Mammal Research (2021) 66:349–369
https://doi.org/10.1007/s13364-021-00555-w

ORIGINAL PAPER

Integrating morphology and DNA barcoding to assess cetacean diversity in Brazil

Vanessa S. Silva[1] · Natália Skueresky[1] · Fernando Lopes[1] · Tabata K. Koch[1] · Paulo Henrique Ott[2,3] · Salvatore Siciliano[4] · André S. Barreto[5] · Eduardo R. Secchi[6] · Ana Carolina O. de Meirelles[7] · Vitor Luz Carvalho[7] · João C. G. Borges[8] · Daniel Danilewicz[3] · Ana Paula C. Farro[9] · Lupércio A. Barbosa[10] · S. José Martins Jr[11] · Camila Domit[12] · Inês Serrano[13] · Tiago Silva[14] · Cristine Trinca[14] · Miriam Marmontel[15] · Neusa Renata Emin-Lima[16] · Victor Hugo Valiati[1] · Eduardo Eizirik[14] · Larissa Rosa de Oliveira[1,3]

Received: 15 September 2020 / Accepted: 13 January 2021 / Published online: 15 February 2021

Abstract

Stranded cetaceans (whales, dolphins, and porpoises) are frequently used to obtain data on species occurrence and demographic trends. Accurate species-level identification of these individuals is crucial, but often challenging or impossible when relying solely on morphological features (e.g., for highly decayed specimens). To aid in the development of a reliable molecular assay for cetacean DNA-based identification, we tested the efficacy of the standardized DNA barcode segment of the *coxI* gene in identifying cetaceans occurring off the Brazilian coast and in its continental waters. We generated *coxI* sequences from 150 specimens (collected by 16 Brazilian institutions), most of which included voucher material (skulls, skeletons and/or images) deposited in scientific collections. This allowed a direct comparison between their morphological and molecular identification. *CoxI* sequences correctly identified ~93% of the samples, comprising 33 species (70% of the 47 cetaceans reported for Brazilian waters). Two species (*Berardius arnuxii* and *Phocoena dioptrica*) were sequenced for *coxI* for the first time. For only two dolphins (*Stenella coeruleoalba* and *S. clymene*) and a right whale (*Eubalaena australis*), *coxI* failed to identify the species due to overlapping distributions of intra- vs. interspecific divergences. Only one right whale species occurs in the southern hemisphere, facilitating identification in this case. *Stenella* dolphins present extensive sympatry and potential inter-species hybridization, suggesting that nuclear markers may be required for their reliable identification. These results indicate that DNA barcoding can reliably identify most stranded cetaceans and highlight the importance of voucher materials to validate the construction of a reliable DNA-based identification system.

Keywords Whales · Dolphins · Stranding · Morphological · Identification · molecular

Introduction

Brazil has one of the world's most extensive coastlines, spanning almost 8000 km (Ab'Saber 2001), as well as some of its largest freshwater basins (FAO 2016). The biological diversity of these ecosystems has been substantially impacted by increasing anthropogenic changes in the freshwater, marine, and coastal regions, threatening the survival of many species and even entire communities (Amaral and Jablonski 2005; Costa et al. 2005).

Knowledge about the existing diversity in the continental, coastal, and oceanic regions of Brazil is essential to understand the functioning of its different ecosystems, as well as to ensure the sustainable use and conservation of their living resources (e.g., Longo and Amado Filho 2014). The current knowledge about the aquatic communities in these regions is still insufficient to guarantee their conservation, especially in view of the growing economic interest in exploring these areas, even with the implementation of important research programs in the Brazilian oceanic regions in the last decades (e.g., REVIZEE, Archipelago Program and Oceanic Islands).

Communicated by: Cino Pertoldi

✉ Larissa Rosa de Oliveira
larissaro@unisinos.br; lari.minuano@gmail.com

Miriam Marmontel
marmontel@mamiraua.org.br

Extended author information available on the last page of the article

Cetaceans (i.e., whales, dolphins and porpoises) comprise one of the taxonomic groups that lack basic information, mainly regarding their ecological function in the aquatic ecosystems, making it difficult to establish effective conservation plans and mitigation strategies in the face of environmental impacts (Zerbini et al. 2004; Ott et al. 2009; Siciliano et al. 2012).

Currently, there are confirmed records of 47 cetacean species in Brazil, out of the 90 that are recognized worldwide (Pinedo et al. 1992, 2002; Zerbini et al. 1997, 2004; ICMBio 2011a, 2011b; Hrbek et al. 2014; Cypriano-Souza et al. 2016; Bastida et al. 2018). Eight of them are classified as threatened, and eight are considered "data deficient" (DD) in the Brazilian Red List (ICMBio 2018). Moreover, six species are classified as globally threatened and 12 as "data deficient" by the IUCN (2020).

Most information about this remarkable cetacean diversity (>50% of the global diversity) is usually based on specimens found dead or stranded along the Brazilian coast and continental waters, mostly related to anthropogenic activities (Greig et al. 2001; Van Bressem et al. 2007; Fruet et al. 2012; Lemos et al. 2013; Prado et al. 2016; Dick et al. 2019). In this context, the Brazilian Stranding Network of Aquatic Mammals (REMAB) was created in 2011. This initiative includes four regional networks: the Northern (REMANOR), the Northeastern (REMANE), the Southeastern (REMASE), and the Southern (REMASUL) aquatic mammal networks. REMAB is coordinated by the National Aquatic Mammal Center (*Centro de Mamíferos Aquáticos*—CMA/ICMBio/MMA) and operates throughout the nation. The purpose of these networks is to exchange information and experience among institutions and to support government decisions on aquatic mammal conservation in Brazil.

However, the completeness and reliability of the information surveyed by these networks hinges upon accurate species-level identification of detected cetaceans, which is hampered by two challenges: (1) many individuals observed in-water are difficult to identify by the few exposed parts of the body, especially given the morphological similarity between some species, and (2) the advanced decomposition state frequently observed in stranded carcasses (Meirelles et al. 2009; Sholl et al. 2013). In this context, unambiguous species identification often depends on the analysis of collected osteological material (e.g., Pinedo et al. 2002; Meirelles and Furtado-Neto 2004) or molecular identification (e.g., Sholl et al. 2013; Siciliano et al. 2016; Cypriano-Souza et al. 2016). It is important to highlight that when diagnostic body parts, such as the skull or teeth, are lost and the original skin color is no longer present, morphology-based identification is virtually impossible for most species.

This was precisely the case in the first record of the Omura's whale (*Balaenoptera omurai*) on the coast of Brazil and the Southwestern Atlantic (Cypriano-Souza et al. 2016). The authors were only able to reach unambiguous identification of the specimen after generating information from three mitochondrial DNA (mtDNA) segments (control region, *cytochrome-b* (*cyt-b*), and *cytochrome oxidase c subunit I* (*coxI*)) and comparing them with sequences of these same segments deposited in molecular databases. Based on these results, it was demonstrated that there is potential cryptic diversity of cetaceans in Brazil, which is "hidden" due to the lack of use of molecular techniques as diagnostic tools for these taxa (Sholl et al. 2008; Cypriano-Souza et al. 2016). A similar situation occurred when Hrbek et al. (2014) found substantial molecular divergence in mtDNA genes supporting the split of the Amazon river dolphin genus *Inia* into two species: *I. geoffrensis* and *I. araguaiaensis*, the latter being the only cetacean species endemic to Brazilian waters. Afterwards, also based on mtDNA control region and *coxI* sequences, Siciliano et al. (2016) detected the presence of the two species of *Inia* and extended the range of the new species *I. araguaiaensis* into the Amazon delta.

In some notable cases, such as in the family Ziphiidae (beaked whales), genetic analyses play a critical role in identifying cryptic diversity (e.g., Dalebout et al. 1998, 2002; Yamada et al. 2019), correcting previous erroneous identifications (e.g., Yamada et al. 2019), or even validating (or revalidating) taxonomic propositions (Dalebout et al. 2004; Yamada et al. 2019). The elusive behavior of these cetaceans, with little exposure on the surface and aversion to vessels, and their common offshore distribution (MacLeod et al. 2006) make information on this family particularly difficult to obtain (Dalebout et al. 1998). Ziphiids are rarely found washed ashore on the Brazilian coast, even in regions with a long time series of beach surveys (e.g., Meirelles et al. 2009; Prado et al. 2016; Vianna et al. 2016; Dick et al. 2019). In general, the identification of beaked whales is based on the analysis of skull and teeth morphology of stranded specimens, mainly adult males (e.g., Reyes et al. 1995; Mead 2008). However, erroneous identifications of beached specimens are not uncommon, mainly due to carcass decomposition (Dalebout et al. 1998) and lack of some of diagnostic features used for species recognition (shape and position of erupted mandibular teeth) in females and juveniles (Reyes et al. 1995). Additionally, the geographic distribution of several beaked whales is poorly known, and their occurrence in some regions can be somewhat unexpected (Siciliano and Santos 2003; MacLeod et al. 2006). Moreover, some morphologically similar species have overlapping distributions, making the identification of these elusive whales even more challenging (Dalebout et al. 1998, 2002). In this context, the inclusion of molecular identification techniques that allow comparisons with reference databases comprising samples that are validated with voucher materials, is crucial for the identification of beaked whale specimens, especially in the case of cryptic or poorly sampled species, such as Perrin's beaked whale (*Mesoplodon perrini*), Longman beaked whale (*Indopacetus*

pacificus) and the newly described minimal-beaked whale (*Berardius minimus*) (e.g., Dalebout et al. 1998, 2002, 2004; Yamada et al. 2019).

To establish the correct identification of these mammals, which are frequently found washed ashore and often in advanced state of decomposition, DNA barcoding becomes a very useful tool (Hebert et al. 2003; Alfonsi et al. 2013). Analysis based on a fragment of the mitochondrial gene *cytochrome c oxidase subunit 1* (*coxI*) is a powerful tool to identify individuals at the species level (Hebert et al. 2003). Recently, Falcão et al. (2017) published a DNA barcoding study on marine mammal species from Brazil and Canada, but it covered a small portion of the Northeastern Brazilian coast and only four individuals of four species (*Physeter macrocephalus*, *Peponocephala electra*, *Sotalia guianensis*, and *Tursiops truncatus*).

There are few studies integrating *coxI* and morphology to identify cetacean species (Amaral et al. 2007; Viricel and Rosel 2011; Alfonsi et al. 2013). Until now, there are virtually no cetacean studies including morphological voucher material, such as skulls, to compare with *coxI* results, probably because they need a large number of cetacean species with both DNA samples and bones collected from the same individual.

In the present study, we evaluate the potential of DNA barcoding for the monitoring of cetacean diversity along the coast of Brazil and its inner waters. Based on the establishment of a consortium of 16 institutions from the Brazilian stranding network, included in the project "Tetrapoda DNA Barcodes[1]" of the Brazilian Barcode o Life (BrBOL) initiative, tissue samples were collected from stranded cetaceans as well as few biopsies taken from live animals along the Brazilian coast. Most DNA samples were associated with voucher material deposited in scientific collections (e.g., skull and/or skeletons) that could be identified to species level based on morphological characters, which allowed a controlled assessment of the molecular identifications performed with the *coxI* gene. We additionally evaluated the quality and reproducibility of the cetacean taxonomic identification performed by the consortium field researchers, by identifying degraded carcasses, describing intraspecific variation for some dolphin species, and by evaluating the hypothesis that *coxI* can be an efficient molecular marker to identify cetacean species (Hebert et al. 2003; Taylor et al. 2017). Finally, we discuss the results with a focus on method validation and its potential inconsistencies in cases of morphological vs. molecular mismatches (Viricel and Rosel 2011).

[1] Tetrapoda DNA Barcodes: building an integrated network DNA barcoding of amphibians, reptiles, birds and mammals.

Methods

Samples

A collaborative stranding network of 16 research institutions investigating aquatic mammal strandings along the Brazilian coast and inner Amazon basin waters obtained tissue samples from 143 cetacean carcasses. The specimens were recovered during regular beach surveys or notified by locals, from 1989 to 2018, including samples from four regions: south, southeast, northeast, and north (see Fig. 1; Table 1). Additionally, we also included seven biopsy samples of cetaceans detected during onboard surveys of oceanic waters. These samples were collected in waters surrounding the São Pedro e São Paulo Archipelago (also known as Saint Paul's Rocks) (00° 56′ S; 29° 22′ W) and Campos and Santos Basins (from 21° 40′ S to 27° 00′ S). These samples were obtained under *SISBIO* (Brazilian Biodiversity authorization and information system) license numbers 12022-1 and 19665-1.

Voucher specimens (osteological material or photos that unequivocally identify the species) from the carcasses sampled in this study are deposited in their respective scientific collections, except for some stranded baleen whales. This is the first cetacean barcoding study that includes voucher material, allowing reproducibility of species identification, performed by field correspondents or researchers from the collaborating institutions. In the field, specimens were initially identified by experienced researchers or trained assistants, following guidelines suggested by the American Society of Mammalogists in the protocol *Acceptable Field Methods in Mammalogy: Preliminary Guidelines Approved by the American Society of Mammalogists* (ad hoc Committee on Acceptable Field Methods in Mammalogy 1987, http://mammalogy.org/uploads/committee_files/ACUC1987.pdf) and by Geraci and Lounsbury (2005); both protocols were adopted by Brazilian stranding marine mammal networks (IBAMA 2005). The identification of each specimen was performed through a combination of diagnostic characters of body and skull morphology, when necessary. Moreover, information related to total length, sex, and the condition of each carcass, including the state of the decomposition (Geraci and Lounsbury 2005), was also recorded whenever possible. Tissue samples were collected and stored in 70% ethanol or 20% DMSO saturated with NaCl and sent to Laboratory of Genetics and Molecular Biology (LGBM) at the University of Vale dos Rio dos Sinos ($n = 140$). A few samples were also sent to the Laboratory of Genomics and Molecular Biology at the Pontifícia Universidade Católica do Rio Grande do Sul ($n = 10$).

DNA was extracted using a phenol/chloroform protocol, and the quality and concentration of DNA were verified via 1% agarose gel electrophoresis. The concentrations of genomic DNA were estimated with Nanodrop UV spectrophotometry (Thermo Scientific Wilmington, DE). The DNA samples were diluted in deionized water until reaching a concentration of approximately 100 ng/ul.

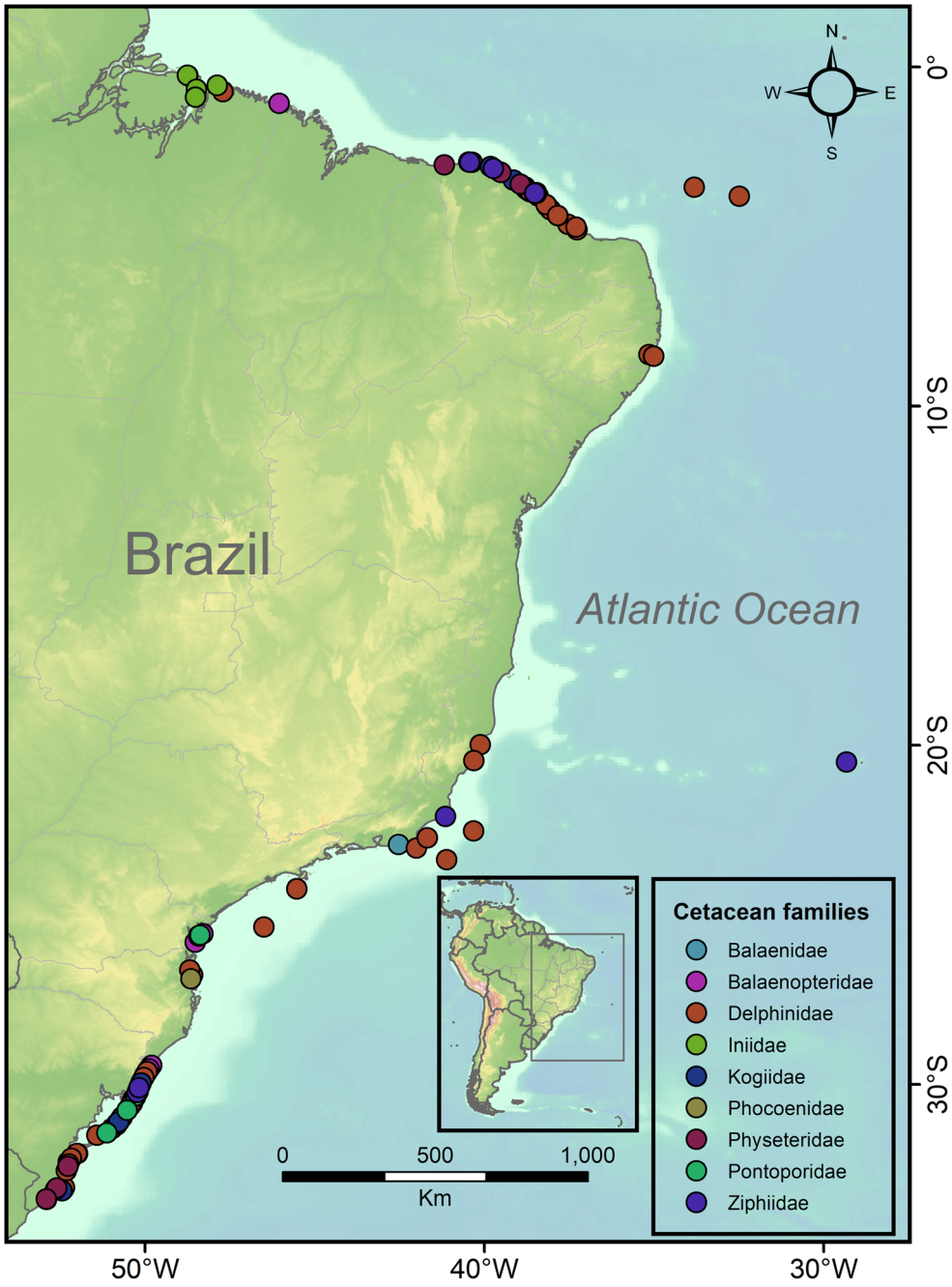

Fig. 1. Sampling sites of 150 cetacean specimens collected along the Brazilian continental, coastal, and oceanic areas. The specimens were grouped by family

We amplified *coxI* fragments with polymerase chain reactions (PCRs) by applying two primer pairs, VF1d, VF1i, VR1, and VR1d, which targeted approximately 800 base pairs (bp) (see Supplementary Material 1 for details). PCR results were verified on 1% agarose gels stained with GelRed (Biotium, Hayward, CA, USA). PCR products were purified using Shrimp Alkaline Phosphatase (SAP) and exonuclease I (New England Biolabs), following the manufacturer's recommendation. Amplicons were sequenced in both directions using universal primers (M13-FP and M13R-pUC, see Supplementary Material 1).

Analysis

We manually selected only high-quality *coxI* sequences, with high and clear peaks for each nucleotide, based on the observation of electropherograms conducted with ChromasPro 2.6.6 (http://www.technelysium.com.au). A total of 150 consensus sequences were automatically aligned (with minor manual correction) in ClustalW implemented in MEGA 7 (Kumar et al. 2016), with subsequent edition in BioEdit 5.0. 9 (Hall 1999). After the alignment, we compared the *coxI* sequences with those available in GenBank (www.ncbi.nlm.

Table 1. Number of sequences of the gene cytochrome c oxidase subunit 1 (*coxI*) obtained from 33 cetaceans species along the Brazilian coast and continental waters by a collaborative stranding network of 16 research institutions. The number of sequences of *coxI* currently (April 2020) available in the NCBI and BOLD databases are also indicated. NA = not available

Common name Delphinidae	Species	NCBI	BOLD	Shared between NCBI/BOLD	Number of sequences obtained*
Common dolphin	*Delphinus delphis*	29	19	16	8
Common bottlenose dolphin	*Tursiops truncatus*	122	125	122	7
Rough-toothed dolphin	*Steno bredanensis*	4	4	4	4
Atlantic spotted dolphin	*Stenella frontalis*	9	10	9	6
Striped dolphin	*Stenella coeruleoalba*	11	13	11	5
Clymene dolphin	*Stenella clymene*	13	13	13	6
Spinner dolphin	*Stenella longirostris*	117	117	117	5
Pantropical spotted dolphins	*Stenella attenuata*	97	97	97	4
Fraser's dolphin	*Lagenodelphis hosei*	4	2	2	8
Guiana dolphin	*Sotalia guianensis*	4	5	2	7
Long-finned pilot whale	*Globicephala melas*	10	11	9	1
False killer whale	*Pseudorca crassidens*	11	8	8	8
Risso's dolphin	*Grampus griseus*	8	11	6	3
Melon-head whale	*Peponocephala electra*	7	8	8	4
Kogiidae					
Pygmy sperm whale	*Kogia breviceps*	4	4	4	2
Dwarf sperm whale	*Kogia sima*	4	7	4	6
Physeteridae					
Sperm whale	*Physeter macrocephalus*	88*	71*	70	10
Pontoporiidae					
Franciscana dolphin	*Pontoporia blainvillei*	3	4	3	11
Phocoenidae					
Spectacled porpoise	*Phocoena dioptrica*	NA	NA	-	1
Burmeister's porpoise	*Phocoena spinipinnis*	1	1	1	3
Iniidae					
Araguaian river dolphin	*Inia araguaiaensis*	47	47	47	3
Amazon river dolphin	*Inia geoffrensis*	39	39	39	2
Ziphiidae					
Arnoux's beaked whale	*Berardius arnuxii*	NA	NA	-	1
Gervais' beaked whale	*Mesoplodon europaeus*	10	10	10	1
Cuvier's beaked whale	*Ziphius cavirostris*	26	29	26	4
Balaenidae					
Southern right whale	*Eubalaena australis*	4	4	4	5
Balaenopteridae					
Humpback whale	*Megaptera novaeangliae*	10	12	10	9
Common minke whale	*Balaenoptera acutorostrata*	5	6	5	4
Antarctic minke whale	*Balaenoptera bonaerensis*	3	3	3	2
Sei whale	*Balaenoptera borealis*	5	5	5	3
Bryde's whale	*Balaenoptera brydei*	4	3	3	5
Fin whale	*Balaenoptera physalus*	158	161	158	1
Omura's whale	*Balaenoptera omurai*	8	8	8	1

*Some sequences attributed to the known synonym *Physeter catodon*.

nih.gov) and BOLD systems (www.boldsystems.org), which are the two main public databases of DNA barcode data for all taxa (Meiklejohn et al. 2019), using the Basic Local Alignment Search Tool (BLAST) (blast.ncbi.nlm.nih.gov).

The molecular identifications suggested by both GenBank and BOLD were based on the percentage of similarity among sequences. The first criterion we used was based on 3% as a suggested lower limit for genetic divergence (dA) between species (Hebert et al. 2003); values close to this limit were considered to attain the lowest level for cetacean species delimitation based on the *coxI* marker (Siciliano et al. 2016; Taylor et al. 2017). The second criterion was a direct assessment of the level of similarity of each sequence with the suggested by GenBank. Here, we highlight that, for those species with no *coxI* sequence currently available in the databases, the similarity search retrieved the closest taxon or no result was returned. Cases of molecular vs. morphology mismatch (Viricel and Rosel 2011; Alfonsi et al. 2013), due to incongruence between the species identification suggested by *coxI* sequences (from GenBank or BOLD) and the morphological identification informed by collaborating researchers, were further investigated. Whenever possible, a revision of the species identification was conducted by requesting skull or carcass images to the field correspondents. External traits or diagnostic characters of the skull were analyzed to confirm the identification. In cases of uncertainties, additional marine mammal specialists were consulted. This procedure was conducted for species of the polyspecific genera such as *Balaenoptera* and *Stenella*, as well as to the monospecific genera *Orca* and *Pseudorca*. In addition, field notes on the specimens collected were also double-checked in the catalogue books of the scientific collections, mainly regarding the decomposition stage (including images from the sampling), which could explain some of the mismatch results (see Discussion section).

Intraspecific and interspecific genetic divergence (dA) were calculated using the K2P model (Kimura 1980) for those species that did not exhibit a clear-cut barcoding gap to establish the interval of genetic separation between them (e.g., some delphinids). A barcoding gap is a lack of overlap between intraspecific and interspecific nucleotide divergence in the investigated taxa (Viricel and Rosel 2011).

To test the hypothesis that all *coxI* sequences belonging to the same cetacean species form a monophyletic cluster, we performed two types of phylogenetic analyses: a maximum likelihood (ML) tree reconstructed with the program RAxML 8.2 (Stamatakis 2014); and as secondary method, a neighbor-joining tree (NJ) tree using the Kimura 2-parameter (K2P) model implemented in the software MEGA 7 (Kumar et al. 2016). For the ML, we used GTR+4G as the substitution model, as estimated with jmodeltest2 (Darriba et al. 2012). To perform these phylogenetic analyses, we assembled and aligned our 150 *coxI* consensus sequences with the 71 sequences available on the BOLD platform, totaling 221 *coxI* sequences representing 33 cetacean taxa. The species *Hippopotamus amphibius*, available on the BOLD platform (GBMA2411-09), was used as the outgroup.

Results

We recovered *coxI* sequences spanning 644 to 847 bp from 150 samples representing 33 species. The recorded species were distributed in nine cetacean families, including both odontocetes (i.e., dolphins, porpoises and toothed whales) and mysticetes (i.e., baleen whales) (Table 1). A total of 865 and 857 *coxI* sequence records were identified in the NCBI and BOLD nucleotide databases, respectively, representing 898 cetacean specimens (Fig. 2a; Table 1). With this study, we are adding 150 sequences which represent a 14.4% growth in the number of specimens and 16.8% of all cetacean samples in the databases (Fig. 2a). The number of individuals per species ranged from one to 11 (mean = 4.6). Two species were sequenced for *coxI* here for the first time (*Berardius arnuxii* and *Phocoena dioptrica*). The molecular identification was in accordance with the external morphology-based identification in 92.7% of the specimens (Table 2).

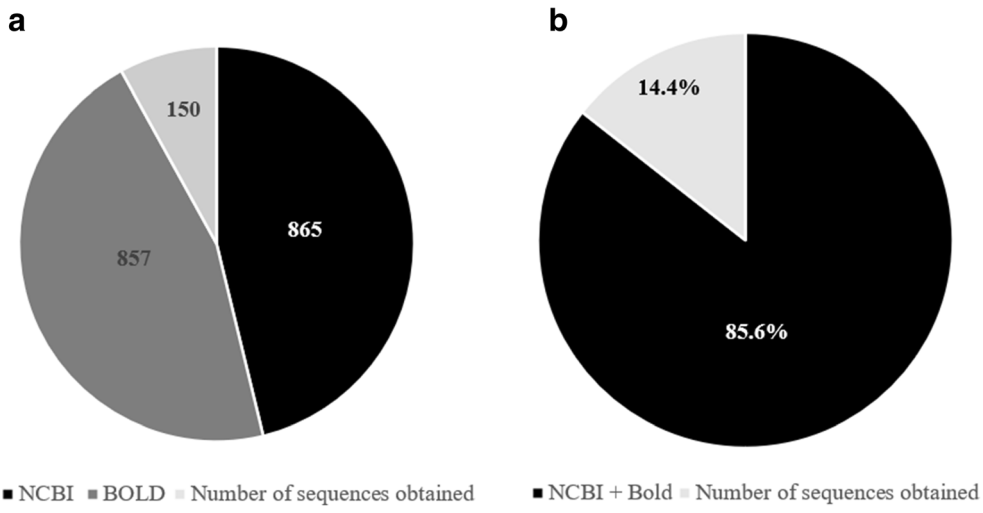

Fig. 2 **a** Number of sequences of the cytochrome c oxidase subunit 1 gene (*coxI*) obtained in this study and currently available for cetaceans in NCBI and BOLD databases. **b** Growth of *coxI* records in the aggregated databases as a result of this study

Table 2 Detailed information on each sample examined: specimen and; institution acronym (institution responsible for collecting); GenBank accession number; MID: morphological identification; NCBI ID: molecular identification suggested by GenBank platform; BOLD ID: molecular identification suggested by BOLD SYSTEM platform; NCBI%: percentage of similarity with the cetacean species deposited in NCBI; BOLD%: percentage of similarity with the cetacean species deposited in BOLD platform; coordinates of the: sampling site. *Specimens with molecular-morphological mismatch

Specimen	GenBank accession number	MID	NCBI ID	BOLD ID	NCBI(%)	BOLD (%)	Lat	Long
Family Balaenidae								
*[a]GEMM-Lagos 051	MW446705	*Eubalaena australis*	*Eubalaena australis*	*Eubalaena glacialis*	99	99.69	22° 55′ 57.86″ S	42° 31′ 25.21″ W
[b]GEMARS 1456	MW446728	*Eubalaena australis*	*Eubalaena australis*	*Eubalaena australis*	100	100	29° 43′ 49.35″ S	49° 59′ 44.92″ W
GEMARS 1467	MW446729	*Eubalaena australis*	*Eubalaena australis*	*Eubalaena australis*	100	100	29° 26′ 53.80″ S	49° 48′ 32.68″ W
*[c]MN 60458	MW446713	*Eubalaena australis*	*Eubalaena australis*	*Eubalaena glacialis*	100	100	22° 26′ 00″ S	42°49′ 00″ W
Family Balaenopteridae								
GEMARS 0469	MW446668	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	99.05	99.04	31° 1′ 30.00″ S	50° 42′ 45.00″ W
GEMARS 1042	MW446681	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	99.08	99.08	30° 37′ 54.50″ S	50° 25′ 44.80″ W
GEMARS 1468	MW446719	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	99.15	99.13	30° 9′ 13.60″ S	50° 11′ 35.30″ W
[d]LEC#119	MW446720	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	*Balaenoptera acutorostrata*	98.90	98.9	25° 48′ 42.85″ S	48° 30′ 51.49″ W
GEMARS 1269	MW446682	*Balaenoptera bonaerensis*	*Balaenoptera bonaerensis*	*Ba.laenoptera bonaerensis*	100	100	29° 26′ 27.10″ S	49° 47′ 57.80″ W
[e]ECOMEGA/FURG minke	MW446721	*Balaenoptera bonaerensis*	*Balaenoptera bonaerensis*	*Balaenoptera bonaerensis*	99.58	99.65	Rio Grande - RS	
*ECOMEGA/FURG 63	MW446679	*Balaenoptera borealis*	*Balaenoptera brydei*	*Balaenoptera brydei*	99.23	99.22	32° 2′ 24.00″ S	52° 0′ 9.97″ W
ECOMEGA/FURG 61	MW446656	*Balaenoptera borealis*	*Balaenoptera borealis*	*Balaenoptera borealis*	100	99.35	31° 26′ 16.91″ S	55° 0′ 0.00″ W
ECOMEGA/FURG 62	MW446657	*Balaenoptera borealis*	*Balaenoptera borealis*	*Balaenoptera borealis*	99.70	99.7	32° 17′ 31.52″ S	52° 15′ 41.58″ W
[f]MPEG 39691	MW446661	*Balaenoptera borealis*	*Balaenoptera borealis*	*Balaenoptera borealis*	100	100	01° 3′ 52.34″ S	46° 2′ 31.21″ W
GEMARS 1406	MW446669	*Balaenoptera brydei*	*Balaenoptera brydei*	*Balaenoptera brydei*	100	100	31° 4′ 23.34″ S	50° 16′ 49.87″ W
GEMARS 1425	MW446727	*Balaenoptera brydei*	*Balaenoptera brydei*	*Balaenoptera brydei*	99.71	99.81	30° 22′ 36.77″ S	50° 16′ 49.87″ W
GEMARS 1694	MW446674	*Balaenoptera brydei*	*Balaenoptera brydei*	*Balaenoptera brydei*	99.54	99.39	30° 10′ 17.99″ S	50° 11′ 53.69″ W
LEC#154	MW446726	*Balaenoptera brydei*	*Balaenoptera brydei*	*Balaenoptera brydei*	100	99.34	25° 33′ 39.69″ S	48° 17′ 27.78″ W
02C0100/421 AQUASIS	MW446678	*Balaenoptera omurai*	*Balaenoptera omurai*	*Balaenoptera omurai*	100	100	3° 32′ 11.60″ S	38° 47′ 51.80″ W
GEMARS 0826	MW446725	*Balaenoptera physalus*	*Balaenoptera physalus*	*Balaenoptera physalus*	97.81	97.79	29° 55′ 14.60″ S	50° 5′ 36.80″ W
[g]AQUASIS 02C0211/418	MW446709	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	100	100	3° 33′ 54.32″ S	38° 47′ 20.84″ W
AQUASIS 02C0212/645	MW446664	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	100	100	3° 36′ 41.30″ S	38° 45′ 19.10″ W
GEMARS 0597	MW446722	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	99.84	99.84	30° 4′ 4.51″ S	50° 9′ 32.01″ W
GEMARS 1409	MW446723	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	99.84	99.84	29° 39′ 54.40″ S	49° 57′ 31.08″ W
GEMARS 1451	MW446724	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	100	99.85	30° 15′ 51.88″ S	50° 14′ 8.16″ W
*GEMARS 1491	MW446662	*Megaptera novaeangliae*	*Eubalaena australis*	*Eubalaena australis*	99.18	98.38	30° 37′ 48.80″ S	50° 25′ 41.20″ W
GEMARS 1683	MW446673	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	100	100	30° 8′ 32.24″ S	50° 11′ 19.50″ W
GEMARS 1684	MW446672	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	100	100	29° 32′ 44.89″ S	49° 52′ 44.12″ W
GEMARS 1685	MW446659	*Megaptera novaeangliae*	*Megaptera novaeangliae*	*Megaptera novaeangliae*	100	100	30° 3′ 37.84″ S	50° 9′ 18.99″ W
Family Physeteridae								
AQUASIS 02C0410/308	MW446781	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	99.84	100	3° 42′ 27.93″ S	38° 27′ 51.71″ W
AQUASIS 02C0410/338	MW446691	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	100	100	3° 6′ 33.00″ S	39° 30′ 38.00″ W
AQUASIS 02C0411/542	MW446663	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	100	100	3° 43′ 3.30″ S	38° 31′ 20.30″ W
AQUASIS 02C0411/809	MW446652	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	100	101	3° 27′ 19.00″ S	38° 56′ 12.00″ W
AQUASIS 02C0412/792	MW446667	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	99.85	99.85	2° 53′ 16.50″ S	41° 10′ 38.90″ W
ECOMEGA/FURG 17	MW446782	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	100	100	32° 25′ 34.10″ S	52° 15′ 57.49″ W
ECOMEGA/FURG 18	MW446783	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	99	100	33° 3′ 39.13″ S	52° 35′ 55.00″ W
ECOMEGA/FURG 19	MW446778	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	100	100	33° 7′ 7.79″ S	52° 38′ 2.76″ W

Table 2 (continued)

Specimen	GenBank accession number	MID	NCBI ID	BOLD ID	NCBI(%)	BOLD (%)	Lat	Long
ECOMEGA/FURG 20	MW446779	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	98	99.7	33° 23′ 11.00″ S	52° 54′ 16.49″ W
GEMARS 0941	MW446780	*Physeter macrocephalus*	*Physeter macrocephalus*	*Physeter macrocephalus*	100	100	30° 36′ 54.90″ S	50° 24′ 55.80″ W
Family Kogiidae								
ECOMEGA/FURG 33	MW446775	*Kogia breviceps*	*Kogia breviceps*	*Kogia breviceps*	100	99,37	33° 8′ 46.03″ S	52° 26′ 33.72″ W
GEMARS 1496	MW446776	*Kogia breviceps*	*Kogia breviceps*	*Kogia breviceps*	99.68	99.68	31° 6′ 40.82″ S	50° 46′ 10.74″ W
AQUASIS 02C0511/703	MW446650	*Kogia sima*	*Kogia sima*	*Kogia sima*	100	99.83	3° 19′ 55.83″ S	39° 8′ 25.13″ W
AQUASIS 02C0511/726	MW446666	*Kogia sima*	*Kogia sima*	*Kogia sima*	99.33	99.33	2° 56′ 7.00″ S	39° 48′ 59.00″ W
AQUASIS 02C0512/585	MW446710	*Kogia sima*	*Kogia sima*	*Kogia sima*	99.33	99.32	3° 19′ 55.83″ S	39° 8′ 25.13″ W
GEMARS 1311	MW446695	*Kogia sima*	*Kogia sima*	*Kogia sima*	100	99.85	29° 57′ 32.00″ S	50° 6′ 40.10″ W
GEMARS 1407	MW446670	*Kogia sima*	*Kogia sima*	*Kogia sima*	99.06	99.84	30° 11′ 59.35″ S	50° 12′ 39.92″ W
GEMARS 1421	MW446777	*Kogia sima*	*Kogia sima*	*Kogia sima*	100	99.85	30° 33′ 25.13″ S	50° 22′ 16.14″ W
Family Ziphiidae								
*GEMARS 1155	MW446774	*Berardius arnuxii*	*Berardius bairdii*	*Berardius bairdii*	99.70	99.69	30° 14′ 29.07″ S	50° 13′ 37.48″ W
MN 84736	MW446686	*Mesoplodon europaeus*	*Mesoplodon europaeus*	*Mesoplodon europaeus*	99	99.41	22° 6′ 1.16″ S	41° 8′ 27.35″ W
02C0810/683	MW446665	*Ziphius* sp.	*Ziphius cavirostris*	*Ziphius cavirostris*	100	100	2° 59′ 18.00″ S	39° 44′ 6.00″ W
02C0812/305	MW446772	*Ziphius cavirostris*	*Ziphius cavirostris*	*Ziphius cavirostris*	100	100	3° 43′ 9.16″ S	38° 30′ 40.05″ W
[h]UNIVALI AB02	MW446708	*Ziphius cavirostris*	*Ziphius cavirostris*	*Ziphius cavirostris*	100	100	20° 29′ 43.01″ S	29° 19′ 41.02″ W
GEMARS 1484	MW446671	*Ziphius cavirostris*	*Ziphius cavirostris*	*Ziphius cavirostris*	99.85	99.85	30° 6′ 0.78″ S	50° 10′ 20.82″ W
Family Iniidae								
*MPEG 38764	MW446742	*Inia geoffrensis*	*Inia araguaiaensis*	*Inia araguaiaensis*	100	99.81	0° 15′ 8.58″ S	48° 22′ 35.91″ W
*MPEG 42122	MW446741	*Inia geoffrensis*	*Inia araguaiaensis*	*Inia araguaiaensis*	100	99.81	0° 14′ 48.81″ S	48° 44′ 51.40″ W
*MPEG 42055	MW446743	*Inia geoffrensis*	*Inia araguaiaensis*	*Inia araguaiaensis*	100	99.81	0° 43′ 21.28″ S	48° 17′ 29.22″ W
MPEG 42179	MW446784	*Inia geoffrensis*	*Inia geoffrensis*	*Inia geoffrensis*	100	100	0° 15′ 3.22″ S	48° 44′ 11.75″ W
MPEG 42180	MW446785	*Inia geoffrensis*	*Inia geoffrensis*	*Inia geoffrensis*	100	100	0° 14′ 48.81″ S	48° 44′ 51.40″ W
Family Pontoporiidae								
GEMARS 0215	MW446738	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	98	99.85	30° 20′ 29.87″ S	50° 16′ 3.18″ W
GEMARS 0424	MW446731	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	99	99.84		
GEMARS 0530	MW446732	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	99	99,85	31° 25′ 57.36″ S	51° 7′ 18.94″ W
GEMARS 0550	MW446730	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	100	100		
GEMARS 0634	MW446734	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	99	100	29° 51′ 5.02″ S	50° 3′ 36.36″ W
GEMARS 0745	MW446735	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	100	100	29° 59′ 3.08″ S	50° 6′ 53.64″ W
GEMARS 0748	MW446733	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	100	100		
GEMARS 0749	MW446736	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	99.82	100		
GEMARS 1487	MW446737	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	100	99.84	RS	
LEC#01	MW446739	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	99.85	100	25° 37′ 46.54″ S	48° 24′ 46.99″ W
LEC#71	MW446740	*Pontoporia blainvillei*	*Pontoporia blainvillei*	*Pontoporia blainvillei*	99.69	99.69	25° 35′ 56.15″ S	48° 22′ 38.95″ W
Family Delphinidae								
GEMM-Lagos # 57	MW446707	*Delphinus delphis*	*Delphinus delphis*	*Delphinus delphis*	99.56	99.69	23° 2′ 14.21″ S	42° 0′ 10.87″ W
GEMM-Lagos BC04	MW446712	*Delphinus delphis*	*Delphinus delphis*	*Delphinus delphis*	99.68	99.67	22° 44′ 0.13″ S	41° 40′ 39.61″ W
GEMARS 0221	MW446680	*Delphinus delphis*	*Delphinus delphis*	*Delphinus delphis*	99.85	99.85	31° 18′ 30.00″ S	50° 58′ 0.00″ W
GEMARS 0419	MW446693	*Delphinus delphis*	*Delphinus delphis*	*Delphinus delphis*	99.68	99.68	29° 57′ 52.00″ S	50° 6′ 51.00″ W
[i]PA288 /IO –USP	MW446687	*Delphinus delphis*	*Delphinus delphis*	*Delphinus delphis*	100	99.84	24° 21′ 00″ S	46° 40′ 00″ W
ECOMEGA/FURG 7	MW446752	*Delphinus* sp.	*Delphinus delphis*	*Delphinus delphis*	100	99.68	33° 3′ 35.30″ S	52° 23′ 52.40″ W
ECOMEGA/FURG 8	MW446753	*Delphinus* sp.	*Delphinus delphis*	*Delphinus delphis*	99	99.23	32° 12′ 8.46″ S	52° 10′ 32.70″ W
ECOMEGA/FURG 6	MW446751	*Delphinus sp*	*Delphinus delphis*	*Delphinus delphis*	98.32	98.57	33° 5′ 35.30″ S	52° 23′ 42.43″ W
ECOMEGA/FURG 38	MW446771	*Globicephala melas*	*Globicephala melas*	*Globicephala melas*	100	99.68	33° 8′ 8.48″ S	52° 25′ 58.58″ W

Table 2 (continued)

Specimen	GenBank accession number	MID	NCBI ID	BOLD ID	NCBI(%)	BOLD (%)	Lat	Long
AQUASIS 02C1812/588	MW446647	*Grampus griseus*	*Grampus griseus*	*Grampus griseus*	99.38	99.37	4° 38′ 39.80″ S	37° 32′ 15.40″ W
GEMARS 1236	MW446694	*Grampus griseus*	*Grampus griseus*	*Grampus griseus*	99.22	99.52	29° 41′ 47.94″ S	49° 58′ 36.30″ W
MPEG 38480	MW446685	*Grampus griseus*	*Grampus griseus*	*Grampus griseus*	100	99.83	0° 43′ 13.14″ S	47° 42′ 13.64″ W
AQUASIS 02C0212/342	MW446645	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	100	99.83	4° 7′ 3.00″ S	38° 8′ 16.00″ W
AQUASIS 02C2512/389	MW446646	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	99.69	99.84	3° 5′ 36.00″ S	39° 31′ 56.00″ W
ECOMEGA/FURG 22	MW446757	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	99.84	99.84	32° 2′ 45.13″ S	52° 0′ 30.53″ W
ECOMEGA/FURG 23	MW446773	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	100	98.89	30° 58′ 39.88″ S	50° 22′ 53.38″ W
GEMARS 0467	MW446701	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	100	99.85	31° 4′ 15.00″ S	50° 44′ 26.00″ W
GEMARS 0488	MW446702	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	100	99.85	30° 57′ 44.40″ S	50° 40′ 4.00″ W
GEMARS 1453	MW446696	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	100	99.84	29° 58′ 36.00″ S	50° 7′ 22.54″ W
GEMARS 0435	MW446758	*Lagenodelphis hosei*	*Lagenodelphis hosei*	*Lagenodelphis hosei*	100	100	30° 8′ 54.88″ S	50° 11′ 28.92″ W
*ECOMEGA/FURG 45	MW446653	*Orcinus orca*	*Pseudorca crassidens*	*Pseudorca crassidens*	100	100	32° 21′ 3.60″ N	52° 14′ 34.80″ W
AQUASIS 02C1511/783	MW446641	*Peponocephala electra*	*Peponocephala electra*	*Peponocephala electra*	100	100	2° 48′ 10.10″ S	40° 27′ 24.80″ W
AQUASIS 02C1511/784	MW446642	*Peponocephala electra*	*Peponocephala electra*	*Peponocephala electra*	100	100	2° 48′ 10.10″ S	40° 27′ 24.80″ W
AQUASIS 02C1512/669	MW446639	*Peponocephala electra*	*Peponocephala electra*	*Peponocephala electra*	100	100	4° 12′ 59.50″ S	38° 2′ 47.10″ W
[j]CEUNES-UFES#6	MW446770	*Peponocephala electra*	*Peponocephala electra*	*Peponocephala electra*	100	100	20° 27′ 23.13″ S	40° 18′ 23.52″ W
ECOMEGA/FURG 01	MW446769	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	100	99.5	31° 55′ 00′ ′ S	-51° 50′ 00′ ′ W
ECOMEGA/FURG 02	MW446767	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	99	99.4	32° 22′ 00′ ′ S	52° 18′ 00′ ′ W
ECOMEGA/FURG 04	MW446766	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	98	99.83	32° 11′ 5.68″ S	52° 9′ 49.46″ W
ECOMEGA/FURG 05	MW446768	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	100	100	31° 26′ 7.98″ S	51° 7′ 6.35″ W
GEMARS 1659	MW446697	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	100	99.85	29° 37′ 19.88″ S	49° 55′ 58.48″ W
GEMARS 1665	MW446684	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	99.53	99.53	30° 12′ 15.70″ S	50° 12′ 46.91″ W
CEUNES-UFES#1	MW446765	*Pseudorca crassidens*	*Pseudorca crassidens*	*Pseudorca crassidens*	99.87	99,87	19° 59′ 2.64″ S	40° 6′ 53.07″ W
GEMM-Lagos s#39	MW446706	*Stenella attenuata*	*Stenella attenuata*	*Stenella attenuata*	99.56	99.55	22° 32′ 3.26″ S	40° 18′ 45.79″ W
AQUASIS 02C1121/614	MW446690	*Stenella attenuata*	*Stenella attenuata*	*Stenella attenuata*	100	100	2° 53′ 19.40″ S	41° 10′ 53.80″ W
GEMM-Lagos BC02	MW446711	*Stenella attenuata*	*Stenella attenuata*	*Stenella attenuata*	99	99.41	21° 40′ S	-
GEMM-Lagos BC03	MW446759	*Stenella attenuata*	*Stenella attenuata*	*Stenella attenuata*	100	101	25° 21′ 54.00″ S	46° 29′ 45.92″ W
AQUASIS 02C1151/531	MW446698	*Stenella clymene*	*Stenella clymene*	*Stenella clymene*	99.35	99.83	4° 23′ 28.70″ S	37° 49′ 44.50″ W
AQUASIS 02C1151/543	MW446699	*Stenella clymene*	*Stenella clymene*	*Stenella clymene*	100	99.83	2° 48′ 35.00″ S	40° 21′ 34.00″ W
*AQUASIS 02C1152/333	MW446644	*Stenella clymene*	*Stenella clymene*	*Stenella frontalis/S. clymene*	100	100	2° 56′ 44.34″ S	39° 47′ 58.58″ W
AQUASIS 02C1152/733	MW446651	*Stenella clymene*	*Stenella clymene*	*Stenella clymene*	100	99.85	4° 3′ 31.30″ S	38° 10′ 50.50″ W
GEMARS 0795	MW446703	*Stenella clymene*	*Stenella clymene*	*Stenella clymene*	100	99.71	30° 0′ 15.40″ S	50° 7′ 49.80″ W
CEUNES-UFES 01C1152/99	MW446750	*Stenella clymene*	*Stenella clymene*	*Stenella clymene*	99.69	100	3° 48′ 47.85″ S	32° 29′ 0.36″ W
AQUASIS 02C1142/295	MW446704	*Stenella coeruleoalba*	*Stenella coeruleoalba*	*Stenella coeruleoalba*	100	100	4° 48′ 6.60″ S	37° 16′ 0.80″ W
GEMARS 0047	MW446692	*Stenella coeruleoalba*	*Stenella coeruleoalba*	*Stenella coeruleoalba*	100	100	30° 15′ 12.32″ S	50° 13′ 54.79″ W
*GEMARS 1240	MW446643	*Stenella coeruleoalba*	*Delphinus delphis*	*Delphinus delphis*	100	99.85	31° 10′ 19.20″ S	50° 49′ 30.00″ W
GEMARS 1346	MW446658	*Stenella coeruleoalba*	*Stenella coeruleoalba*	*Stenella coeruleoalba*	99.7	99.69	30° 5′ 46.80″ S	50° 10′ 14.90″ W
GEMARS 1416	MW446748	*Stenella coeruleoalba*	*Stenella coeruleoalba*	*Stenella coeruleoalba*	100	100	30° 27′ 9.36″ S	50° 21′ 26.46″ W
GEMARS 1478	MW446749	*Stenella coeruleoalba*	*Stenella coeruleoalba*	*Stenella coeruleoalba*	100	100	30° 13′ 25.50″ S	50° 12′ 8.89″ W
ECOMEGA/FURG 29	MW446744	*Stenella frontalis*	*Stenella frontalis*	*Stenella frontalis*	100	100	32° 21′ 19.51″ S	52° 14′ 49.24″ W
ECOMEGA/FURG 30	MW446746	*Stenella frontalis*	*Stenella frontalis*	*Stenella frontalis*	99	100	31° 30′ 11.77″ S	51° 24′ 45.18″ W
GEMARS 1174	MW446745	*Stenella frontalis*	*Stenella frontalis*	*Stenella frontalis*	99.69	99.68	30° 32′ 26.63″ S	50° 21′ 32.81″ W
GEMARS 1488	MW446747	*Stenella frontalis*	*Stenella frontalis*	*Stenella frontalis*	99	99.69		
GEMM-Lagos BC009	MW446787	*Stenella frontalis*	*Stenella frontalis*	*Stenella frontalis*	100	100	24° 14′ 28.32″ S	45° 31′ 23.16″ W
GEMM-Lagos BC 051	MW446660	*Stenella frontalis*	*Stenella frontalis*	*Stenella frontalis*	99.85	99.84	23° 22′ 57.32″ S	41° 6′ 28.98″ W

Table 2 (continued)

Specimen	GenBank accession number	MID	NCBI ID	BOLD ID	NCBI(%)	BOLD (%)	Lat	Long
AQUASIS 02C1131/226	MW446677	*Stenella longirostris*	*Stenella longirostris*	*Stenella longirostris*	100	100	3° 43′ 38.69″ S	38° 27′ 29.67″ W
AQUASIS 02C1131/672	MW446640	*Stenella longirostris*	*Stenella longirostris*	*Stenella longirostris*	100	100	3° 32′ 35.70″ S	33° 48′ 38.70″ W
AQUASIS 02C1131/681	MW446649	*Stenella longirostris*	*Stenella longirostris*	*Stenella longirostris*	100	100	4° 43′ 39.90″ S	37° 17′ 48.60″ W
AQUASIS 02C1132/403	MW446689	*Stenella longirostris*	*Stenella longirostris*	*Stenella longirostris*	100	100	3° 48′ 28.60″ S	38° 24′ 40.40″ W
GEMARS 1317	MW446683	*Stenella longirostris*	*Stenella longirostris*	*Stenella longirostris*	100	100	29° 48′ 9.44″ S	50° 2′ 2.65″ W
AQUASIS 02C1210/601	MW446648	*Steno bredanensis*	*Steno bredanensis*	*Steno bredanensis*	100	99.85	3° 35′ 52.20″ S	38° 46′ 12.00″ W
ECOMEGA/FURG 11	MW446764	*Steno bredanensis*	*Steno bredanensis*	*Steno bredanensis*	100	100	33° 3′ 2.99″ S	52° 22′ 2.06″ W
GEMARS 0512	MW446638	*Steno bredanensis*	*Steno bredanensis*	*Steno bredanensis*	96	99.56	31° 33′ 0.68″ S	51° 13′ 47.37″ W
GEMARS 1621	MW446715	*Steno bredanensis*	*Steno bredanensis*	*Steno bredanensis*	99	100	30° 57′ 57.13″ S	50° 40′ 13.69″ W
AQUASIS 02C1412/290	MW446761	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	100	99.69	4° 3′ 20.76″ S	38° 10′ 55.39″ W
AQUASIS 02C1412/406	MW446762	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	92	99,82	3° 39′ 18.00″ S	38° 41′ 9.00″ W
AQUASIS 02C1412/508	MW446717	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	99.26	99.55	3° 41′ 10.63″ S	38° 38′ 14.15″ W
AQUASIS 02C1412/523	MW446763	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	98	100	3° 43′ 26.80″ S	38° 30′ 7.70″ W
LEC#92	MW446760	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	99.54	99.82	25° 36.973′ S	48° 24′ 4.41″ W
PA186 /IO –USP	MW446716	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	92	99.69		
PA226 /IO –USP	MW446718	*Sotalia guianensis*	*Sotalia guianensis*	*Sotalia guianensis*	100	100	3° 43′ 38.69″ S	38° 27′ 29.67″ W
AQUASIS 02C1312/696	MW446700	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	100	100	3° 48′ 16.00″ S	38° 24′ 49.00″ W
GEMARS 1485	MW446714	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	98.96	99.54	30° 10′ 37.81″ S	50° 12′ 8.89″ W
GEMARS_ ASPSP_C	MW446756	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	97.22	97.21	8° 30′ 38.27″ S	34° 52′ 41.16″ W
GEMARS_ ASPSP_E	MW446754	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	97.06	96.92	8° 32′ 32.83″ S	34° 52′ 4.10″ W
GEMARS_ ASPSP_N	MW446755	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	100	99.85	8° 32′ 34.68″ S	34° 51′ 12.00″ W
UNIVALI ii015573	MW446676	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	100	99.85	26° 38′ 2.83″ S	48° 40′ 50.81″ W
UNIVALI ii014622	MW446688	*Tursiops truncatus*	*Tursiops truncatus*	*Tursiops truncatus*	100	100	26° 46′ 59.05″ S	48° 35′ 45.49″ W
Family Phocoenidae								
*UNIVALI ii 47907	MW446675	*Phocoena dioptrica*	*Phocoena spinipinnis*	*	98	*	26° 53′ 31.48″ S	48° 38′ 24.91″ W
ECOMEGA/FURG 68	MW446655	*Phocoena spinipinnis*	*Phocoena spinipinnis*	*Phocoena spinipinnis*	100	98.99	32° 33′ 17.89″ S	52° 18′ 53.28″ W
ECOMEGA/FURG 69	MW446654	*Phocoena spinipinnis*	*Phocoena spinipinnis*	*Phocoena spinipinnis*	100	100	33° 21′ 3.02″ S	53° 5′ 27.71″ W
ECOMEGA/FURG 70	MW446786	*Phocoena spinipinnis*	*Phocoena spinipinnis*	*Phocoena spinipinnis*	98.92	98.91	Rio Grande—RS	

[a] GEMM-Lagos: Grupo de Estudos de Mamíferos, Aves e Répteis Marinhos e Costeiros da Região dos Lagos

[b] GEMARS: Grupo de Estudos de Mamíferos Aquáticos do Rio Grande do Sul

[c] MN: Museu Nacional da Universidade Federal do Rio de Janeiro

[d] LEC: Laboratório de Ecologia e Conservação de Mamíferos do Centro de Estudos do Mar, Universidade Federal do Paraná

[e] ECOMEGA/FURG: Laboratório de Ecologia e Conservação da Megafauna Marinha da Universidade Federal do Rio Grande

[f] MPEG: Museu Paraense Emílio Goeldi/ Grupo de Estudos de Mamíferos Aquáticos da Amazônia

[g] AQUASIS: Associação de Pesquisa e Preservação de Ecossistemas Aquáticos

[h] UNIVALI: Universidade do Vale do Itajaí

[i] Instituto Oceanográfico da Universidade São Paulo

[j] Departamento de Ciências Agrárias e Biológicas da Universidade Federal do Espírito Santo

Regarding the 11 mismatches between the molecular and morphological identifications among 150 cetacean carcasses (i.e., ~7% of the sample) (Table 2), we can assign them to four causes: (1) incorrect morphological identification; (2) recent taxonomic changes (species splitting); (3) incomplete molecular databases, and (4) absence of barcoding gap between species. Each of them will be treated separately below.

Incorrect morphological identification

The first mismatch case between morphological and molecular identifications was found in the ECOMEGA/FURG 45 specimen. The specimen was in an advanced state of decomposition and was identified during fieldwork as a killer whale (*Orcinus orca*), but both molecular databases indicated a complete match (100% identity) with the false killer whale (*Pseudorca crassidens*). Unfortunately, the skull was missing, but the pictures from the head of the dead specimen were sent to two marine mammal specialists, who concluded based mainly on external morphology and tooth counts (likely nine) that the specimen was probably a *P. crassidens* (Fig. 3a). Despite a little overlap between the dental formula of these two species (typically, 7 to 10 teeth per tooth row in *P. crassidens* and 10 to 12 in *O. orca*), the number of teeth is generally smaller in *P. crassidens* (Jefferson et al. 1993).

Two other molecular-morphological mismatches due to incorrect morphological identification in the field were reported: (a) GEMARS 1491, putatively identified during fieldwork as a humpback whale (*Megaptera novaeangliae*), but identified with both molecular databases as a southern right whale (*Eubalaena australis*) (NCBI = 99.18% identity; BOLD = 98.38% identity) and (b) ECOMEGA/FURG 63, morphologically identified as a sei whale (*Balaenoptera borealis*) but identified with both molecular databases as a Bryde's whale (*Balaenoptera brydei*) (NCBI = 99.23% identity; BOLD = 99.22% identity). In both cases, the specimens were found in an advanced state of decomposition, indicating code 4 according to the classification determined by Geraci and Lounsbury (2005). Based on the carcass conditions, we presume that the morphological evaluation of the species identity was very difficult, leading the collectors to misidentify the two specimens.

Recent taxonomic changes (species splitting)

Three specimens of river dolphins (MPEG 38764, MPEG 42122 and MPEG 42055) were identified by the field researchers as *Inia geoffrensis*, but the molecular identification with both databases indicated that they should be classified as *I. araguaiaensis* (NCBI=100% identity; BOLD=99.81% identity for all cases). These mismatches are explained by the fact that, at the time the samples, were collected and

Fig. 3 ECOMEGA/FURG 45 specimen: **a** *Pseudorca crassidens* found stranded in advanced state of decomposing. The species identification was based on teeth counting as well as DNA barcoding analysis. Photo: ECOMEGA/FURG. **b** GEMARS 1491 specimen found on the coast of Rio Grande do Sul and identified as *Megaptera novaeangliae* cf., but genetically, it was *Eubalaena australis*. Photo: image bank of GEMARS

deposited in the museum collection (between 2007 and 2012; for details, see Siciliano et al. 2016), *I. araguaiaensis* had not been formally described (Hrbek et al. 2014). Until the formal description of this taxon in 2014 and the deposit of its sequences in the molecular databases, Amazon and Araguaia-Tocantins river dolphins were jointly identified as *I. geoffrensis*.

Incomplete molecular databases

The GEMARS 1155 specimen was morphologically identified as Arnoux's beaked whale (*Berardius arnuxii*), while the molecular identification performed with both databases indicated that it was Baird's beaked whale (*Berardius bairdii*) (NCBI=99.70% identity; BOLD=99.69% identity). These species show very slight morphological differences, and the validity of these species had already been questioned (Balcomb 1989 in Jefferson et al. 1993). However, studies based on the mitochondrial *cytochrome b* gene supported clear-cut molecular differences and recognized them as distinct species (Dalebout et al. 2004). At the same time, it is noteworthy that these two species exhibit antitropical distributions, with *B. bairdii* occurring only in the North Pacific Ocean (Kasuya 2009) and that *B. arnuxii coxI* sequences were not previously represented in these databases. Thus, we conclude that the molecular identification in this case did not match the morphological identification purely because of the lack of *B. arnuxii* reference sequences, making *B. bairdii* the closest available species for similarity-based clustering.

A similar result was observed with the UNIVALI ii 47907 specimen, which had been morphologically identified as a spectacled porpoise (*Phocoena dioptrica*) based on the unique pigmentation pattern of the species (e.g., double eye patch) and the large and rounded dorsal fin typical of males (Goodall 2009) (Fig. 4). However, the molecular approach identified it as Burmeister's porpoise (*Phocoena spinipinnis*) (NCBI=97.99% identity; BOLD=97.98% identity). This mismatch resulted from the lack of *coxI* sequences of *P. dioptrica* in both GenBank and BOLD databases

Absence of barcoding gap between species

The sample AQUASIS 02C1152/333 was morphologically identified as a Clymene dolphin (*Stenella clymene*). This identification was confirmed by GenBank (NCBI=100% identity), but it was ambiguous in the BOLD database, which reported 100% similarity with both *Stenella frontalis* and *Stenella clymene*. This specimen was very weak when it was rescued, according to the Marine Mammal Rehabilitation Center (CRMM), and it died a few hours after arrival. The fresh conditions of the carcass allowed the precise observation of a typical *S. clymene* coloration pattern, including the three-part color of the body, the dark mark on the upper side of the beak ("moustache") and the distinct eye-stripe, some of the most distinctive features of the species (Perrin 2009; Jefferson et al. 1993) (Fig. 5).

Likewise, the molecular results suggested that the GEMARS 1240 specimen was a short-beaked common dolphin (*Delphinus delphis*) with both databases (NCBI = 100% identity; BOLD = 99.85% identity), but the specimen was morphologically identified during fieldwork and also after the skull examination by a marine mammal expert as a striped dolphin (*Stenella coeruleoalba*). Taking into account the morphological diagnosis of deep palatal grooves in the *D. delphis* skull and the fact that in the GEMARS 1240 specimen this trait was absent, we are confident in the morphological identification as *S. coeruleoalba* (Fig. 6a and b). In addition to these dolphin species, we found two cases that seem to reflect the inexistence of a barcoding gap among right whale species. According to the external morphology, the samples MN60458 and GEMM-Lagos 051 were identified as southern right whales (*Eubalaena australis*), and these identifications were supported by a BLAST comparison against GenBank (MN60458, NCBI=100% identity; GEMM-Lagos 051, NCBI=99% identity). However, the BOLD analysis identified both samples as *E. glacialis* (MN60458, BOLD=100% identity; GEMM-Lagos 051, BOLD=99.69% identity), a species that only occurs in the North Atlantic (Rosenbaum et al. 2000). Although these findings could also be related to an erroneous deposit of sequences in the BOLD platform, we believe that the results are more likely derived from a weak or absent barcoding

Fig. 4. UNIVALI ii47907 specimen of spectacled porpoise (*Phocoena dioptrica*). Photo: PMP-BS (2020) Ocorrência de Fauna Alvo Individual - ii 047907. Available at https://simba.petrobras.com.br/simba/web/sistema/pmp/1/individualfaunaoccurrence/33573

Fig. 5. AQUASIS 02C1152/333 specimen of Clymene dolphin (*Stenella clymene*) still alive during its treatment. Photo: Aquasis photo bank

gap between these species, as noticed by Viricel and Rosel (2011).

Inter- and intraspecific distances of *coxI*

Intra- and interspecific genetic divergences for *Delphinus delphis*, *Stenella clymene*, *Stenella coeruleoalba*, *Stenella frontalis* and *Tursiops truncatus* of the family Delphinidae are detailed in Table 3. Measurements of intraspecific variation ranged from 0 to 0.56%, while interspecific variation ranged from 0.38 to 2.56%, with a mean divergence of 1.5%. The neighbor-joining tree correctly distinguished all the analyzed cetaceans (Fig. 7), except the species of Delphinidae, which presented a small inter-specific genetic

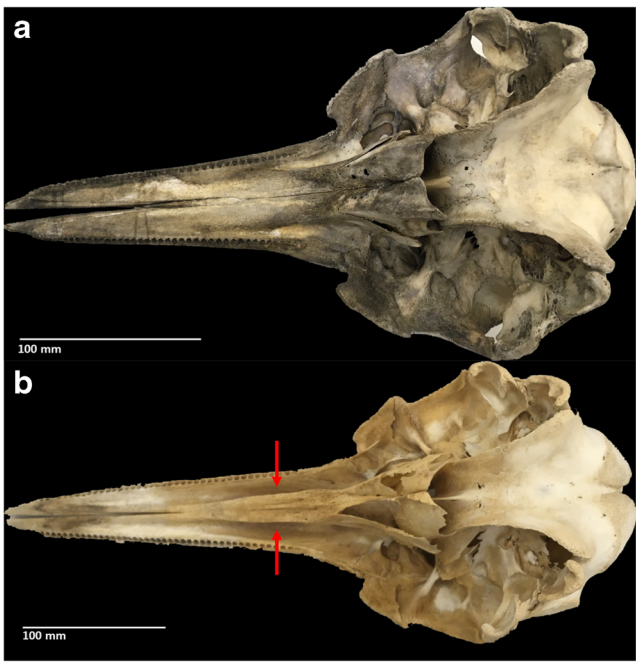

Fig. 6. Ventral view of skulls: **a** Striped dolphin (*Stenella coeruleoalba*) (GEMARS 1240). **b** common dolphin (*Delphinus delphis*), highlighting the prominence of the palatal grooves (pointed out by the arrows)

Table 3 The inter- and intra-specific divergences (K2P pairwise distances) between cetacean species of the subfamily Delphininae of the present study that the *coxI* marker was not efficient to identify at species level

Genetic divergences (%)							
		Between species					Within species
Species		1	2	3	4	5	
1	*Delphinus delphis*						0.56
2	*Stenella clymene*	1.56					0.00
3	*Stenella coeruleoalba*	1.73	2.56				0.27
4	*Stenella frontalis*	0.38	1.16	1.33			0.00
5	*Tursiops truncatus*	1.03	1.97	2.15	0.70		0.28

divergence. However, some species of this family formed clades with high bootstrap support values (>90%): *Sotalia guianensis*, *Steno bredanensis*, *Grampus griseus*, *Stenella attenuata*, and *Globicephala melas*.

The same comparative scenario for *coxI* intra- and inter-specific genetic divergences for the three species of *Eubalaena* (*E. australis*, *E. glacialis*, and *E. japonica*) is presented in Table 4, based on the analysis of only 11 sequences deposited in both the GenBank and BOLD databases. The measurements of inter-specific variation for the *coxI* marker of the three species of *Eubalaena* were very small, less than 1%. Moreover, when the standard deviations are taken into account, the limits of divergence among the three species did not support three groups, suggesting the lack of a gap among right whales. However, these results must be interpreted with caution, because of the small sample size available for this analysis. Although *coxI* was able to correct the misidentification of the specimen GEMARS 1491 (*Megaptera novaeangliae* cf.) to a right whale, the highest identity score (98.38%) of the BLAST search for this sequence in the BOLD platform (i.e., the most similar sequences to the query) was shared among four sequences, two *E. australis* and two *E. glacialis*. Moreover, this same searching tool of the BOLD platform identified two other southern right whale samples (MN 60458 and GEMM-Lagos 051) as *E. glacialis* and even in the cases that the Brazilian samples were correctly identified as *E. australis* (GEMARS 1456 and GEMARS 1467), and the first five results of the target sequences also included *E. glacialis* and *E. japonica*.

Phylogenetic reconstruction using maximum-likelihood

Although there were problems with determining inter-specific limits for some species of Delphinidae, both phylogenetic analyses had similar results, but especially in the maximum likelihood (ML) tree reconstructed most species as well-defined clades (Fig. 8), supporting the use of *coxI* as a useful marker for species identification in cetaceans, except for

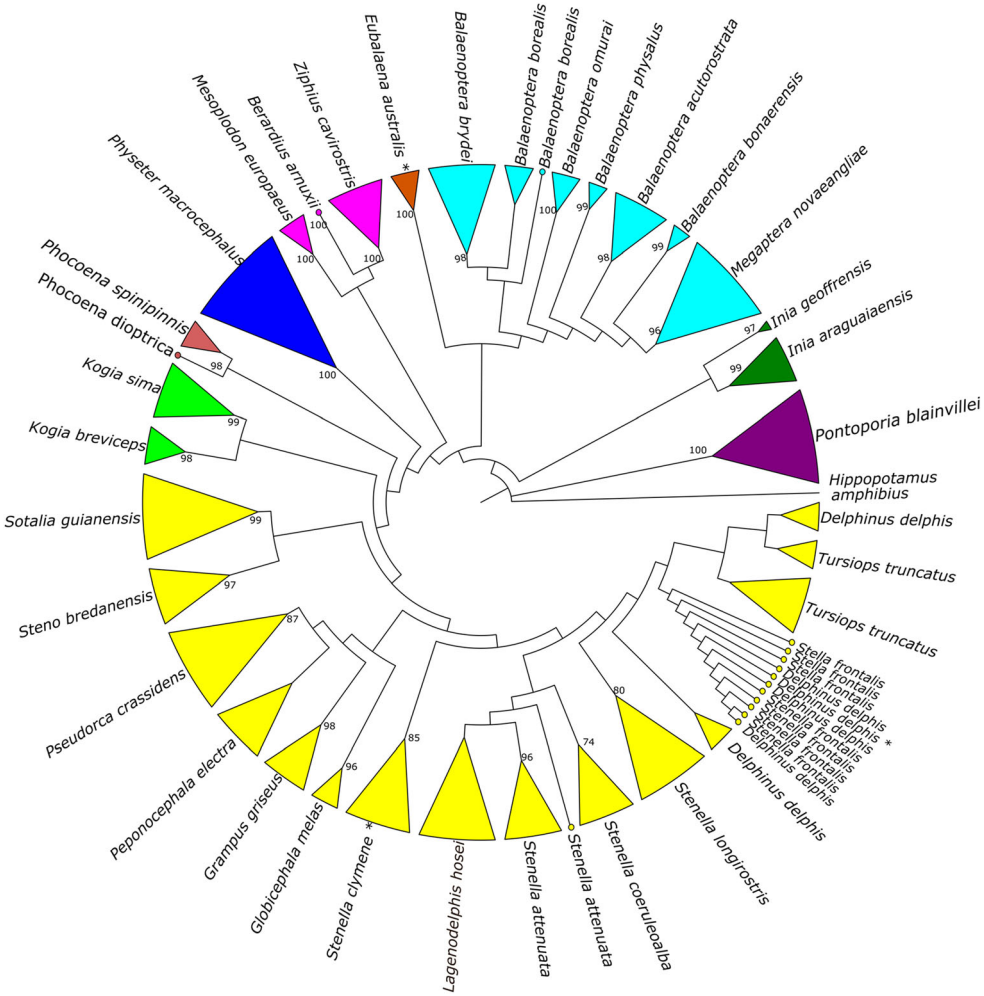

Fig. 7 Neighbor-joining tree generated from pre-existing sequences in BoldSystem and the 150 sequences generated in this study. The colors indicate different families of cetaceans: dark green: Iniidae, brown: Balaenidae, purple: Pontoporiidae, blue: Physeteridae, light green: Kogiidae, pink: Ziphiidae, light blue: Balaenopteridae, coral: Phocoenidae and yellow: Delphinidae

Delphinus delphis, the only species that did not form a monophyletic group.

Discussion

This study generated 150 sequences from the *coxI* region of 33 cetacean species, which represent 70% of the Brazilian diversity of this taxon. The molecular identification was in accordance with external morphology-based identification in ~93% of the specimens. We detected 11 cases of molecular-morphological mismatched identifications; all were resolved in favor of the molecular identification, except for three cases in which we observed an absence of barcoding gap between delphinid species (genera *Stenella* and *Delphinus*) and probably two cases among the right whales (*Eubalaena* spp.). Overall, these results demonstrate that DNA barcoding is highly efficient as a tool for taxonomic identification of cetacean species along the Brazilian coastal and continental waters.

Alfonsi et al. (2013) were able to generate good-quality *coxI* sequences from 150 highly degraded carcasses of marine mammals found along the Brittany coast of France. They correctly identified all specimens, which represent ca. 16% of the specimens recovered every year along the coast of France, and concluded that DNA barcoding, even with certain constraints, is very useful for the French stranding network. In view of their findings, Alfonsi et al. (2013) suggested that DNA barcoding could be useful for the monitoring of marine mammal strandings at three levels:

Table 4 *CoxI* pairwise inter- and intra-specific distances among species of *Eubalaena*, including the two specimens of the present study and sequences deposited in both GenBank and BOLD System databases

Genetic divergence (%)				
		Between species		Within species
Species		1	2	
1	*E. australis*			0.42 ± 0.2
2	*E. glacialis*	0.56 ± 0.2		0.55 ± 0.2
3	*E. japonica*	0.82 ± 0.3	0.72 ± 0.3	0.00 ± 0.0

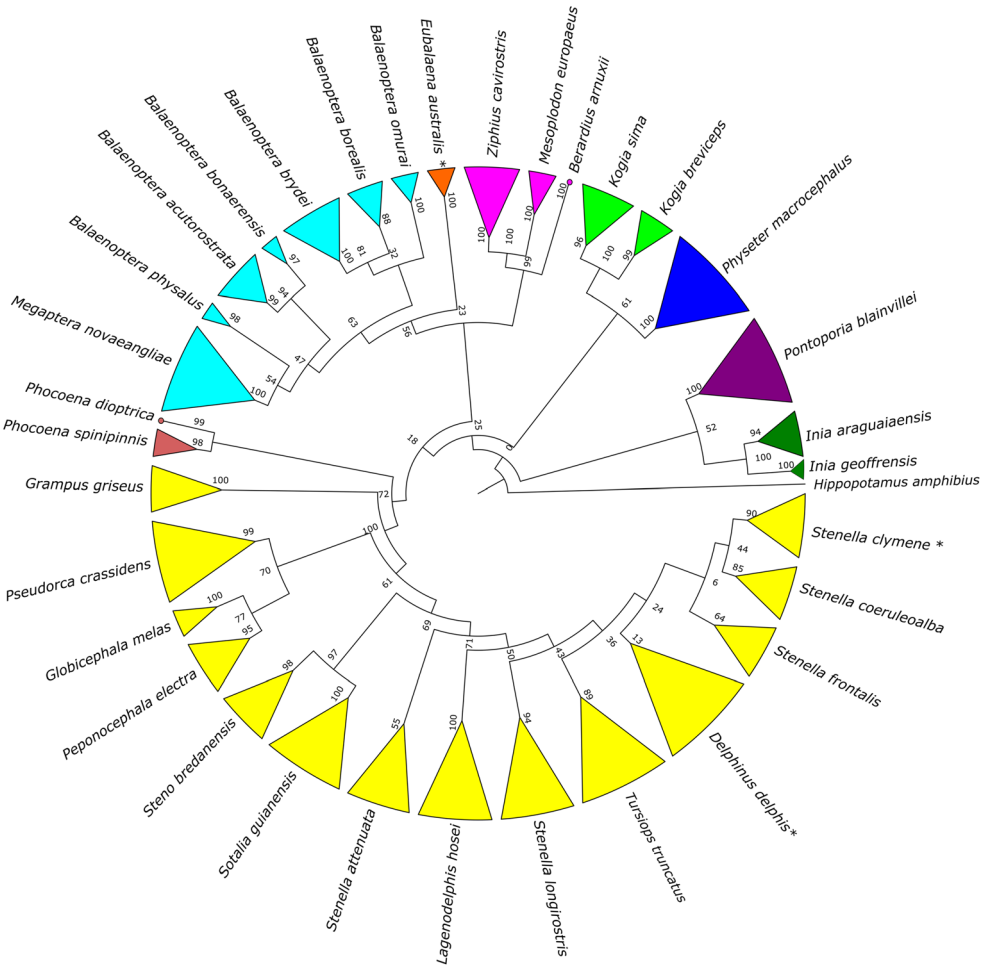

Fig. 8. Maximum-likelihood tree generated from pre-existing sequences in BoldSystem and the 150 sequences generated in this study. The colors indicate different families of cetaceans: dark green: Iniidae, brown: Balaenidae, purple: Pontoporiidae, blue: Physeteridae, light green: Kogiidae, pink: Ziphiidae, light blue: Balaenopteridae, coral: Phocoenidae and yellow: Delphinidae

(i) by providing a confirmation or an additional degree of taxonomic determination of rare species identified by field researchers, mainly in uncommon stranding events of rare or deep-living species (Thompson et al. 2012);
(ii) by helping the identification at species level when it is not possible to identify the animal by the external morphology due to highly degraded carcasses or even when morphology-based identification only reaches the genus or family levels, due to an incomplete skeleton or skull
(iii) by potentially allowing an assessment of intraspecific genetic variability, which enables genetic structure analysis and possibly monitoring population movements (Pauls et al. 2012).

In general, most species identified here with the molecular approach were very common in the coastal region, with no challenging identification, such as franciscana dolphins (*Pontoporia blainvillei*) and the common bottlenose dolphin (*Tursiops truncatus*). There were also records of rarely found stranded specimens belonging to Ziphiidae and Phocoenidae and oceanic and deep-diving species, such as pygmy, dwarf, and sperm whales (Pinedo et al. 2002; Prado et al. 2016), and the only endemic cetacean species for Brazil, the recently described Araguaian River dolphin. It is worth mentioning that the present study is one of the few involving DNA barcoding sequences of samples associated with voucher materials deposited in scientific collections, enabling morphological checking whenever necessary and thus providing greater reliability of the use of the molecular marker. According to Hanner (2009), as part of the BOLD quality control, DNA barcodes must be associated with specimen records linked to institutional (e.g., museum) material making them the most valuable as reference accessions. This is particularly important in cases of rare species, which usually have no sequences deposited in molecular platforms. The accuracy of DNA barcoding relies upon the level of taxonomic representation for each group and the amount of intraspecific genetic diversity represented in the databases (Gaubert et al. 2015).

It is important to mention that the present study contributed with the inclusion of the first *coxI* sequences of the spectacled porpoise (*Phocoena dioptrica*) and Arnoux's beaked whale (*Berardius arnuxii*), in both GenBank and Bold databases. The spectacled porpoise is a small cetacean with circumpolar distribution in Antarctic and subantarctic waters, with only one previous record published for the Brazilian coast (Pinedo et al. 2002).

There was another unpublished record in August 2016 for Cassino beach (ca. 32° 11′ S; 52° 09′ W, in Rio Grande do Sul State—Ecomega, unpubl. data), southern Brazil. The specimen analyzed in the present study was collected at Navegantes Beach, Santa Catarina State (26° 53′ 40″ S; 48° 38′ 32″ W) in July 2017, and represents the northernmost record of this species in the Atlantic Ocean (Barreto, unpubl. data).

Arnoux's beaked whale was first reported in Brazilian waters based on the collection of a floating dead specimen close to the coast of São Sebastião, São Paulo State, in southeastern Brazil (Siciliano and Santos 2003). The specimen sequenced in the present study (GEMARS 1155) stranded in the municipality of Balneário Pinhal, Rio Grande do Sul State (30° 14′ 29″ S; 50° 13′ 37″ W), in January 2004, representing the second confirmed record of the species in Brazilian waters (Ott et al. 2013).

Another record of a poorly known cetacean for which we provide new *coxI* sequences is Fraser's dolphin (*Lagenodelphis hosei*). There was a mass stranding event of 10 dolphins along 156 km of sandy beaches in the Rio Grande do Sul State coast, between September and November 1997 (Pinedo et al. 2001; Moreno et al. 2003), and four of these specimens were analyzed in this study. This stranding was not an isolated event; other stranded animals were reported in Uruguay as well as in Rio de Janeiro state coast. As a final counting, around 100 specimens were reported for the Southwestern Atlantic coast in 1997 (for a review, see Moreno et al. 2003).

According to Galimberti et al. (2015), there is a hidden diversity within the mammal record. The BOLD System had barcoded about 2850 mammal species by the end of May 2015, with at least 300 unnamed clusters (i.e., not assigned to a species). Currently, there are approximately 3587 species with recognized barcodes in the MammaliaBoL, 75 of which are cetaceans. Taking into account the requirement of *coxI* sequences associated to voucher material, Galimberti et al. (2015) emphasized that the standardized molecular reexamination of museum-deposited voucher specimens and the comparison with other reference information would allow the fast detection of misidentification or uncertainties that typically occur in the field.

This reexamination of voucher specimens and their information was particularly true for the case of specimen GEMARS 1491 found on the coast of Rio Grande do Sul, putatively identified in the field as a humpback whale (*Megaptera novaeangliae* cf.), but genetically as a southern right whale (*Eubalaena australis*). As mentioned earlier, when we examined the field notes presented in the catalogue book of the scientific collection, we found that the specimen was in an advanced state of decomposition, almost buried in sand, and that there was a highlighted note in the labels saying cf. (*confero*, in Latin), which means "needs to be confirmed" or "needs to be compared with" (Sigovini et al. 2016), which supports the care referred to by Galimberti et al. (2015). Moreover, according to the field notes, the specimen had some sessile whale barnacles still attached to its exposed skin, which led researchers to believe it was a humpback whale or a southern right whale. Considering that there was no clear clue in the notes in favor of humpback whale identity, we conclude that the molecular identification is correct.

Francis et al. (2010) commented that field identification for many mammals is difficult because it is based on the analysis of internal structures such as skull or dentition, which is particularly true for cetaceans. In these cases, the existence of voucher material as well as DNA samples in scientific collections becomes crucial to confirm the identification of specimens through complementary approaches (i.e., DNA barcodes and voucher material). For cetacean taxonomy, one of the main constraints lies in the small number of reference collections, which are in general spread among several museums. The present study had the privilege of including 16 institutions in Brazil with vast scientific collections, which allowed us to detect cases of doubtful or incorrect morphological identification in the field, as was the case of ECOMEGA/FURG 45. This specimen was identified during fieldwork as a killer whale (*Orcinus orca*), but both molecular databases indicated greater similarity to the false killer whale (*Pseudorca crassidens*). Due to this incongruence, the available voucher material was reexamined, and taking into account the number of tooth pairs visible on the photographs of the stranded animal and the range of tooth pairs described for both species, the specimen was considered to have a higher probability of being *P. crassidens*, in agreement with the molecular identifications. Although these two species have completely different external appearance, skull morphology is quite similar (Heyning and Dahlheim 1988; Baird 2009). Thus, in the field, when some of the main external morphological traits are missing or are not clearly visible, as in the case of this specimen, misidentification can occur, highlighting the importance of molecular analyses. However, two other cases involving the combination of field identification, barcoding information and the reexamination of the skull morphology from two dolphin specimens revealed unsolved morphological-molecular mismatches. In the case of GEMARS 1240, both molecular databases suggested that the specimen was a short-beaked common dolphin (*Delphinus delphis*), but the absence of a prominent trapezoid-shaped palatal ridge and the deep palatal grooves on the skull of the voucher specimen supported the morphological identification as *S. coeruleoalba* (Jefferson et al. 1993). In the case of the AQUASIS 02C1152/333 specimen, it showed a typical coloration pattern of *S. clymene*, and this identification was corroborated by one of the molecular databases (NCBI). Nevertheless, the search in the BOLD System database resulted in an ambiguous identification with equal support for *Stenella frontalis* and *Stenella clymene*. It is worth mentioning that both cases above involve member of the subfamily

Delphininae, which show an overlap between intra- and interspecific *coxI* genetic variations, suggesting that *coxI* is an imperfect barcode for these species. Therefore, for these taxa, additional markers must be developed for accurate species-level molecular identification, including complementary mitochondrial segments and likely biparentally inherited nuclear markers as well.

In this context, we cannot rule out that the morphological and molecular mismatch of these specimens represent cases of hybridization between *S. coeruleoalba* and *D. delphis* (GEMARS1240) and between *S. clymene* and *S. frontalis* (AQUASIS 02C1152/333). The introgressive hybridization between *S. coeruleoalba* and *D. delphis*, where males of *D. delphis* mate and produce fertile hybrids with females of *S. coeruleoalba*, has been recently reported in the Mediterranean (Antoniou et al. 2018). Moreover, the existence of other presumed interspecific hybrids in the genus *Stenella* (*S. clymene* x *S. longirostris* and *S. attenuata* x *S. longirostris*) has been reported in Brazilian waters (Silva et al. 2005). To investigate this possibility, informative nuclear markers must be developed, since the uniparentally-inherited mtDNA is insufficient for such questions. This development is an important avenue to pursue in the field of cetacean genetics and molecular identification.

Regardless of putative hybridization as a potential cause, two unsolved mismatches (AQUASIS 02C1152/333 e GEMARS 1240) between the morphological and molecular identifications found in this study involved delphinids (i.e., Delphinidae family), as already reported in other studies (e.g., Amaral et al. 2007; Viricel and Rosel 2011; Alfonsi et al. 2013), corroborating the limited efficiency of this marker in identifying these species, especially within the subfamily Delphininae. Moreover, the neighbor-joining analysis showed that *D. delphis*, *S. frontalis*, and *T. truncatus* species do not form monophyletic groups, possibly due to introgression processes, as reported for *D. delphis* and *S. coeruleoalba* (Kessler 2019) or due to insufficient time of divergence of some species within the taxon (Zhou et al. 2011). On the other hand, through phylogenetic reconstruction with maximum likelihood, it was possible to recover a greater number of monophyletic groups that corresponded to the sequences identified at species level for all cetaceans in this study, except for *D. delphis*. Moreover, *D. delphis*. *T. truncatus*. *S. coeruleoalba*. *S. frontalis*, and *S. clymene* presented very low interspecific *coxI* distances, which ranged from 2.56% (*S. clymene* vs. *S. coeruleoalba*) to 0.38% (*D. delphis* vs. *S. frontalis*). Due to the difficulty of species delimitation, the Delphinidae has been the target of studies that seek to resolve evolutionary relationships among its members using information regarding morphology, genetics, and, recently, acoustics and historical biogeography (Amaral et al. 2007; Vollmer et al. 2019). Additional work is required to clarify species boundaries in this group, thus allowing a more direct assessment of the power of DNA barcoding for their accurate identification.

In addition to the members of the subfamily Delphininae, our results also indicated a poor performance of *coxI* for discriminating among right whales species (*Eubalaena* spp.). Although *coxI* was able to correct the misidentification of the specimen GEMARS 1491 (*Megaptera novaeangliae* cf.) to a right whale, it was unable to conclusively discriminate among right whale species, as previously observed with another mtDNA region (*cytochrome b*) by Viricel and Rosel (2011). Taking into account the recent divergence of these species (Rosenbaum et al. 2000), our results are not surprising. However, since only *E. australis* is distributed in the southern hemisphere and all three extant species have an antitropical distribution (Rosenbaum et al. 2000), this limitation of *coxI* would not be a problem for discriminating the southern right whale from other large baleen whales in Brazilian waters.

In summary, the main concerns regarding the identification of cetaceans using the *coxI* gene are related to (i) cetaceans that seem not to have a "barcoding gap"; (ii) potential hybrids, which would require the use of biparentally inherited nuclear genes to establish the identification of the species; (iii) taxonomic updates that have not been incorporated in specimen identifications. All these concerns are relevant but, according to Galimberti et al. (2015), "...reference sequences constitute the main core of the DNA barcoding initiative and their absence or the lack of control of the correct identification of the source specimens by expert taxonomists, can irremediably affect the assignment of newly generated query sequences." This is why the existence of voucher material related to every *coxI* sequence is important.

Although DNA barcoding still generates some controversy, when it is considered a "taxonomic service," it becomes a very interesting tool, able to contribute to the knowledge of mammal diversity, providing information on the biology, distribution, and conservation of mammals, especially in the case of rare or poorly investigated taxa (Galimberti et al. 2015). A hidden diversity is also observed in large whales, which had their last species described in 2003 (*Balaenoptera omurai*), based on comparisons of external morphology, osteology, and mitochondrial DNA data (Wada et al. 2003). The species distribution was recently expanded to Brazilian waters based on a stranded specimen identified by *cytochrome b* and *coxI* sequences (Cypriano-Souza et al. 2016), since identification through its external morphology had been compromised due to the decomposition process. Moreover, DNA barcoding proved to be effective in discriminating cryptic or morphologically similar species, such as the species of genus *Inia*. The DNA barcoding approach allowed the researchers to recognize the existence of a distinct lineage confined to the Araguaia-Tocantins basin (Hrbek et al. 2014) as well as Marajó Bay (Siciliano et al. 2016), in northern Brazil.

Twelve cetaceans recorded for Brazil are classified by IUCN as "Data Deficient", mainly due to the lack of taxonomic or ecological information about these animals (ICMBio

2018; Hrbek et al. 2014; Cypriano-Souza et al. 2016; IUCN 2020). This scarcity of data and the accelerated process of degradation and pollution of the marine and freshwater environments occupied by these species highlight the need for studies that can help enhance the knowledge about this group, enabling the elaboration of effective conservation plans.

Considering this scenario, stranded cetacean carcasses can provide valuable information about the richness and patterns of occurrence of this group in Brazilian waters (Sholl et al. 2008; Meirelles et al. 2009; Prado et al. 2016; Dick et al. 2019; Milmann et al. 2020), once correctly identified. Therefore, despite some recognized limitations (Galimberti et al. 2015), our results reinforce that DNA barcodes, when properly used, can be a valuable tool for the scientific community involved in the stranding networks and to support decision-makers and conservation policies.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s13364-021-00555-w.

Acknowledgements The authors would like to thank all members of 16 institutions involved in field work and sampling activity: Grupo de Estudos de Mamíferos Aquáticos do Rio Grande do Sul (GEMARS), Ecossistemas Aquáticos (Aquasis), Laboratório de Biologia Molecular da Universidade do Vale dos Sinos, Fundação Osvaldo Cruz (FIOCRUZ), Universidade Federal do Espírito Santo (UFES), Universidade de São Paulo (USP), Universidade Federal de Rio Grande (FURG), Universidade Federal do Paraná (UFPR), Grupo de Estudos de Mamíferos Aquáticos da Amazônia (GEMMAM), Universidade do Vale do Itajaí (UNIVALI), Fundação Mamíferos Aquáticos (FMA), Grupo de Estudos de Mamíferos, Aves e Répteis Marinhos e Costeiros da Região dos Lagos (GEMM/Lagos), Organização Consciência Ambiental (ORCA/ES), Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio), Instituto de Desenvolvimento Sustentável Mamirauá (IDSM). We also thank the curators MSc. Maurício Tavares from the Museu de Ciências e História Natural (MUCIN) of the Universidade Federal do Rio Grande do Sul (UFRGS), Dr. João Oliveira from the Museu Nacional do Rio de Janeiro (MNRJ), Dr. Marcos César de Oliveira Santos from the Instituto Oceanográfico da Universidade de São Paulo (IO-USP), Dr. Silvina Botta, and the lab. assistents Lilia Fidélix and Wagner Vaz of the Laboratório de Ecologia e Conservação da Megafauna Marinha (Ecomega-FURG), the staff of the Centro de Biodiversidade Subtropical (CBS-FURG), as well as all students who have been working with all the cited institutions for the collection and maintenance of part of the specimens analyzed in this study.

Authors' contributions L.R.O. and E.E. developed the conceptualization of the study. L.R.O., E.E., and VHV designed the experiments. P.H.O., L.R.O., D.D., R.M. A.B., E.R.S., A.C.O.M., V.L.C., J.C.G.B., L.A.B., J.M.S.Jr., C.D., I.S., T.S., C.T., M.M., and N.R.E. conducted the sampling activity. V.S.S., N.S. A.P.F., and T.K.K., conducted mtDNA sequences generation in the laboratory and V.H.V., V.S.S., and F.L. performed the bioinformatics analysis. L.R.O., V.H.V., E.E., and P.H.O. conducted the validation of the data. L.R.O. and E.E. were responsible for funding acquisition and project administration. V.S.S., L.R.O., V.H.V., S.S., E.E., P.H.O., F.L., D.D., R.M. A.B., E.R.S., A.C.O.M., V.L.C., J.C.G.B., L.A.B., J.M.S.Jr., C.D., I.S., T.S., C.T., M.M., and N.R.E. wrote the original draft. L.R.O., E.E., and P.H.O. reviewed and edited the final version of the manuscript.

Funding Coordenação e Aperfeiçoamento de Pessoal de Nível Superior (CAPES-PROSUC) (CAPES) (Finance Code 001) for the provision of the master's degree to VSS and Conselho National de Pesquisa e Desenvolvimento Científico e Tecnológico (CNPq), which provided research fellowship to LRO (CNPq 303813/2011-3, 308650/2014-0 and 310621/2017-8), ERS (PQ 310597/2018–8), SS (CNPq 306076/2019-5) and EE (PQ 305040/2008-1, 311327/2011-7, 310803/2015-2 and 309068/2019-3). The research groups Ecologia e Conservação da Megafauna Marinha (Ecomega-FURG/CNPq) and Observa Litoral (Uergs/CNPq) contributed to this study. This study was financed in part by the project "Tetrapoda DNA Barcodes: construction of a DNA barcoding database for amphibians, reptiles, birds and mammals," part of the Brazilian Barcode of Life (BrBOL) initiative (MCT/CNPq/FNDCT N°. 50/2010). S. Siciliano is supported by Program INOVA Fiocruz. Samples collected by Aquasis (Projeto Manatí) were sponsored by Petrobras through Petrobras Socioambiental Program. Samples ii015573, ii014622, and ii047907 were collected under permit ABIO n° 640/2015, issued by IBAMA. Long-term beach surveys performed by Ecomega-FURG has been sponsored by Yaqu Pacha (Germany).

Data availability All barcode sequences and their respective accession numbers are available in GenBank.

Compliance with ethical standards

Ethics approval and consent to participate The study was based on voucher specimens deposited in scientific collections. All DNA samples used for this research derived from animals stranded and naturally dead, or from biopsied animals. No animal was intentionally caught or killed during the summarized research. The sampling permits (see methods) issued by local authorities in Brazil (*SISBIO* - Brazilian Biodiversity authorization and information system) attest that the authors did not violate any ethical rule for collecting the animal samples. All authors (Vanessa S. Silva, Natália Skueresky, Fernando Lopes, Tabata K. Koch, Paulo Henrique Ott, Salvatore Siciliano, André S. Barreto, Eduardo R. Secchi, Ana Carolina O. de Meirelles, Vitor Luz Carvalho, João C. G. Borges, Daniel Danilewicz, Ana Paula C. Farro, Lupércio A. Barbosa, José Martins S. Jr., Camila Domit, Inês Serrano, Tiago Silva, Cristine Trinca, Miriam Marmontel, Neusa Renata Emin-Lima, Victor Hugo Valiati, Eduardo Eizirik, Larissa Rosa de Oliveira) declare that they consent to participate in the manuscript.

Consent for publication All authors (Vanessa S. Silva, Natália Skueresky, Fernando Lopes, Tabata K. Koch, Paulo Henrique Ott, Salvatore Siciliano, André S. Barreto, Eduardo R. Secchi, Ana Carolina O. de Meirelles, Vitor Luz Carvalho, João C. G. Borges, Daniel Danilewicz, Ana Paula C. Farro, Lupércio A. Barbosa, José Martins S. Jr., Camila Domit, Inês Serrano, Tiago Silva, Cristine Trinca, Miriam Marmontel, Neusa Renata Emin-Lima, Victor Hugo Valiati, Eduardo Eizirik, and Larissa Rosa de Oliveira) declare that they consent for publication of the manuscript.

Conflict of interest The authors declare that they have no conflict of interest.

Code availability Not applicable

References

Ab'Saber AN (2001) Litoral do Brasil. Meta Livros, São Paulo

Alfonsi E, Méheust E, Fuchs S, Carpentier FG, Quillivic Y, Viricel A, Hassani S, Jung JL (2013) The use of DNA barcoding to monitor the

marine mammal biodiversity along the French Atlantic coast. ZooKeys. 365:5–24. https://doi.org/10.3897/zookeys.365.5873

Amaral ACZ, Jablonski S (2005) Conservation of marine and coastal biodiversity in Brazil. Conserv Biol 19:625–631. https://doi.org/10.1111/j.1523-1739.2005.00692.x

Amaral ARM, Sequeira M, Coelho MM (2007) A first approach to the usefulness of cytochrome c oxidase I barcodes in the identification of closely related delphinid cetacean species. Mar Freshw Res 58: 505. https://doi.org/10.1071/MF07050

Antoniou A, Frantzis A, Alexiadou P, Paschou N, Poulakakis N (2018) Evidence of introgressive hybridization between *Stenella coeruleoalba* and *Delphinus delphis* in the Greek Seas. Mol Phylogenet Evol 129:325–337. https://doi.org/10.1016/j.ympev.2018.09.007

Baird RW (2009) False killer whale. *Pseudorca crassidens*. In: Perrin WF, Wursig B, Thewissen JGM (eds) Encyclopedia of Marine Mammals, 2nd edn. Academic Press, Cambridge, pp 405–406

Bastida RO, Rodríguez D, Secchi E, da Silva V (2018) Mamíferos Aquáticos da América do Sul e Antártica. Vázquez Mazzini Editores, Buenos Aires

Costa LP, Leite LR, Mendes SL, Ditchfield AD (2005) Mammal Ccnservation in Brazil. Conserv Biol 19:672–679

Cypriano-Souza AL, Meirelles ACO, Luz V, Bonatto SL (2016) Rare or cryptic? The first report of an Omura's whale (*Balaenoptera omurai*) in the South Atlantic Ocean. Marine Mammal Sci 33:80–95. https://doi.org/10.1111/mms.12348

Dalebout ML, Van Helden A, Van Waerebeek K, Baker CS (1998) Molecular genetic identification of southern hemisphere beaked whales (Cetacea: Ziphiidae). Mol Ecol 7:687–694. https://doi.org/10.1046/j.1365-294x.1998.00380.x

Dalebout ML, Mead JG, Baker CS, Baker NA, Van Helden AL (2002) A new species of beaked whale *Mesoplodon perrini* sp. n. (Cetacea: Ziphiidae) discovered through phylogenetic analyses of mitochondrial DNA sequences. Marine Mammal Sci. https://doi.org/10.1111/j.1748-7692.2002.tb01061.x

Dalebout ML, Baker CS, Mead JG, Cockcroft VG, Yamada TK (2004) A comprehensive and validated molecular taxonomy of beaked whales, family Ziphiidae. J Hered 95:459–473. https://doi.org/10.1093/jhered/esh054

Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models. new heuristics and parallel computing. Nat Methods 9:772–772

Dick et al. (2019), Strandings of marine mammals, sea turtles and seabirds along the central-north Santa Catarina coast, Brazil, from 2015 to 2018, Dryad, Dataset. https://doi.org/10.5061/dryad.x95x69pd9

Falcão LHO, Campos AS, Freitas JEP, Furtado-Neto MAA, Faria VV (2017) Molecular identification of cetaceans from the West Atlantic using the E3-I5 region of COI. Genet Mol Res 16. https://doi.org/10.4238/gmr16029607

FAO Food and Agriculture Organization of the United Nations (2016). The state of world fisheries and aquaculture: contributing to food security and nutrition for all. Rome

Francis CM, Borisenko AV, Ivanova NV, Eger JL, Lim BK, Guillén-Servent A, Kruskop SV, Mackie I, Hebert PDN (2010) The role of DNA barcodes in understanding and conservation of mammal diversity in Southeast Asia. PLoS One 5:e12575. https://doi.org/10.1371/journal.pone.0012575

Fruet PF, Kinas PG, Silva KG, Di Tullio JC, Monteiro DS, Dalla Rosa L, Estima SC, Secchi ER (2012) Temporal trends in mortality and effects of by-catch on common bottlenose dolphins, *Tursiops truncatus*, in southern Brazil. J Mar Biol Assoc U K 92:1865–1876. https://doi.org/10.1017/S0025315410001888

Galimberti A, Sandionigi A, Bruno A, Bellati A, Casiraghi M (2015) DNA barcoding in mammals: what's new and where next? Hystrix Italian J Mammal. https://doi.org/10.4404/hystrix-26.1-11347

Gaubert P, Njiokou F, Olayemi A, Pagani P, Dufour S, Danquah E, Dernat R (2015) Bushmeat genetics: setting up a reference framework for the DNA typing of African forest bushmeat. Mol Ecol Resour 15:633–651. https://doi.org/10.1111/1755-0998.12334

Geraci JR, Lounsbury VJ (2005) Marine mammals ashore: a field guide for strandings, 2nd edn. National Aquarium in Baltimore, Baltimore

Goodall RNP (2009) Spectacled porpoise. *Phocoena dioptrica*. In: Perrin WF, Wursig B, Thewissen JGM (eds) Encyclopedia of Marine Mammals, 2nd edn. Academic Press, Cambridge, pp 1087–1091

Greig AB, Secchi ER, Zerbini AN, Rosa LD (2001) Stranding events of southern right whales, *Eubalaena australis*, in southern Brazil. J Cetacean Res Manag Special Issue 2:157–160

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41:95–98

Hanner R (2009) Data Standards for BARCODE Records in INSDC (BRIs). http://barcoding.si.edu/PDF/DWGdatastandards.pdf. Accessed 10 September 2020

Hebert PDN, Cywinska A, Ball SL, Dewaard JR (2003) Biological identifications through DNA barcodes. Proc R Soc B Biol Sci 270:313–321. https://doi.org/10.1098/rspb.2002.2218

Heyning JE, Dahlheim ME (1988) *Orcinus orca*. Mamm Species:1. https://doi.org/10.2307/3504225

Hrbek T, Silva VMF, Dutra N, Gravena W, Martin AR, Farias IP (2014) A new species of river dolphin from Brazil or: how little do we know our biodiversity. PLoS ONE 9:e83623. https://doi.org/10.1371/journal.pone.0083623

Ibama (2005). Protocolo para encalhe de mamíferos aquáticos/ Rede de encalhe de mamíferos aquáticos do Nordeste. https://www.icmbio.gov.br/portal/images/stories/plano-de-manejo/12protocolodeencalhesAPAdabaleiafranca.pdf. Accessed 07 September 2020

Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio) (2011a) Plano de Ação Nacional para Conservação dos Mamíferos Aquáticos: Pequenos cetáceos. Brasília: Instituto Chico Mendes de Conservação da Biodiversidade. https://www.icmbio.gov.br/portal/images/stories/docs-pan/pan-pequenos-cetaceos/1-ciclo/pan-pequenos-cetaceos-livro.pdf. Accessed 07 September 2020

Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio) (2011b) Plano de Ação para a Conservação dos Mamíferos Aquáticos – Grandes Cetáceos e Pinípedes. In: Rocha-Campos et al. (Orgs). Brasília: Instituto Chico Mendes de Conservação da Biodiversidade. https://www.icmbio.gov.br/portal/faunabrasileira/plano-de-acao-nacional-lista/861-plano-de-acao-para-conservacao-dos-grandes-cetaceos-e-pinipedes Accessed 07 September 2020

Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio) (2018). Listas de espécies ameaçadas do Brasil.

IUCN (2020) The IUCN Red List of Threatened Species. Version 2020-2. http://www.iucnredlist.org. Accessed 11 March 2020

Jefferson TA, Leatherwood S, Webber MA (1993) FAO Species Identification Guide. Marine Mammals of the World. FAO, Rome

Kasuya T (2009) Giant beaked whales. *Berardius bairdii* and *Berardius arnuxii*. In: Perrin WF, Wursig B, Thewissen JGM (eds) Encyclopedia of Marine Mammals, 2nd edn. Academic Press, Cambridge, pp 498–500

Kessler A (2019) Genômica da origem híbrida do golfinho *Stenella clymene*. Dissertation, Pontifícia Universidade Católica do Rio Grande do Sul (PUCRS)

Kimura MJ (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J Mol Evol 16:111–120. https://doi.org/10.1007/BF01731581

Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Mol Biol Evol. https://doi.org/10.1093/molbev/msw054

Lemos LS, Moura JF, Hauser-Davis RA, De Campos RC, Salvatore S (2013) Small cetaceans found stranded or accidentally captured in

southeastern Brazil: bioindicators of essential and non-essential trace elements in the environment. Ecotoxicol Environ Saf 97: 166–175. https://doi.org/10.1016/j.ecoenv.2013.07.025

Longo LL, Amado Filho GM (2014) O conhecimento da fauna marinha bentônica brasileira através dos tempos. História, Ciências, Saúde-Manguinhos 21:995–1010. https://doi.org/10.1590/S0104-59702014000300011

MacLeod CD, Perrin WF, Pitman R, Barlow J, Balance L, D'amico A, Gerrodette T, Joyce G, Mullin KD, Palka DL, Waring GT (2006) Known and inferred distributions of beaked whale species (Cetacea: Ziphiidae). J Cetacean Res Manag 7:271–286

Mead JG (2008) Beaked Whales, Overview. Ziphiidae. In: Perrin WF, Wursig B, Thewissen JGM (eds) Encyclopedia of Marine Mammals, 2nd edn. Academic Press, Cambridge, pp 94–97

Meiklejohn KA, Damaso N, Robertson JM (2019) Assessment of BOLD and GenBank – their accuracy and reliability for the identification of biological materials. PLoS ONE 14. https://doi.org/10.1371/journal.pone.0217084

Meirelles ACO, Furtado-Neto MAA (2004) Stranding of an Antartic minke whale, *Balaenoptera bonaerenis* (Burmeister 1867), on the northern coast of South America. Lat Am J Aquat Mamm 3:81–82

Meirelles ACO, Monteiro-Neto C, Martins AMA, Costa AF, Barros HMDR, Alves MDO (2009) Cetacean strandings on the coast of Ceará, north-eastern Brazil (1992– 2005). J Mar Biol Assoc U K 89:1083–1090. https://doi.org/10.1017/S002531540900221

Milmann L, Siciliano S, Morais I, Tribulato AS, Machado R, Zerbini AN, Baumgarten JE, Ott PH (2020) A review of Balaenoptera strandings along the east coast of South America. Reg Stud Mar Sci 37:101343. https://doi.org/10.1016/j.rsma.2020.101343

Moreno IB, Danilewicz D, Borges-Martins M, Ott PH, Caon G, Oliveira LR (2003) Fraser's dolphin (*Lagenodelphis hosei* Fraser, 1956) in southern Brazil. Lat Am J Aquat Mamm 2. https://doi.org/10.5597/lajam00029

Ott PH, Tavares M, Moreno IB, Oliveira LR, Danilewicz D (2009) Os cetáceos do Arquipélago de São Pedro e São Paulo. In: Mohr LV, Castro, JWA, Costa, PMS, Alves, RJV (Orgs) Ilhas Oceânicas Brasileiras: da Pesquisa ao Manejo. MMA/Secretaria de Biodiversidade e Floresta, Brasília, pp 283-300

Ott PH, Tavares M, Secchi ER, Di Tullio JC (2013) Cetacea. In: Weber MM, Roman C, Cáceres NC, (Orgs) Mamíferos do Rio Grande do Sul, 1st edn. UFSM, Santa Maria, pp 457-550

Pauls SU, Nowak C, Bálint M, Pfenninger M (2012) The impact of global climate change on genetic diversity within populations and species. Mol Ecol 22:925–946. https://doi.org/10.1111/mec.12152

Perrin WF (2009) Coloration. In: Perrin WF, Wursig B, Thewissen JGM (eds) Encyclopedia of Marine Mammals, 2nd edn. Academic Press, Cambridge, pp 243–249

Pinedo MC, Rosas FCW, Marmontel M (1992) Cetáceos e Pinípedes do Brasil. UNEP/FUA, Manaus

Pinedo MC, Lamardo M, Barreto AS (2001) Review of *Ziphius cavirostris*, *Mesoplodon grayi* and *Lagenodelphis hosei* (Cetacea: Ziphiidae and Delphinidae) in Brazilian waters, with new records from southern Brazil. Atlântica 23:67–76

Pinedo MC, Barreto AS, Lammardo MP, Andrade ALV, Geracitano L (2002) Northernmost records of the spectacled porpoise, Layard's beaked whale, Commerson's dolphin and Peale's dolphin in the southwestern Atlantic Ocean. Aquat Mamm 28:32–37

Prado HF, Mattos PH, Silva KG, Secchi ER (2016) Long-term seasonal and interannual patterns of marine mammal strandings in subtropical western South Atlantic. PLoS One 11. https://doi.org/10.1371/journal.pone.0146339

Reyes JC, Van Waerebeek K, Cardenas JC, Anez JLY (1995) *Mesoplodon bahamondi* sp.n. (Cetacea, Ziphiidae), a new living beaked whale from the Juan Fernandez Archipelago, Chile. Bol Mus Nac Hist Nat Chile 45:31–44

Rosenbaum HC, Brownell RL Jr, Brown MW, Schaeff C et al (2000) Worldwide genetic differentiation of *Eubalaena*: questioning the number of right whale species. Mol Ecol 9:1793–1802. https://doi.org/10.1046/j.1365-294x.2000.01066.x

Sholl TGC, Nascimento FF, Leoncini O, Bonvicino CR, Siciliano S (2008) Taxonomic identification of dolphin love charms commercialized in the Amazonian region through the analysis of cytochrome b DNA. J Mar Biol Assoc U K 88:1207–1210. https://doi.org/10.1017/S002531540800043X

Sholl TGC, Moura JF, Ott PH, Bonvicino CR, Reis EC, Tavares DC, Siciliano S (2013) Cytochrome b sequencing for the species identification of whale carcasses washed ashore in Brazil. Marine Biodivers Records 6. https://doi.org/10.1017/S175526721200115

Siciliano S, Santos MCO (2003) On the occurrence of the Arnoux's beaked whale (*Berardius arnuxii*) in Brazil. J Mar Biol Assoc U K 83:887–888. https://doi.org/10.1017/S0025315403007999h

Siciliano S, Moura JF, Filgueiras HR, Rodrigues PP, Leite NO Jr (2012) Sightings of humpback whales on the Vitória-Trindade chain and around Trindade Island, Brazil. Braz J Oceanogr 60:455–459. https://doi.org/10.1590/S1679-87592012000300016

Siciliano S, Valiati VH, Emin-Lima R, Costa AF, Sartor J, Dorneles T, Silva Júnior JS, Oliveira LR (2016) New genetic data extend the range of river dolphins Inia in the Amazon. Delta Hydrobiol. https://doi.org/10.1007/s10750-016-2794-7

Sigovini M, Keppel E, Tagliapietra D (2016) Open nomenclature in the biodiversity era. Methods Ecol Evol 7:1217–1225. https://doi.org/10.1111/2041-210X.12594

Silva JM Jr, Silva FJL, Sazima I (2005) Two presumed interspecific hybrids in the genus *Stenella* (Delphinidae) in the Tropical West Atlantic. Aquat Mamm 31:468–472. https://doi.org/10.1578/AM.31.4.2005.468

Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30:312–1313

Taylor BL, Archer FI, Martien KK (2017) Guidelines and quantitative standards to improveconsistency in cetacean subspecies and species delimitation relying on molecular genetic data. Marine Mammal Sci 33:132–155. https://doi.org/10.1111/mms.12411

Thompson K, Baker CS, Van Helden A, Patel S, Millar C, Constantine R (2012) The world's rarest whale. Curr Biol 22:R905–R906. https://doi.org/10.1016/j.cub.2012.08.055

Van Bressem MF, Van Waerebeek K, Reyes J, Félix F, Echegaray M, Siciliano S, Di Beneditto AP, Flach L, Viddi F, Avila IC, Herrera JC, Tobon IC, Bolanos-Jimenez J, Moreno IB, Ott PH, Sanino GP, Castineira E, Montes D, Crespo E, Flores PAC, Haase B, Souza SMFM, Laeta M, Fragoso AB (2007) A preliminary overview of skin and skeletal diseases and traumata in small cetaceans from South American waters. Lat Am J Aquat Mamm 6:7–42

Vianna TS, Loch C, Castilho PV, Cremer MJ, Simões-Lopes CP (2016) Review of thirty-two years of toothed whale strandings in Santa Catarina. Southern Brazil (Cetacea: Odontoceti). Zoologia. https://doi.org/10.1590/S1984-4689zool-20160089

Viricel A, Rosel PE (2011) Evaluating the utility of cox1 for cetacean species identification. Marine Mammal Sci **28**:**37**–**62**. https://doi.org/10.1111/j.1748-7692.2010.00460.x

Vollmer NL, Ashe E, Brownell RL Jr, Cipriano F, Mead JG, Reeves RR, Soldevilla MS, Williams R (2019) Taxonomic revision of the dolphin genus *Lagenorhynchus*. Marine Mammal Sci 35:957–1057. https://doi.org/10.1111/mms.12573

Wada S, Oishi M, Yamada TK (2003) A newly discovered species of living baleen whale. Nature. 426:278–281. https://doi.org/10.1038/nature02103

Yamada TK, Kitamura S, Abe S, Tajima Y, Matsuda A, Mead JG, Matsuishi TF (2019) Description of a new species of beaked whale (Berardius) found in the North Pacific. *Sci Rep* 9:12723. https://doi.org/10.1038/s41598-019-46703-w

Zerbini NA, Secchi ER, Siciliano S, Simões-Lopes PC (1997) A review of the occurrence and distribution of whales of the Genus *Balaenoptera* along the Brazilian coast. Report Int Whaling Commis 47:407–417

Zerbini AN, Secchi ER, Bassoi M, Dalla Rosa L, Higa A, Sousa L, et al.(2004) Distribuição e abundância relativa de cetáceos na Zona Econômica Exclusiva da região sudeste-sul do Brasil. Série de Documentos Revizee-Score Sul. http://www.mma.gov.br/o-ministerio/organograma/item/7605-programa-revizee-s%C3%A9rie-de-documentos. Accessed 11 March 2020

Zhou X, Xu S, Yang Y, Zhou K, Yang G (2011) Phylogenomic analyses and improved resolution of Cetartiodactyla. Mol Phylogenet Evol 61:255–264. https://doi.org/10.1016/j.ympev.2011.02.009

Affiliations

Vanessa S. Silva[1] · Natália Skueresky[1] · Fernando Lopes[1] · Tabata K. Koch[1] · Paulo Henrique Ott[2,3] · Salvatore Siciliano[4] · André S. Barreto[5] · Eduardo R. Secchi[6] · Ana Carolina O. de Meirelles[7] · Vitor Luz Carvalho[7] · João C. G. Borges[8] · Daniel Danilewicz[3] · Ana Paula C. Farro[9] · Lupércio A. Barbosa[10] · S. José Martins Jr[11] · Camila Domit[12] · Inês Serrano[13] · Tiago Silva[14] · Cristine Trinca[14] · Miriam Marmontel[15] · Neusa Renata Emin-Lima[16] · Victor Hugo Valiati[1] · Eduardo Eizirik[14] · Larissa Rosa de Oliveira[1,3]

1 Universidade do Vale do Rio dos Sinos (UNISINOS), São Leopoldo, RS, Brazil

2 Universidade Estadual do Rio Grande do Sul (UERGS), Porto Alegre, RS, Brazil

3 Grupo de Estudos de Mamíferos Aquáticos do Rio Grande do Sul (GEMARS), Tôrres, RS, Brazil

4 Fundação Oswaldo Cruz (FIOCRUZ), Rio de Janeiro, RJ, Brazil

5 Universidade do Vale do Itajaí, Itajaí, SC, Brazil

6 Universidade Federal do Rio Grande (FURG), Rio Grande, RS, Brazil

7 Associação de Pesquisa e Preservação de Ecossistemas Aquáticos (Aquasis), Caucaia, CE, Brazil

8 Fundação Mamíferos Aquáticos (FMA), São Cristóvão, SE, Brazil

9 Departamento de Ciências Agrárias e Biológicas, CEUNES, Universidade Federal do Espírito Santo (UFES), São Mateus, ES, Brazil

10 Organização Consciência Ambiental (ORCA/ES), Guarapari, ES, Brazil

11 Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio)/Projeto Golfinho Rotador, Fernando de Noronha, PE, Brazil

12 Centro de Estudos do Mar, Universidade Federal do Paraná (UFPR), Pontal do Paraná, PR, Brazil

13 Instituto Chico Mendes de Conservação da Biodiversidade (ICMBIO), Estrada Estadual Bocaina, SP, Brazil

14 Pontifícia Universidade Católica do Rio Grande do Sul (PUCRS), Porto Alegre, RS, Brazil

15 Instituto de Desenvolvimento Sustentável Mamirauá, Tefé, AM, Brazil

16 Museu Paraense Emílio Goeldi, Grupo de Estudos de Mamíferos Aquáticos da Amazônia (GEMAM), Belém, PA, Brazil