GOVERNMENT OF WESTERN AUSTRALIA
Department of **Biodiversity, Conservation and Attractions**
Biodiversity and Conservation Science

Report on genetic identification of unknown beaked whale species tissue samples T023798 and T023800 (Fauna lab)

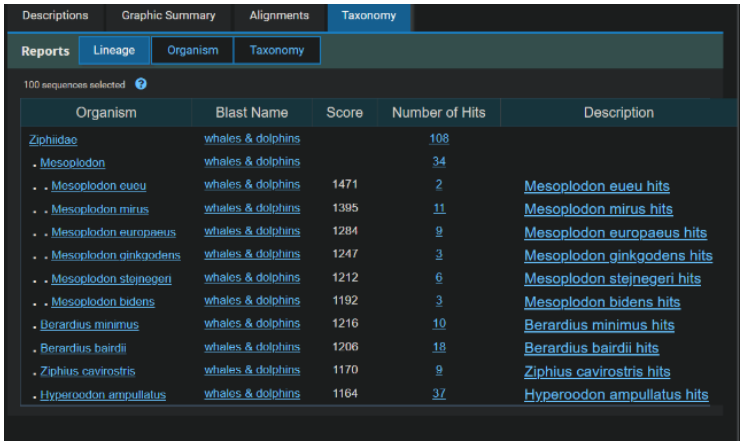
MA Millar 03/02/2026

The tissue samples (T023798 and T023800) were collected from animals stranded at Yeagerup Beach, Western Australia in December 2025 and received from Tiana Jones, DBCA, in December 2025. T023798 was from a mature adult male and T023800 from a juvenile female. The samples were confirmed via sequencing analysis to be a Ramari's beaked whale or *Mesoplodon eueu*.

DNA was extracted from blubber tissue samples using a TNES extraction method. The Displacement Loop primers Wada-D-Loop Forward/Wada-D-Loop Reverse were used to amplify non-coding mitochondrial D-Loop DNA using a Shaw hot start PCR program. This region produced a strong single PCR product. The PCR product was sequenced using the same Forward and Reverse primers at the Western Australian State Agricultural Biotechnology Centre (SABC) Murdoch University. Sequence data was edited, Forward and Reverse sequences aligned and a consensus sequences obtained using the Geneious sequence alignment editor.

The sequenced regions produced clean sequence reads of 1777bp (seq1) and 1775bp (seq2) respectively. The sequence regions were queried using the blastn suite (megablast) for highly similar sequences (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

The queried sequences were significantly aligned to 108 and 110 sequences of the Ziphidiidae family of cetaceans respectively. For seq1 there were 34 sequence alignments with 6 different Mesoplodon species, 28 with Cuvier's beaked whale, *Ziphius cavirostris*, 9 with 2 different Berardius species and 37 with the Northern bottlenose whale, *Hyperoodon ampullatus*, (Fig 1). Of the sequences producing significant alignment, the top 2 with the highest Maximum Scores, highest Total Scores, highest Query Coverages, lowest E values, and highest Percent Identities were from Ramari's beaked whale, *Mesoplodon eueu* (Fig 2).



Descriptions | Graphic Summary | Alignments | Taxonomy

Reports | Lineage | Organism | Taxonomy

100 sequences selected

Organism	Blast Name	Score	Number of Hits	Description
Ziphiidae	whales & dolphins		108	
. Mesoplodon	whales & dolphins		34	
. . Mesoplodon eueu	whales & dolphins	1471	2	Mesoplodon eueu hits
. . Mesoplodon mirus	whales & dolphins	1395	11	Mesoplodon mirus hits
. . Mesoplodon europaeus	whales & dolphins	1284	9	Mesoplodon europaeus hits
. . Mesoplodon ginkgodens	whales & dolphins	1247	3	Mesoplodon ginkgodens hits
. . Mesoplodon stejnegeri	whales & dolphins	1212	6	Mesoplodon stejnegeri hits
. . Mesoplodon bidens	whales & dolphins	1192	3	Mesoplodon bidens hits
. Berardius minimus	whales & dolphins	1216	10	Berardius minimus hits
. Berardius bairdii	whales & dolphins	1206	18	Berardius bairdii hits
. Ziphius cavirostris	whales & dolphins	1170	9	Ziphius cavirostris hits
. Hyperoodon ampullatus	whales & dolphins	1164	37	Hyperoodon ampullatus hits

Figure 1. Number of significant alignments (Hits) by taxon for tissue sample T023798.

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Biodiversity and Conservation Science

select all 100 sequences selected | GenBank | Graphics | Distance tree of results | MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Mesoplodon eueu voucher SWFSC Z34216 mitocho...	Mesopl...	1471	2905	98%	0.0	96.22%	16342	OK326892.1
Mesoplodon eueu voucher NMNZ MM003000 (MmiN...	Mesopl...	1459	2888	98%	0.0	96.00%	16342	OK326893.1
Mesoplodon mirus mitochondrion, complete genome	Mesopl...	1395	2759	97%	0.0	95.24%	16342	NC_042217.1
Mesoplodon mirus voucher USNM:MAMM:504724 m...	Mesopl...	1393	2750	97%	0.0	95.24%	16342	OK326888.1
Mesoplodon mirus voucher USNM:MAMM:571357 m...	Mesopl...	1393	2750	97%	0.0	95.24%	16342	OK326887.1
Mesoplodon mirus voucher MMI:301112 mitochondri...	Mesopl...	1393	2750	97%	0.0	95.24%	16342	OK326891.1
Mesoplodon mirus genome assembly, organelle: mit...	Mesopl...	1393	2755	97%	0.0	95.24%	16346	OZ205435.1
Mesoplodon mirus voucher USNM:MAMM:175019 m...	Mesopl...	1393	2750	97%	0.0	95.24%	16342	OK326890.1
Mesoplodon mirus voucher USNM:MAMM:504612 m...	Mesopl...	1387	2738	97%	0.0	95.13%	16342	OK326889.1
Mesoplodon mirus voucher USNM:MAMM:593609 m...	Mesopl...	1371	2711	97%	0.0	94.79%	16342	OK326886.1
Mesoplodon mirus voucher USNM:MAMM:594404 m...	Mesopl...	1371	2711	97%	0.0	94.79%	16342	OK326884.1
Mesoplodon mirus voucher USNM:MAMM:594039 m...	Mesopl...	1371	2711	97%	0.0	94.79%	16342	OK326885.1
Mesoplodon europaeus isolate SWFSC ID z0074259...	Mesopl...	1284	2533	97%	0.0	92.66%	16343	KC776693.2
Mesoplodon europaeus isolate SWFSC ID z0002698...	Mesopl...	1279	2522	97%	0.0	92.55%	16343	NC_021434.2
Mesoplodon europaeus isolate SWFSC ID z0074252...	Mesopl...	1273	2506	97%	0.0	92.44%	16343	KC776692.2
Mesoplodon europaeus isolate SWFSC ID z0004120...	Mesopl...	1267	2500	97%	0.0	92.32%	16343	KC776691.2
Mesoplodon europaeus isolate SWFSC ID z0002817...	Mesopl...	1267	2500	97%	0.0	92.32%	16343	KC776689.2
Mesoplodon europaeus isolate SWFSC ID z0003853...	Mesopl...	1267	2506	97%	0.0	92.35%	16344	KC776690.2
Mesoplodon europaeus isolate SWFSC ID z0074265...	Mesopl...	1264	2497	97%	0.0	92.25%	16345	KC776694.2
Mesoplodon europaeus isolate SWFSC ID z0094578...	Mesopl...	1262	2495	97%	0.0	92.24%	16340	KC776695.1
Mesoplodon ginkgodens SNH22005 mitochondrial D...	Mesopl...	1247	2463	96%	0.0	92.07%	892	LC870191.1
Mesoplodon ginkgodens voucher NMNS17594 mitoc...	Mesopl...	1240	2443	94%	0.0	91.81%	16339	NC_027593.1
Berardius minimus isolate Bsp0618 tRNA-Pro gene,...	Berardi...	1216	2386	100%	0.0	90.22%	1019	MK605248.1
Berardius minimus haplotype b2 tRNA-Pro gene, D-l...	Berardi...	1216	2386	100%	0.0	90.22%	1032	OL906296.1
Mesoplodon stejnegeri voucher CRI000090 mitocho...	Mesopl...	1212	2417	97%	0.0	91.20%	16349	NC_036997.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, c...	Mesopl...	1210	2386	96%	0.0	93.41%	877	LC017820.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, c...	Mesopl...	1210	2386	96%	0.0	93.41%	877	LC017819.1
Berardius minimus isolate Bsp0515 tRNA-Pro gene,...	Berardi...	1210	2375	100%	0.0	90.12%	1020	MK605247.1
Berardius minimus mitochondrial DNA, D-loop, comp...	Berardi...	1206	2382	99%	0.0	90.25%	931	AB572008.2
Berardius bairdii haplotype b3 tRNA-Pro gene, partia...	Berardi...	1206	2382	99%	0.0	90.25%	970	KT936579.1
Berardius minimus mitochondrial genes, tRNA-Pro,...	Berardi...	1206	2382	99%	0.0	90.25%	931	LC175773.1
Berardius minimus mitochondrial genes, tRNA-Pro,...	Berardi...	1206	2382	99%	0.0	90.25%	931	LC175772.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, c...	Mesopl...	1205	2375	96%	0.0	93.28%	877	LC017817.1
Berardius minimus mitochondrial DNA, D-loop, comp...	Berardi...	1201	2371	99%	0.0	90.14%	931	AB572007.2
Berardius bairdii haplotype b5 tRNA-Pro gene, partia...	Berardi...	1201	2371	99%	0.0	90.14%	970	KT936581.1
Berardius minimus mitochondrial DNA, D-loop, comp...	Berardi...	1195	2360	99%	0.0	90.03%	931	AB572006.2

Figure 2. Sequences producing significant alignments for tissue sample T023798.

For seq2 there were 58 sequence alignments with Mesoplodon species, 28 with Berardius species and 24 with *Ziphius cavirostris* (Fig 3). Of the sequences producing significant alignment, the top 2 with the highest Maximum Scores, highest Total Scores, highest Query Coverages, lowest E values, and highest Percent Identities were again from Ramari's beaked whale, *Mesoplodon eueu* (Fig 4).

Descriptions | Graphic Summary | Alignments | Taxonomy

Reports | Lineage | Organism | Taxonomy

100 sequences selected

Organism	Blast Name	Score	Number of Hits	Description
Ziphiidae	whales & dolphins		110	
. Mesoplodon	whales & dolphins		58	
. . Mesoplodon eueu	whales & dolphins	1445	2	Mesoplodon eueu hits
. . Mesoplodon mirus	whales & dolphins	1358	11	Mesoplodon mirus hits
. . Mesoplodon europaeus	whales & dolphins	1254	9	Mesoplodon europaeus hits
. . Mesoplodon ginkgodens	whales & dolphins	1219	3	Mesoplodon ginkgodens hits
. . Mesoplodon stejnegeri	whales & dolphins	1199	6	Mesoplodon stejnegeri hits
. . Mesoplodon bidens	whales & dolphins	1181	3	Mesoplodon bidens hits
. . Mesoplodon grayi	whales & dolphins	1153	14	Mesoplodon grayi hits
. . Mesoplodon densirostris	whales & dolphins	1138	10	Mesoplodon densirostris hits
. Berardius minimus	whales & dolphins	1170	10	Berardius minimus hits
. Ziphius cavirostris	whales & dolphins	1170	24	Ziphius cavirostris hits
. Berardius bairdii	whales & dolphins	1170	18	Berardius bairdii hits

Figure 3. Number of significant alignments (Hits) by taxon for tissue sample T023800.

Descriptions | Graphic Summary | Alignments | Taxonomy

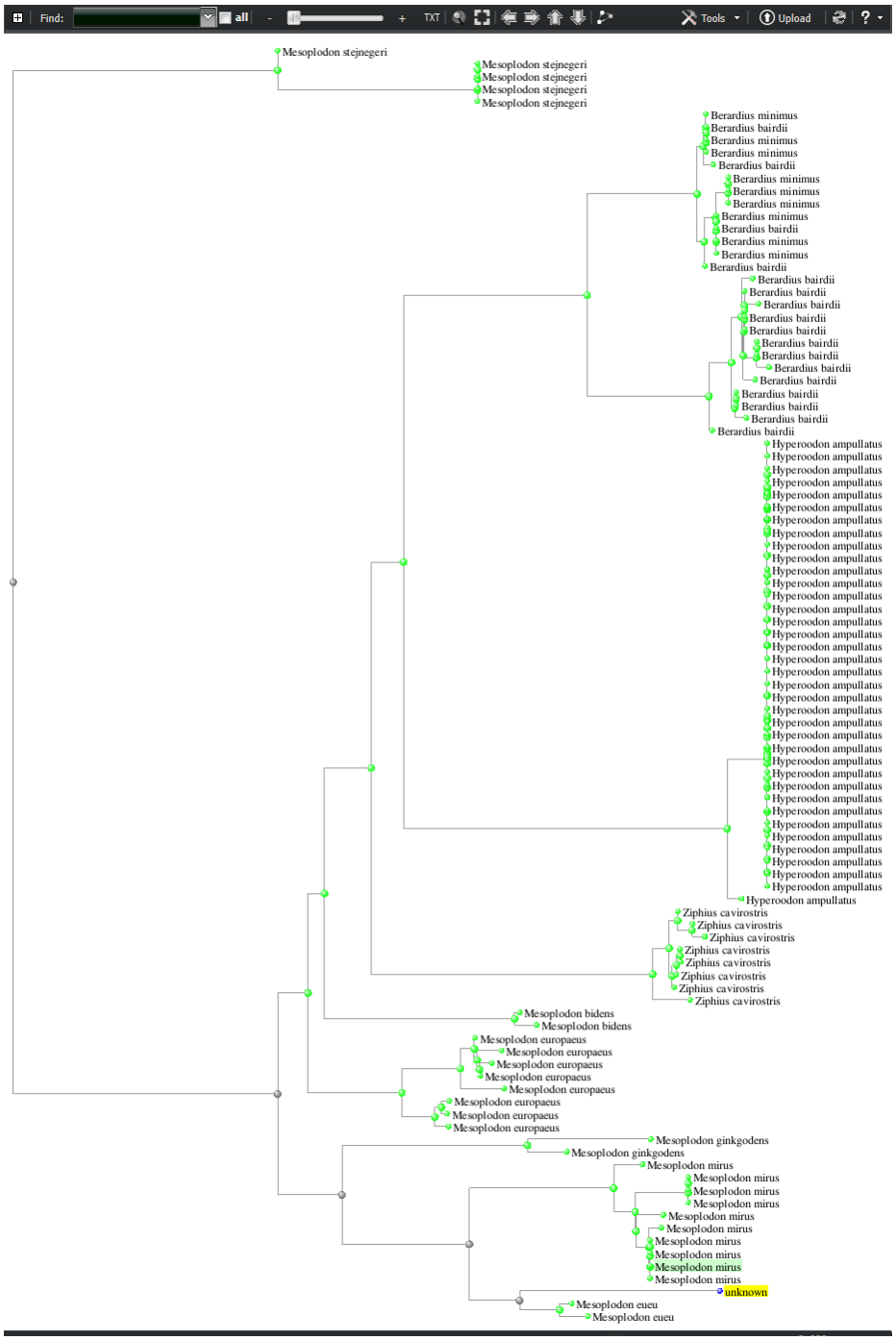
Sequences producing significant alignments Download Select columns Show 100

select all 100 sequences selected GenBank Graphics Distance tree of results MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Mesoplodon eueu voucher NMNZ MM003000 (MmiNZ01) mitochondrion, comp...	Mesoplodon...	1445	2851	97%	0.0	98.42%	16342	OK326893.1
Mesoplodon eueu voucher SWFSC Z34216 mitochondrion, complete genome	Mesoplodon...	1441	2847	97%	0.0	98.30%	16342	OK326892.1
Mesoplodon mirus mitochondrion, complete genome	Mesoplodon...	1358	2702	96%	0.0	96.70%	16342	NC_042217.1
Mesoplodon mirus genome assembly, organelle: mitochondrion	Mesoplodon...	1351	2687	96%	0.0	96.57%	16346	OZ205435.1
Mesoplodon mirus voucher USNM:MAMM:504612 mitochondrion, complete ge...	Mesoplodon...	1351	2692	96%	0.0	96.57%	16342	OK326889.1
Mesoplodon mirus voucher USNM:MAMM:504724 mitochondrion, complete ge...	Mesoplodon...	1347	2683	96%	0.0	96.45%	16342	OK326888.1
Mesoplodon mirus voucher USNM:MAMM:571357 mitochondrion, complete ge...	Mesoplodon...	1347	2683	96%	0.0	96.45%	16342	OK326887.1
Mesoplodon mirus voucher MMI:301112 mitochondrion, complete genome	Mesoplodon...	1347	2683	96%	0.0	96.45%	16342	OK326891.1
Mesoplodon mirus voucher USNM:MAMM:175019 mitochondrion, complete ge...	Mesoplodon...	1347	2683	96%	0.0	96.45%	16342	OK326890.1
Mesoplodon mirus voucher USNM:MAMM:593609 mitochondrion, complete ge...	Mesoplodon...	1339	2665	96%	0.0	96.33%	16342	OK326886.1
Mesoplodon mirus voucher USNM:MAMM:594404 mitochondrion, complete ge...	Mesoplodon...	1339	2665	96%	0.0	96.33%	16342	OK326884.1
Mesoplodon mirus voucher USNM:MAMM:594039 mitochondrion, complete ge...	Mesoplodon...	1339	2665	96%	0.0	96.33%	16342	OK326885.1
Mesoplodon europaeus isolate SWFSC ID z0074259 mitochondrion, complete_...	Mesoplodon...	1254	2489	97%	0.0	94.41%	16343	KC776693.2
Mesoplodon europaeus isolate SWFSC ID z0002698 mitochondrion, complete_...	Mesoplodon...	1249	2478	97%	0.0	94.29%	16343	NC_021434.2
Mesoplodon europaeus isolate SWFSC ID z0003853 mitochondrion, complete_...	Mesoplodon...	1249	2469	97%	0.0	94.29%	16344	KC776690.2
Mesoplodon europaeus isolate SWFSC ID z0094578 mitochondrion, complete_...	Mesoplodon...	1243	2458	97%	0.0	94.17%	16340	KC776695.1
Mesoplodon europaeus isolate SWFSC ID z0074265 mitochondrion, complete_...	Mesoplodon...	1243	2458	97%	0.0	94.17%	16345	KC776694.2
Mesoplodon europaeus isolate SWFSC ID z0004120 mitochondrion, complete_...	Mesoplodon...	1238	2456	97%	0.0	94.05%	16343	KC776691.2
Mesoplodon europaeus isolate SWFSC ID z0074252 mitochondrion, partial gen...	Mesoplodon...	1238	2461	97%	0.0	94.05%	16343	KC776692.2
Mesoplodon europaeus isolate SWFSC ID z0002817 mitochondrion, complete_...	Mesoplodon...	1238	2456	97%	0.0	94.05%	16343	KC776689.2
Mesoplodon ginkgodens SNH22005 mitochondrial DNA, tRNA-Pro, D-loop, tRN...	Mesoplodon...	1219	2425	97%	0.0	93.87%	892	LC870191.1
Mesoplodon ginkgodens voucher NMNS17594 mitochondrion, complete genome	Mesoplodon...	1214	2413	97%	0.0	93.73%	16339	NC_027593.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, complete sequence, specim...	Mesoplodon...	1199	2325	96%	0.0	93.18%	877	LC017820.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, complete sequence, specim...	Mesoplodon...	1199	2325	96%	0.0	93.18%	877	LC017819.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, complete sequence, specim...	Mesoplodon...	1194	2314	96%	0.0	93.06%	877	LC017817.1
Mesoplodon stejnegeri voucher CRI000090 mitochondrion, complete genome	Mesoplodon...	1194	2353	97%	0.0	93.06%	16349	NC_036997.1
Mesoplodon stejnegeri mitochondrial DNA, D-loop, complete sequence, specim...	Mesoplodon...	1182	2292	96%	0.0	92.81%	877	LC017818.1
Mesoplodon bidens genome assembly, organelle: mitochondrion	Mesoplodon...	1181	2330	96%	0.0	92.99%	16348	OZ073234.1
Berardius minimus mitochondrial DNA, D-loop, complete sequence, specimen_...	Berardius m...	1170	2314	99%	0.0	92.57%	931	AB572008.2
Ziphius cavirostris isolate SWFSC ID z0004472 mitochondrion, complete genome	Ziphius cavi...	1170	2295	96%	0.0	92.48%	16349	NC_021435.1
Berardius bairdii haplotype b3 tRNA-Pro gene, partial sequence; D-loop and tR...	Berardius b...	1170	2314	99%	0.0	92.57%	970	KT936579.1
Mesoplodon bidens mitochondrion, complete genome	Mesoplodon...	1170	2308	96%	0.0	92.74%	16347	NC_042218.1
Berardius minimus mitochondrial genes, tRNA-Pro, D-loop, tRNA-Phe, partial a...	Berardius m...	1170	2314	99%	0.0	92.57%	931	LC175773.1
Ziphius cavirostris isolate SWFSC ID z0007445 mitochondrion, complete genome	Ziphius cavi...	1170	2295	96%	0.0	92.48%	16344	KC776705.1
Berardius minimus mitochondrial genes, tRNA-Pro, D-loop, tRNA-Phe, partial a...	Berardius m...	1170	2314	99%	0.0	92.57%	931	LC175772.1
Ziphius cavirostris isolate SWFSC ID z0079898 mitochondrion, complete genome	Ziphius cavi...	1170	2295	96%	0.0	92.48%	16351	KC776701.1
Ziphius cavirostris isolate SWFSC ID z0074262 mitochondrion, complete genome	Ziphius cavi...	1168	2293	96%	0.0	92.65%	16339	KC776698.1
Berardius minimus mitochondrial DNA, D-loop, complete sequence, specimen_...	Berardius m...	1164	2303	99%	0.0	92.45%	931	AB572007.2
Berardius minimus isolate Bsp0618 tRNA-Pro gene, D-loop, and tRNA-Phe gen...	Berardius m...	1164	2314	100%	0.0	92.45%	1019	MK605248.1
Berardius bairdii haplotype b5 tRNA-Pro gene, partial sequence; D-loop and tR...	Berardius b...	1164	2303	99%	0.0	92.45%	970	KT936581.1
Berardius minimus haplotype b2 tRNA-Pro gene, D-loop, and tRNA-Phe gene,...	Berardius m...	1164	2314	100%	0.0	92.45%	1032	OI906296.1
Berardius bairdii mitochondrial DNA, D-loop, complete sequence, specimen_vo...	Berardius b...	1164	2303	98%	0.0	93.02%	931	AB572005.2
Ziphius cavirostris isolate SWFSC ID z0094591 mitochondrion, complete genome	Ziphius cavi...	1164	2284	96%	0.0	92.35%	16349	KC776703.1
Ziphius cavirostris isolate SWFSC ID z0079893 mitochondrion, complete genome	Ziphius cavi...	1162	2282	96%	0.0	92.35%	16346	KC776700.1
Ziphius cavirostris isolate SWFSC ID z0014950 mitochondrion, complete genome	Ziphius cavi...	1160	2286	95%	0.0	92.80%	16351	KC776697.1
Ziphius cavirostris isolate SWFSC ID z0024816 mitochondrion, complete genome	Ziphius cavi...	1158	2279	96%	0.0	92.23%	16352	KC776707.1
Berardius minimus mitochondrial DNA, D-loop, complete sequence, specimen_...	Berardius m...	1158	2292	99%	0.0	92.33%	931	AB572006.2
Ziphius cavirostris isolate SWFSC ID z0004967 mitochondrion, complete genome	Ziphius cavi...	1158	2284	96%	0.0	92.25%	16352	KC776706.1

Figure 4. Sequences producing significant alignments for tissue sample T023800.

Results were also visualised as a Fast Minimum Evolution distance tree (Fig 5).


Find:
all
TXT
Tools
Upload
Mesoplodon stejnegeri
Mesoplodon stejnegeri
Mesoplodon stejnegeri
Mesoplodon stejnegeri
Berardius minimus
Berardius bairdii
Berardius minimus
Berardius minimus
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Berardius bairdii
Berardius bairdii
Berardius bairdii
Berardius bairdii
Berardius bairdii
Berardius bairdii
Berardius bairdii
Hyperoodon ampullatus
Hyperoodon ampullatus
Hyperoodon ampullatus

Conclusion

Both tissue samples T023798 and T023800 have the greatest sequence alignment with and are identified as Ramiri's beaked whale, *M. eueu*. This species formerly represented the Indian Ocean population of True's beaked whale (*M. mirus*) although genetic studies showed divergence in the early Pleistocene and *M. eueu* was described genetically and morphologically at the species level in 2021.