First record of Ramari's beaked whale *Mesoplodon eueu* (Cetacea: Ziphiidae) for Uruguay

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Abstract

We report the first record of Ramari's beaked whale (*Mesoplodon eueu*) from the temperate Southwestern Atlantic. Our analysis is based on an adult female and a plausibly associated calf/juvenile that stranded on the coast of Canelones Department, Uruguay. The species of the two individuals was identified via a combination of morphometric and molecular mitochondrial data and provide new insights into the Ramari's beaked whale, including previously unknown polymorphisms in the mitochondrial genome and a re-estimated date of divergence from *Mesoplodon mirus* at 2.5902 Mya.

Introduction

Beaked whales (ziphiids) are diverse and wide-ranging, yet remain poorly understood. *Mesoplodon* exemplifies this contradiction: with 16 members, it is the most speciose cetacean genus (Committee on Taxonomy, 2022) but also amongst the most enigmatic large mammals on Earth (Jefferson *et al.*, 2015). Notable knowledge gaps persist regarding species distributions, abundance estimates and even basic biology, with several species having never been recorded alive (MacLeod *et al.*, 2006; Pitman, 2018). *Mesoplodon* occurs from cold subpolar latitudes to the tropics, but can be difficult to observe owing to a preference for deep-water habitats (Reeves *et al.*, 2003; MacLeod *et al.*, 2006).

Ramari's beaked whale (*Mesoplodon eueu,* Carroll *et al.*, 2021) is the most recently described mesoplodont with records from South Africa, Australia, and Aotearoa New Zealand. Until recently, *M. eueu* was thought to be a southern, antitropical population of the North Atlantic True's beaked whale (*Mesoplodon mirus* True, 1913), but molecular and morphological data now confirm a deep independent history warranting species status (Ross, 1969, 1984; MacLeod *et al.*, 2006; Carroll *et al.*, 2021).

A previously reported stranding of True's beaked whale in Brazil also plausibly represents *M. eueu*, which may therefore range across the Southern Hemisphere (Souza *et al.*, 2005); however, to date no South American records of Ramari's beaked whale have been genetically confirmed. Here, we provide the first such record, based on two stranded individuals from Uruguay, and explore the implications of our new molecular data for the diversity and evolutionary history of the species.

Materials and methods

Our analysis is based on two beaked whales that stranded in Canelones Department, Uruguay, in 2019 (Figure 1). On 27th October 2019, the fresh carcass (Code 2 of Pugliares *et al.*, 2007) of a 338 cm long female calf/juvenile was found on San Luis Beach (34°46′31.6″ S, 55°35′24.09″ W; Figure 2). Three days later, a 528 cm long adult female washed up on Marindia Beach (34°46′48.19″ S; 55°49′9.41″ W), 24 km west from the first individual. This specimen showed a moderate state of decomposition (Code 3) suggesting that it died some time prior to the stranding (Figure 3).

Biological information and several photographs were recorded for both specimens. The skulls of both specimens along with muscle, blubber and skin samples and – for the second stranding only – the stomach contents were deposited at the National Museum of Natural History (Montevideo) under registration numbers MNHN 8211 and 8212, respectively. Tissue samples of both specimens were preserved in 95% ethanol and stored in a freezer at −20°C. As far as the position of the carcasses on the beach permitted, body measurements were taken following Norris (1961).
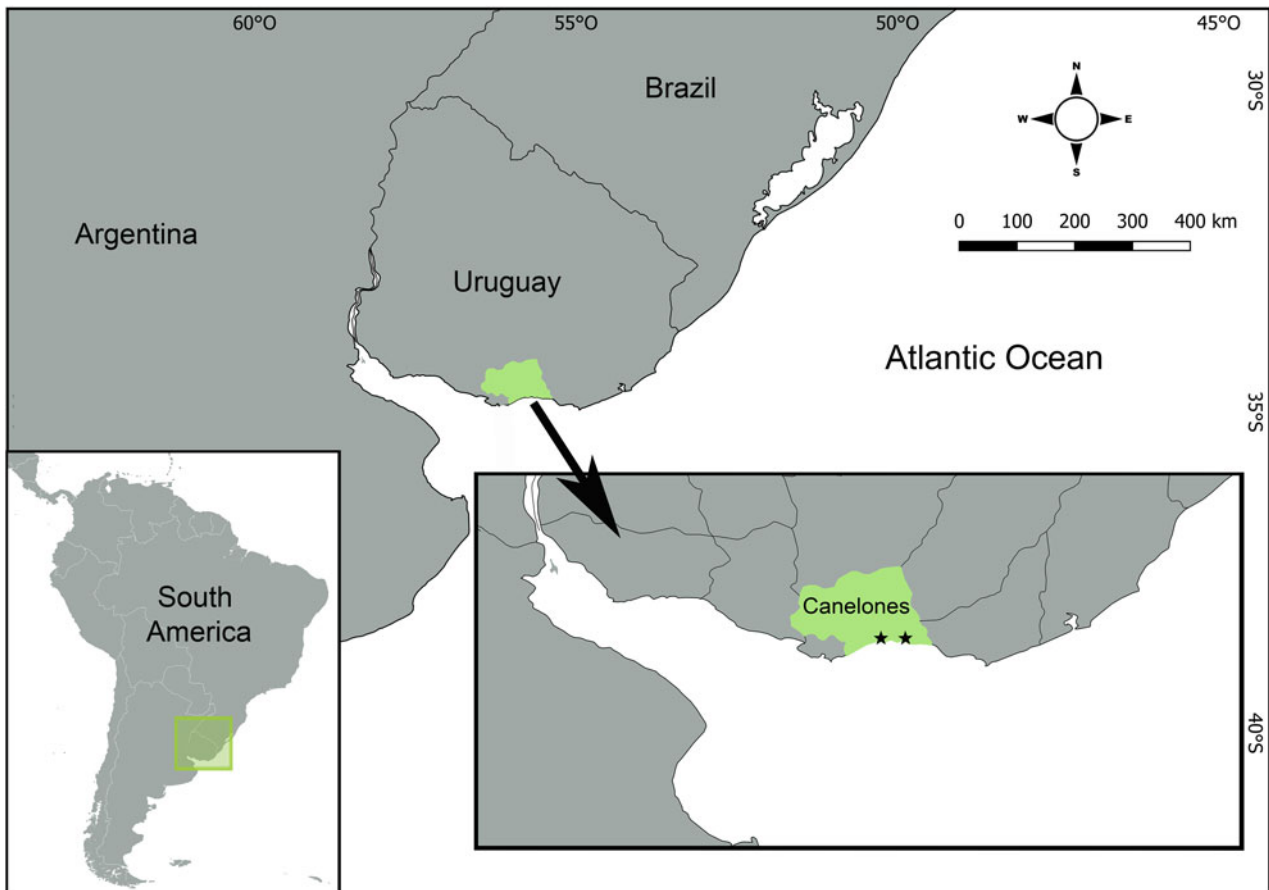
Figure 1. Location of the *Mesoplodon eueu* strandings in Canelones department (Uruguay), stars indicate the two stranding sites.

Figure 2. Left lateral view of the head (A) and ventral view (B) of a juvenile female of *Mesoplodon eueu* (MNHN 8211) stranded on the coast of Uruguay on 27th October 2019.

Figure 3. Dorsolateral view of an adult female *Mesoplodon eueu* (MNHN 8212) stranded on the coast of Uruguay on 30th October 2019.

Skull morphometrics

Following Carroll *et al.* (2021) we used eight measurements of the skull and mandible to test whether our individuals more closely resemble *M. eueu* or *M. mirus*. Measurements were taken to the nearest mm, adjusted for size by dividing them by the bizygomatic width, and log-transformed prior to further analysis. Finally, we combined our observations with those of Carroll *et al.* (2021) and summarized the entire dataset via principal component analysis (PCA) in PAST 4.03 (Hammer *et al.*, 2001).

DNA extraction, control region sequencing and genomic sequencing

Total genomic DNA was extracted from muscle following Medrano *et al.* (1990). The control region was sequenced using t-Pro (Dalebout *et al.*, 1998) and HS-5 primers (Okumura, 2004). The PCR cycling profile was the following: an initial denaturation at 94°C for 3 min, followed by 35 cycles of 94°C for 1 min, 60°C for 1 min, 72°C for 1 min, and a final extension at 72°C for 7 min. The amplified products were sequenced by MACROGEN (Seoul, Korea) using the Sanger sequencing method.

The genome of MNHN 8211 was sequenced on a DNBseq sequencing platform (BGITech Solutions, Hong Kong) using a 150 paired-end strategy and low coverage (1x ≈ 2.5 Gb, genome size of Gervais' beaked whale *Mesoplodon densirostris*; Yuan *et al.*, 2021). Adaptor clean-up and quality filtering were performed by BGI. Mitogenome assembly was carried out using Novoplasty (Dierckxsens *et al.*, 2017) with the control region

sequence acting as a seed. In addition, we assembled the mitogenome of MNHN 8211 via Bowtie2 (Langmead and Salzberg, 2012), Samtools 1.10 (Li *et al.*, 2009) and Trinity v. 2.6.6 (Grabherr *et al.*, 2011), using the mitogenome of *M. eueu* (GenBank accession number OK326893) as a reference. Both mitogenome assemblies were congruent and the average coverage of the entire mitochondrial genome was 748. The average Phred scores for MNHN 8211 and 8212 were 48.6 and 57.3, respectively. Control region sequences for both individuals and the annotated mitogenome of MNHN 8211 assembled by Novoplasty were deposited in Genbank as OP994180, OP994181, and OP994173, respectively.

Genetic analyses

We used sequences retrieved from GenBank to generate two data sets: one comprising the mitochondrial control region (CR) of the two stranded specimens, 49 individuals representing various species of *Mesoplodon* (*M. bidens*, *M. densirostris*, *M. eueu*, *M. europaeus*, *M. ginkgodens*, *M. grayi*, *M. mirus,* and *M. stejnegeri*), and two northern bottlenose whales that acted as outgroup; and one comprising the entire mitogenomes of MNHN 8211 and 25 additional individuals representing *M. bidens*, *M. eueu*, *M. europaeus*, *M. ginkgodens,* and *M. mirus* (Supplemental Tables S1 and S2).

CR sequences were aligned in Clustal W 1.8 (Thompson *et al.*, 1994) and then subjected to phylogenetic analysis via Maximum Likelihood (ML) and Bayesian inference (BI). JModelTest v.2.1.17 (Darriba *et al.*, 2012) identified TPM3uf + I as the best-fitting nucleotide substitution model based on the Bayesian information

criterion (Schwarz, 1978). The ML analysis was carried out in PhyML 3.1 (Guindon and Gascuel, 2003) using NNI (fast-nearest neighbour interchange search) and 1000 bootstrap pseudoreplicates to estimate branch support. BI was implemented in MrBayes 3.2.7 (Ronquist *et al.*, 2012) on the CIPRES Portal (Miller *et al.*, 2010) and comprised two Markov chains in twelve separate runs of 20 million generations. Genetic differentiation between our specimens and other *Mesoplodon* spp. was assessed by computing pairwise *P*-distances in MEGA v. 11 (Kumar *et al.*, 2018).

Divergence times were estimated based on the mitogenomes, including protein-coding genes (split by codon position), transfer and ribosomal RNA genes, and the D-loop region. Substitution models were determined via PartitionFinder2 (Lanfear *et al.*, 2017) and subsets (Supplemental Table S3) linked with a relaxed clock log normal and a linked Yule tree model. We implemented three calibration points derived from the divergence dating analysis of Carroll *et al.* (2021), (Supplemental Table S4). The analysis was run in BEAST v.2.6.7 (Bouckaert *et al.*, 2019) in three separate runs of 15 million generations, sampled every 10,000 generations. The results were then combined in Log Combiner (Bouckaert *et al.*, 2019) after a 10% burn-in, convergence assessed via Tracer v1.7 (Rambaut *et al.*, 2018), and a Maximum Clade Credibility summary tree calculated via TreeAnnotator (Bouckaert *et al.*, 2019) with a burn-in of 20%. Finally, we estimated the mitochondrial nucleotide diversity (π) of individuals identified as *M. eueu* and *M. mirus* using DnaSP v.6 (Rozas *et al.*, 2017).

Results and discussion

External appearance

Ramaris's and True's beaked whales cannot be consistently distinguished based on their external appearance (Carroll *et al.*, 2021). Both share with our specimens the presence of a proportionally small head with a pronounced forehead bulge, a relatively short but distinct beak, a straight mouth line, and a single pair of teeth at the tip of the mandible (Supplementary Figure S1). As is normal in females (Moore, 1968), the teeth in MNHN 8211 and 8212 have not erupted.

The overall body colour of both species appears to be one of basic countershading (medium grey on top, lighter grey on the bottom), in addition to a dark patch around the eye and an area of whiter pigmentation that extends from the anus to the genital slit (Mead, 1989; Pitman, 2018; Carroll *et al.*, 2021). The same pattern occurs in our stranded specimens, albeit less clearly so in MNHN 8212 owing to its advanced state of decomposition. In some individuals of *M. eueu* a pale area stretches from the dorsal fin back towards the flukes (MacLeod, 2018; Carroll *et al.*, 2021). A similar patch can be seen in MNHN 8212 but not MNHN 8211 (Figure 4), suggesting ontogenetic variation in coloration patterns as observed in other ziphiids (Mead, 2009).

Skull morphometrics

The first two principal components of our PCA account for 83.8% of the variance and place our stranded individuals either side of the morphospace occupied by *M. eueu* (Table 1; Figure 5). Principal component 1 separates MNHN 8211 from all other specimens, with its shorter rostrum and mandibular symphysis likely reflecting its immature state. MNHN 8212 is located roughly halfway between the previously defined morphospace areas of *M. eueu* and *M. mirus*. Overall, these results are consistent with – though not conclusive proof of – both of our specimens representing *M. eueu*.

Figure 4. Caudal fins of both *Mesoplodon eueu* specimens stranded, dashed lines indicate the pale area over the peduncle that extends towards the flukes on MNHN 8212 (A) which is absent on MNHN 8211 (B).

Genetic analyses

The CR sequences of MNHN 8211 and 8212 are identical, suggesting that they are closely related. We hypothesize that they represent a mother-calf dyad, given that (i) one is an adult female and the other a calf/juvenile, (ii) both stranded within days of each other and in geographical proximity, and (iii) the more advanced decay of the adult (found three days later), which in turn suggests

Table 1. Cranial measurements taken in *Mesoplodon eueu* specimens stranded in Uruguay

	MNHN 8211	MNHN 8212
CBL	602.7	803.3
CH	247	330
RL	342.3	470.3
RW	174	204
PFW	110.3	118.3
PCW	137.3	159
BZW	274.7	343.7
ML	505.3	682.7
SL	99.7	185.3

CBL, Condylobasal length; CH, Cranial height; RL, Rostrum length; RW, Rostrum width between antorbital notches; PFW, Premaxillary sac fossa width; PCW, Width across prenarial crest; BZW, Bizygomatic width; ML, Mandible length; SL, Symphysis length.
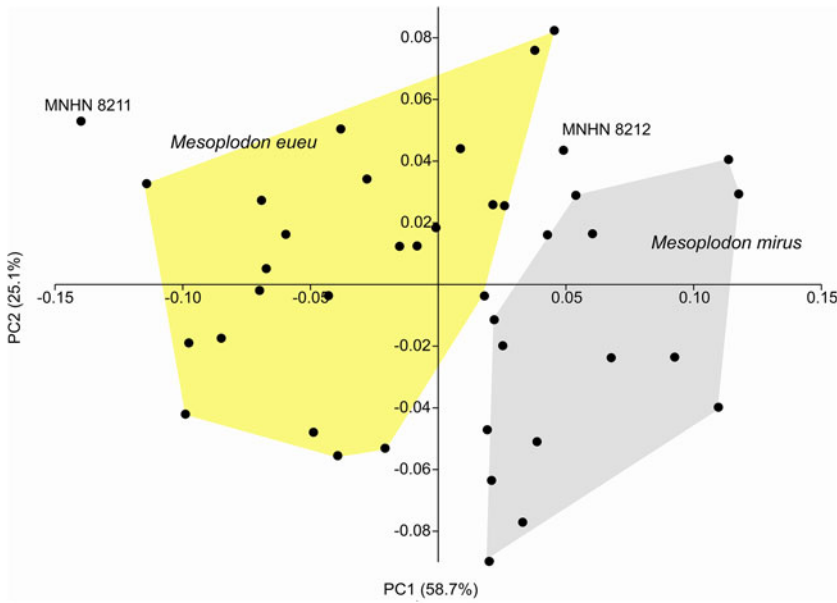All measurements are in mm

Figure 5. Principal component analysis of eight cranial and mandibular measurements shows that the two stranded Mesoplodon specimens from Uruguay (MNHN 8211 and 8212) plausibly cluster with *M. eueu*. Comparative data from Carroll et al. (2021).

that both may have died at a similar time. Alternatively, they could belong to the same population.

Breeding knowledge of beaked whales is scarce but the lactation period is thought to be of one to several years of duration (MacLeod, 2018). In some species it has been estimated to last from 3 to 5 years, and weaning occurs when the calf approximately doubles its size at birth (MacLeod and D'Amico, 2006; Feyrer et al., 2020). The size at birth varies among species but offspring of some beaked whales range from 190 to 460 cm (Ferguson et al., 2023), specifically for *M. mirus* a neonate of 220 cm of length has been reported (Ross, 1984). Taking this information into account and given the body length recorded on MNHN 8211, we suggest that this individual was still dependent on its mother.

Phylogenetic analysis of the CR data clusters our specimens with Ramari's beaked whales and, consistent with our morphometric results, strongly supports their referral to *M. eueu* (Figure 6). The specimens thus correspond to the first confirmed record of this species from Uruguay and the Southwest Atlantic. Furthermore, it is probable that the previously reported stranding of True's beaked whale from Southeastern Brazil (Souza et al., 2005) may also represent *M. eueu*, given the currently known geographic distribution for *M. mirus* and *M. eueu* and that the latter was described after the stranding recorded in Brazil. This would imply an extension of the distribution range of *M. eueu* to the tropics.

As found previously (Carroll et al., 2021), we recover *M. mirus* as sister to *M. eueu*. The *P*-distance between the Uruguayan
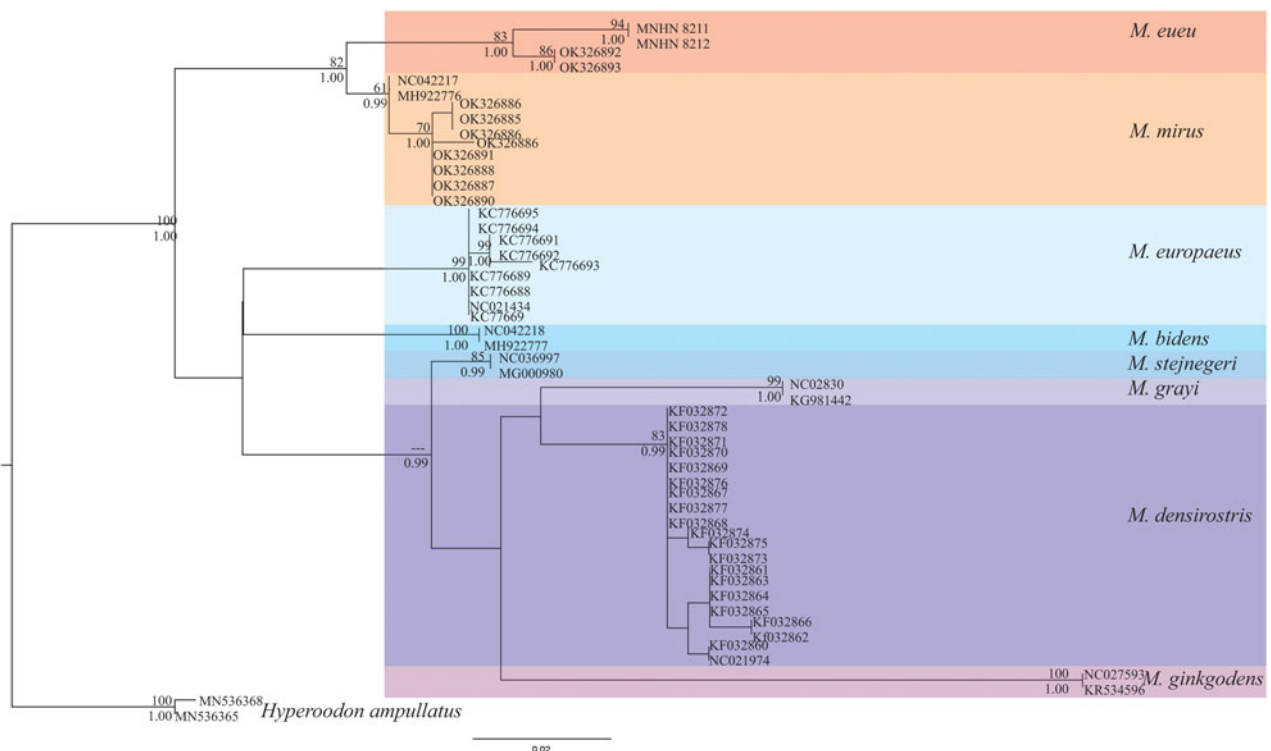

Figure 6. Bayesian phylogeny of Mesoplodon based on 51 mitochondrial control regions. Values above branches are ML bootstrap support, those below are Bayesian posterior probabilities.

individuals and other members of *M. eueu* is 0.0208 (variance = 0.0086), and that between the same specimens and *M. mirus* is 0.0432 (variance = 0.0105). Mitogenome analysis dates the last common ancestor of *M. eueu* to 0.8606 Ma (95% HPD: 0.118–1.7422 Ma) and the divergence of *M. eueu* from *M. mirus* to 2.5902 Ma (1.4201–3.9211 Ma; Supplementary Figure S2).

Our divergence time estimates somewhat predate those of Carroll *et al.* (2021) and reveal greater genetic diversity within Ramari's beaked whales than previously thought. This is reflected in the notable genetic distance between our individuals and previously analysed specimens of *M. eueu*. Specifically, we found a total of 164 substitutions between the mitochondrial genome of MNHN 8211 and the *M. eueu* sequences of Carroll *et al.* (2021), compared to 814 substitutions between *M. eueu* (including MNHN 8211) and *M. mirus*. With the inclusion of MNHN 8211, the mitochondrial nucleotide diversity of *M. eueu* now stands at 0.0070 (standard deviation = 0.0031). This is notably higher than in *M. mirus* (0.0024; SD = 0.0003), confirming the pattern previously described, and suggests a greater effective population size and/or possible population structuring, as seen in other ziphiids like bottlenose whales (Ellegren and Galtier, 2016).

Conclusion

We report the first confirmed record of Ramari's beaked whale from Uruguay and the wider Southwest Atlantic. Our findings expand the range and genetic diversity of this recently described species and suggest possible population structuring. Further samples from across the range of Ramari's beaked whale are needed to test this idea. Identifying a new species of marine mammal in Uruguayan waters calls for further resource allocation both to stranding responses and long-term systematic surveys of the regional coast.

References

Bouckaert R, Vaughan TG, Barido-Sottani J, Duchêne S, Fourment M, Gavryushkina A, Heled J, Jones G, Kühnert D, De Maio N and Matschiner M (2019) BEAST 2.5: an advanced software platform for Bayesian evolutionary analysis. *PLoS Computational Biology* **15**, e1006650.

Carroll EL, McGowen MR, McCarthy ML, Marx FG, Aguilar N, Dalebout ML, Dreyer S, Gaggiotti OE, Hansen SS, van Helden A, Onoufriou AB, Baird RW, Baker S, Berrow S, Cholewiak D, Claridge R, **Constantine R, Davison NJ, Eira C, Fordyce E, Gatesy J, Greg Hofmeyr GJ, Vidal M, Mead JG, Mignucci-Giannoni AA, Morin PA, Reyes C, Rogan E, Rosso M, Silva MA, Springer MS, Steel D and Olsen MT** (2021) Speciation in the deep: genomics and morphology reveal a new species of beaked whale *Mesoplodon eueu*. *Proceedings of the Royal Society B* **288**, 20211213.

Committee on Taxonomy (2022) List of marine mammal species and subspecies. Society for Marine Mammalogy. Available at www.marinemammalscience.org (Accessed 29 March 2023).

Dalebout ML, van Helden A, Van Waerebeek K and Baker CS (1998) Molecular genetic identification of southern hemisphere beaked whales (Cetacea: Ziphiidae). *Molecular Ecology* **7**, 687–694.

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

Dierckxsens N, Mardulyn P and Smits G (2017) NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Research* **45**, e18–e18.

Ellegren H and Galtier N (2016) Determinants of genetic diversity. *Nature Reviews Genetics* **17**, 422–433.

Ferguson SH, Higdon JW, Schmidt C, Pomerleau C and Matthews CJ (2023) Investigating the relationship between body shape and life history traits in toothed whales: can body shape predict fast-slow life histories? *Evolutionary Biology* **50**, 1–18.

Feyrer LJ, Zhao ST, Whitehead H and Matthews CJ (2020) Prolonged maternal investment in northern bottlenose whales alters our understanding of beaked whale reproductive life history. *PLoS One* **15**, e0235114.

Grabherr MG, Haas BJ, Yassour M, Levin JZ, Thompson DA, Amit I, Adiconis X, Fran L, Raychowdhury R, Zeng Q, Chen Z, Mauceli E, Hacohen N, Gnirke A, Rhind N, di Palma F, Birren BW, Nusbaum C, Lindblad-Toh K, Friedman N and Regev A (2011) Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nature Biotechnology* **29**, 644–652.

Guindon S and Gascuel O (2003) A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Systematic Biology* **52**, 696–704.

Hammer Ø, Harper DA and Ryan PD (2001) PAST: paleontological statistics software package for education and data analysis. *Palaeontologia Electronica* **4**, 9.

Jefferson TA, Pitman RL and Webber MA (2015) *Marine Mammals of the World*, 2nd Edn. Cambridge, USA: Elsevier.

Kumar S, Stecher G, Li M, Knyaz C and Tamura K (2018) MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution* **35**, 1547–1549.

Lanfear R, Frandsen PB, Wright AM, Senfeld T and Calcott B (2017) PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Molecular Biology and Evolution* **34**, 772–773.

Langmead B and Salzberg SL (2012) Fast gapped-read alignment with Bowtie 2. *Nature methods* **9**, 357–359.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G and Durbin R (2009) 1000 Genome project data processing subgroup. 2009. The sequence alignment/map format and SAMtools. *Bioinformatics (Oxford, England)* **25**, 2078–2079.

MacLeod CD (2018) Beaked whales, overview. In Wursig B, Thewissen JGM and Kovacs KM (eds), *Encyclopedia of Marine Mammals*. London, UK: Elsevier, pp. 80–83.

MacLeod CD and D'Amico A (2006) A review of beaked whale behaviour and ecology in relation to assessing and mitigating impacts of anthropogenic noise. *Journal of Cetacean Research Management* **7**, 211–221.

MacLeod CD, Perrin WF, Pitman R, Barlow J, Ballance L, D'Amico A, Gerrodette T, Joyce G, Mullin KD and Palka DL (2006) Known and inferred distributions of beaked whale species (Cetacea: Ziphiidae). *Journal of Cetacean Research and Management* **7**, 271–286.

Mead JG (1989) Beaked whales of the genus Mesoplodon. In Ridgway SH and Harrison R (eds), *Handbook of Marine Mammals*. Cambridge, USA: Academic Press, pp. 349–430.

Mead JG (2009) Beaked whales, overview: Ziphiidae. In Wursig B, Thewissen JGM, Kovacs KM (eds), *Encyclopedia of Marine Mammals*. Burlington, USA: Academic Press, pp. 94–97.

Medrano JF, Aasen E and Sharrow L (1990) DNA extraction from nucleated red blood cells. *Biotechniques* **8**, 43.

Miller MA, Pfeiffer W and Schwartz T (2010) Creating the CIPRES science gateway for inference of large phylogenetic trees. In Miller MA (ed.), *Proceedings of the Gateway Computing Environments Workshop (GCE)*. New Orleans: IEEE Press, pp. 1–8.

Moore JC (1968) Relationships among the living genera of beaked whales, with classification, diagnoses and keys. *Fieldiana Zoology* **53**, 206–298.

Norris KS (1961) Standardized methods for measuring and recording data on the smaller cetaceans. The committee on marine mammals American society of mammalogists. *Committee on Marine Mammals Journal of Mammalogy Cetacean* **42**, 471–476.

Okumura H (2004) Complete sequence of mitochondrial DNA control region of the Japanese serow *Capricornis crispus* (Bovidae: Caprinae). *Mammal Study* **29**, 137–145.

Pitman (2018) Mesoplodon beaked whales. In Wursig B, Thewissen JGM and Kovacs KM (eds), *Encyclopedia of Marine Mammals*. London, UK: Elsevier, pp. 595–602.

Pugliares KR, Bogomolni A, Touhey KM, Herzig SM and Harry CT (2007) Marine mammal necropsy: an introductory guide for stranding responders and field biologists. Woods Hole, MA., *Woods Hole Oceanographic Institution*, 1–133. (WHOI Technical Report 2007-06). https://doi.org/10.1575/1912/1823

Rambaut A, Drummond AJ, Xie D, Baele G and Suchard MA (2018) Posterior summarization in Bayesian phylogenetics using Tracer 1.7. *Systematic Biology* **67**, 901–904.

Reeves RR, Smith BD, Crespo EA and di Sciara GN (2003) Dolphins, Whales and Porpoises: 2002–2010 Conservation Action Plan for the World's Cetaceans. IUCN/SSC Cetacean Specialist Group. IUCN, Gland, Switzerland and Cambridge, UK.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA and Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* **61**, 539–542.

Ross GJB (1969) Evidence for a southern breeding population of True's beaked whale. *Nature* **222**, 585.

Ross GJB (1984) The smaller cetaceans of the south-east coast of Southern Africa. *Annals of the Cape Provincial Museums (Natural History)* **15**, 173–410.

Rozas J, Ferrer-Mata A, Sánchez-DelBarrio JC, Guirao-Rico S, Librado P, Ramos-Onsins SE and Sánchez-Gracia A (2017) DnaSP 6: DNA sequence polymorphism analysis of large data sets. *Molecular Biology and Evolution* **34**, 3299–3302.

Schwarz G (1978) Estimating the dimension of a model. *The Annals of Statistics* **6**, 461–464.

Souza SP, Siciliano S, Cuenca S and Sanctis B (2005) A True's beaked whale (*Mesoplodon mirus*) on the coast of Brazil: adding a new beaked whale species to the Western Tropical Atlantic and South America. *Latin American Journal of aquatic mammals* **4**, 129–136.

Thompson JD, Higgins DG and Gibson TJ (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Research* **22**, 4673–4680.

True FW (1913) Diagnosis of a new beaked whale of the genus Mesoplodon from the coast of North Carolina. *Smithsonian Miscellaneous Collections* **60**, 1–2.

Yuan Y, Zhang Y, Zhang P, Liu C, Wang J, Gao H, Hoelzel AR, Seim I, Lv M, Lin M, Dong L, Gao H, Yang Z, Caruso F, Lin W, da Fonseca RR, Wang D, Wang X, Rasmussen MH, Liu M, Zheng J, Zhao L, Campos PF, Kang H, Iversen M, Song Y, Guo X, Guo J, Qin Y, Pan S, Xu Q, Meng L, A Y, Liu S, Lee SM-Y, Liu X, Xu X, Yang H, Fan G, Wang K and Li S (2021) Comparative genomics provides insights into the aquatic adaptations of mammals. *Proceedings of the National Academy of Sciences* **118**, e2106080118.