**Supplementary material for**

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

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**This document contains Supplementary table S1-S4 and figures S1-S2.**

**Table S1:** GenBank accession numbers of control region sequences from Mesoplodon specimens used in phylogenetic analyses.

|  |  |
| --- | --- |
| Accession Number Genbank | Species |
| MH922777.1 | *M. bidens* |
| NC042218.1 | *M. bidens* |
| KF032860.2 | *M. densirostris* |
| NC021974.2 | *M. densirostris* |
| KF032871.2 | *M. densirostris* |
| KF032861.2 | *M. densirostris* |
| KF032862.2 | *M. densirostris* |
| KF032863.2 | *M. densirostris* |
| KF032864.2 | *M. densirostris* |
| KF032869.2 | *M. densirostris* |
| KF032870.2 | *M. densirostris* |
| KF032867.2 | *M. densirostris* |
| KF032868.2 | *M. densirostris* |
| KF032872.2 | *M. densirostris* |
| KF032873.1 | *M. densirostris* |
| KF032874.2 | *M. densirostris* |
| KF032875.2 | *M. densirostris* |
| KF032876.2 | *M. densirostris* |
| KF032877.2 | *M. densirostris* |
| KF032878.2 | *M. densirostris* |
| KF032865.1 | *M. densirostris* |
| KF032866.2 | *M. densirostris* |
| KC776688.2 | *M. europaeus* |
| NC021434.2 | *M. europaeus* |
| KC776689.2 | *M. europaeus* |
| KC776690.2 | *M. europaeus* |
| KC776691.2 | *M. europaeus* |
| KC776692.2 | *M. europaeus* |
| KC776693.2 | *M. europaeus* |
| KC776694.2 | *M. europaeus* |
| KC776695.1 | *M. europaeus* |
| KR534596.1 | *M. ginkgodens*  |
| NC027593.1 | *M. ginkgodens*  |
| KF981442.1 | *M. grayi* |
| NC023830.1 | *M. grayi* |
| MH922776.1 | *M. mirus* |
| NC042217.1 | *M. mirus* |
| OK326891.1 | *M. mirus* |
| OK326890.1 | *M. mirus* |
| OK326889.1 | *M. mirus* |
| OK326888.1 | *M. mirus* |
| OK326887.1 | *M. mirus* |
| OK326886.1 | *M. mirus* |
| OK326885.1 | *M. mirus* |
| OK326884.1 | *M. mirus* |
| OK326893.1 | *M. eueu* |
| OK326892.1 | *M. eueu* |
| MG000980.1 | *M. stejnegeri* |
| NC036997.1 | *M. stejnegeri* |

**Table S2.** GenBank accession numbers of whole mitochondrial genome from Mesoplodon specimens used in divergence time estimation analysis.

|  |  |
| --- | --- |
| Accession Number Genbank | Species |
| MH922777.1 | *M. bidens* |
| NC042218.1 | *M. bidens* |
| KC776688.2 | *M. europaeus* |
| NC021434.2 | *M. europaeus* |
| KC776689.2 | *M. europaeus* |
| KC776690.2 | *M. europaeus* |
| KC776691.2 | *M. europaeus* |
| KC776692.2 | *M. europaeus* |
| KC776693.2 | *M. europaeus* |
| KC776694.2 | *M. europaeus* |
| KC776695.1 | *M. europaeus* |
| KR534596.1 | *M. ginkgodens*  |
| NC027593.1 | *M. ginkgodens*  |
| MH922776.1 | *M. mirus* |
| NC042217.1 | *M. mirus* |
| OK326891.1 | *M. mirus* |
| OK326890.1 | *M. mirus* |
| OK326889.1 | *M. mirus* |
| OK326888.1 | *M. mirus* |
| OK326887.1 | *M. mirus* |
| OK326886.1 | *M. mirus* |
| OK326885.1 | *M. mirus* |
| OK326884.1 | *M. mirus* |
| OK326893.1 | *M. eueu* |
| OK326892.1 | *M. eueu* |

**Table S3:** Subsets of the mitochondrial genome identified with PartitionFinder2 (Lanfear et al., 2017) and evolutive models identified and used on BEAST v.2.6.7 (Bouckaert et al. 2014).

| Subset | Partition names | Model | Number of sites | Beast model used |
| --- | --- | --- | --- | --- |
| 1 | ND6\_pos2 | TRN+G+X | 3855 | TN93 |
| tRNA-P (CCA) |
| tRNA-L (CTA) |
| tRNA-G (GGA) |
| tRNA-R (CGA) |
| tRNA-D (GAC) |
| tRNA-K (AAA) |
| tRNA-I (ATC) |
| tRNA-H (CAC) |
| tRNA-S (AGC) |
| tRNA-M (ATG) |
| tRNA-N (AAC) |
| tRNA-V (GTA) |
| tRNA-L (TTA) |
| tRNA-Q (CAA) |
| tRNA-F (TTC) |
| 12s |
| tRNA-E (GAA) |
| 16s |
| 2 | tRNA-A (GCA) | TRN+G+X | 3002 | TN93 |
| COX3\_pos1 |
| tRNA-T (ACA) |
| tRNA-S (TCA) |
| ND4L\_pos1 |
| CYTB\_pos1 |
| ND3\_pos1 |
| tRNA-W (TGA) |
| ND2\_pos1 |
| ATP6\_pos1 |
| ND5\_pos1 |
| ND4pos2 |
| 3 | ND4L\_pos2 | HKY+I+X | 2023 | HKY |
| ND2\_pos2 |
| ND3\_pos2 |
| ATP6\_pos2 |
| ND5\_pos2 |
| ND6\_pos3 |
| ND4\_pos3 |
| 4 | ATP8\_pos3 | TRN+G+X | 1755 | TN93 |
| ND6\_pos1 |
| ND4\_pos1 |
| ND4L\_pos3 |
| ATP6\_pos3 |
| COX2\_pos3 |
| COX1\_pos3 |
| 5 | ATP8\_pos1 | HKY+G+X | 593 | HKY |
| COX3\_pos3 |
| ATP8\_pos2 |
| 6 | tRNA-C (TGC) | TRNEF+G | 1164 | TN93 |
| COX1\_pos1 |
| COX2\_pos1 |
| ND1\_pos2 |
| 7 | COX1\_pos2 | HKY+I | 1445 | HKY |
| COX2\_pos2 |
| CYTB\_pos2 |
| ND1\_pos2 |
| 8 | tRNA-Y (TAC) | HKY+I+G+X | 1436 | HKY |
| D-loop |
| COX3\_pos2 |
| 9 | ND5\_pos3 | TRN+G+X | 1763 | TN93 |
| CYTB\_pos3 |
| ND3\_pos3 |
| ND1\_pos3 |
| ND2\_pos3 |

**Table S4.** Time to the Most Recent Common Ancestor node priors used to calibrate divergence time analysis. Mean Age (mya) is based on the analysis of Carroll et al. (2021); see for more information on how these were derived.

|  |  |  |
| --- | --- | --- |
| **Priors** | **Mean Age (mya)** | **Standard Deviation (mya)** |
| *M.mirus + M. eueu + M. europaeus + M. ginkgodens + M. bidens*  | 7.02 | 6.20-7.84 |
| *M.mirus + M. eueu + M. europaeus + M. ginkgodens*  | 5.40 | 4.66-6.14 |
| *M.mirus + M. eueu mitogenomes + M. europaeus*  | 4.66 | 4.08-5.24 |

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**Figure S1.** Dorsal view of skulls and lateral view of left mandible of the *M. eueu* stranded in Uruguay (left MNHN 8211, right MNHN 8212).



**Figure S2.** Mitogenome coalescence tree analysis of BEAST v.2.6.7 (Bouckaert et al. 2014). Red circles mark calibration nodes (Table S4). Purple boxes in nodes show 95% HPD (highest posterior density). The bottom bar shows millions of years before present. Bars on the left indicate the Mesoplodon species.