GOVERNMENT OF WESTERN AUSTRALIA

Department of **Biodiversity, Conservation and Attractions**

Biodiversity and **Conservation Science**

Report on genetic identification of Baleen Whale tissue sample T16092 (T00140).

MA Millar 14/12/2023

The sample from a Baleen whale carcass was collected from Table Island, Esperance, and received from Kelly Waples October 2023.

DNA was extracted from the tissue sample using a TNES extraction method. The Displacement D-Loop primers Wada-D-Loop Forward/Wada-D-Loop Reverse were used to PCR non-coding mitochondrial D-Loop DNA using a Shaw hot start PCR program. PCR products were sequenced using the same Forward and Reverse primers at the Western Australian State Agricultural Biotechnology Centre (SABC) Murdoch University and sequence data for each region was aligned and edited using the Geneious Sequence Alignment Editor.

The sequenced region produced a contiguous alignment sequence read of 934bp. This sequence region was queried using the blastn suite (megablast) for highly similar sequences (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

Of the top 100 sequences producing significant alignments 100% were from *Balaenoptera physalus*, the fin whale, also known as finback whale or common rorqual and formerly known as herring whale or razorback whale, belonging to the parvorder of baleen whales (Fig 1)

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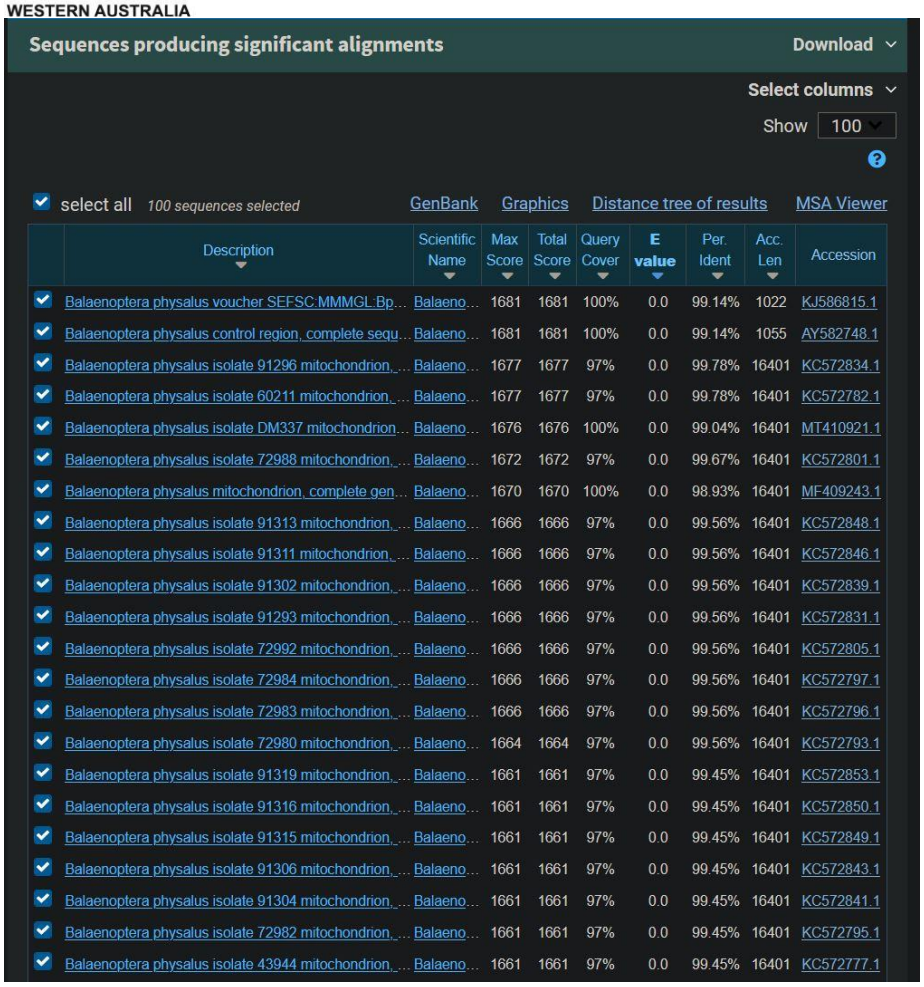
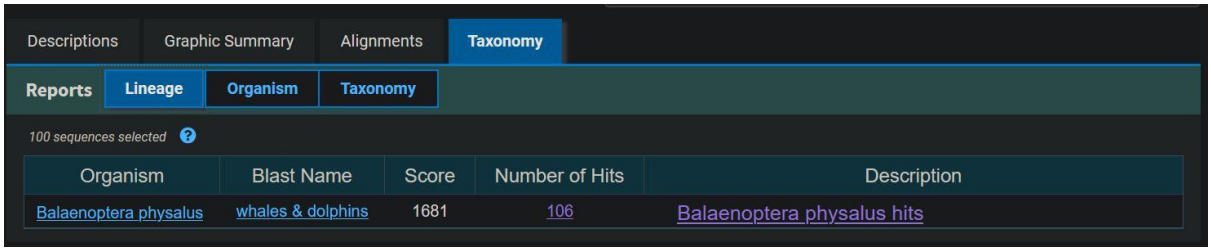


Sequences producing significant alignments — Download — Select columns — Show 100

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
Balaenoptera physalus voucher SEFSC:MMMGL:Bp...	Balaeno...	1681	1681	100%	0.0	99.14%	1022	KJ586815.1
Balaenoptera physalus control region, complete sequ...	Balaeno...	1681	1681	100%	0.0	99.14%	1055	AY582748.1
Balaenoptera physalus isolate 91296 mitochondrion,...	Balaeno...	1677	1677	97%	0.0	99.78%	16401	KC572834.1
Balaenoptera physalus isolate 60211 mitochondrion,...	Balaeno...	1677	1677	97%	0.0	99.78%	16401	KC572782.1
Balaenoptera physalus isolate DM337 mitochondrion...	Balaeno...	1676	1676	100%	0.0	99.04%	16401	MT410921.1
Balaenoptera physalus isolate 72988 mitochondrion,...	Balaeno...	1672	1672	97%	0.0	99.67%	16401	KC572801.1
Balaenoptera physalus mitochondrion, complete gen...	Balaeno...	1670	1670	100%	0.0	98.93%	16401	MF409243.1
Balaenoptera physalus isolate 91313 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572848.1
Balaenoptera physalus isolate 91311 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572846.1
Balaenoptera physalus isolate 91302 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572839.1
Balaenoptera physalus isolate 91293 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572831.1
Balaenoptera physalus isolate 72992 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572805.1
Balaenoptera physalus isolate 72984 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572797.1
Balaenoptera physalus isolate 72983 mitochondrion,...	Balaeno...	1666	1666	97%	0.0	99.56%	16401	KC572796.1
Balaenoptera physalus isolate 72980 mitochondrion,...	Balaeno...	1664	1664	97%	0.0	99.56%	16401	KC572793.1
Balaenoptera physalus isolate 91319 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572853.1
Balaenoptera physalus isolate 91316 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572850.1
Balaenoptera physalus isolate 91315 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572849.1
Balaenoptera physalus isolate 91306 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572843.1
Balaenoptera physalus isolate 91304 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572841.1
Balaenoptera physalus isolate 72982 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572795.1
Balaenoptera physalus isolate 43944 mitochondrion,...	Balaeno...	1661	1661	97%	0.0	99.45%	16401	KC572777.1

Figure 1. Sequences producing significant alignments for tissue sample T16092.
The queried sequence was significantly aligned to 106 accessions of *B. physalus* and no others (Fig 2.).



Descriptions | Graphic Summary | Alignments | **Taxonomy**

Reports | **Lineage** | **Organism** | **Taxonomy**

100 sequences selected

Organism	Blast Name	Score	Number of Hits	Description
Balaenoptera physalus	whales & dolphins	1681	106	Balaenoptera physalus hits

Figure 2. Number of significant alignments (Hits) for tissue sample T16092.

Results were also visualised as a Fast Minimum Evolution distance tree (Fig. 3).

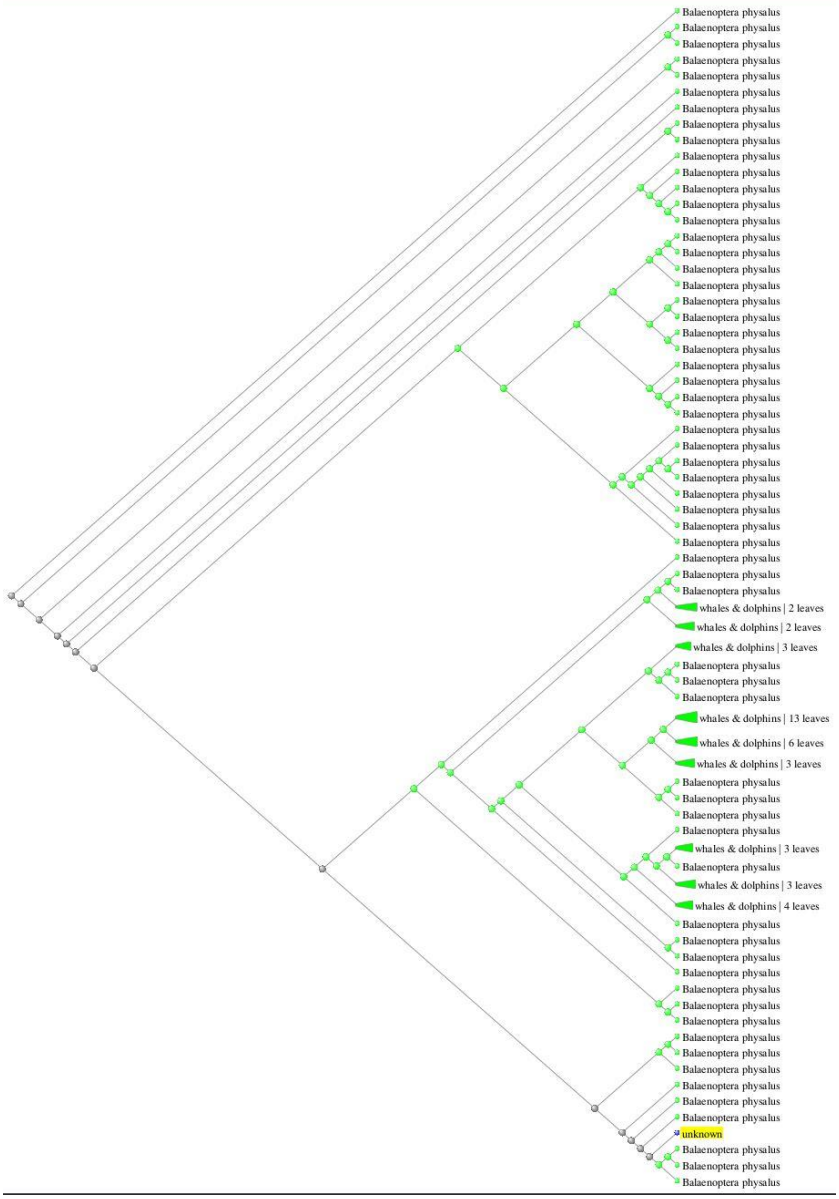


Figure 3. Yellow includes the queried (sample) region. Green are GenBank sequence accessions.

Conclusion

T16092 has the greatest sequence alignment with and is identified as a fin whale, *B. physalus*. As of 2023, four subspecies of *B. physalus* are named, so the sample is likely to be from an individual of *B. p. quoyi* which occupies the Southern Hemisphere.