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

Report on genetic identification of unknown whale tissue sample T018827 (Fauna lab) T01702 (Marine)

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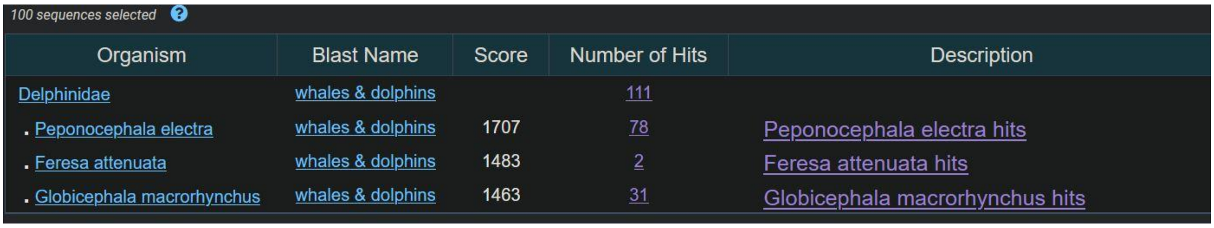
The tissue sample (T018827), suspected to be a Melon headed whale (*Peponocephala electra*) was collected from an animal stranded at Roebuck Bay (13/01/2025) and received from Kelly Waples in Jan 2025.

DNA was extracted from the tissue sample using a TNES extraction method. The Displacement Loop primers Wada-D-Loop Forward/Wada-D-Loop Reverse (Region 1) 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 region produced a consensus alignment sequence read of 948bp. This sequence region was queried using the blastn suite (megablast) for highly similar sequences (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

The queried sequence was significantly aligned to 111 sequences of the Delphinidae family, (Fig 1). Of the sequences producing significant alignment, the top 78 hits had the highest Maximum Scores, highest Total Scores, highest Query Coverages, lowest E values, and highest Percent Identities, with *Peponocephala electra* (Fig 2).



100 sequences selected

Organism	Blast Name	Score	Number of Hits	Description
Delphinidae	whales & dolphins		111	
. Peponocephala electra	whales & dolphins	1707	78	Peponocephala electra hits
. Feresa attenuata	whales & dolphins	1483	2	Feresa attenuata hits
. Globicephala macrorhynchus	whales & dolphins	1463	31	Globicephala macrorhynchus hits

Figure 1. Number of significant alignments (Hits) for tissue sample T018827.

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1707	1707	100%	0.0	99.16%	16389	ON652885.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1701	1701	100%	0.0	99.05%	16389	ON652882.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1701	1701	100%	0.0	99.05%	16389	ON652895.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1701	1701	100%	0.0	99.05%	16389	ON652901.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1701	1701	100%	0.0	99.05%	16389	ON652879.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1701	1701	100%	0.0	99.05%	16389	ON652900.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1696	1696	100%	0.0	98.95%	16389	ON652893.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1696	1696	100%	0.0	98.95%	16389	ON652905.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1690	1690	100%	0.0	98.84%	16389	ON652899.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1690	1690	100%	0.0	98.84%	16389	ON652880.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1690	1690	100%	0.0	98.84%	16389	ON652881.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1690	1690	100%	0.0	98.84%	16389	ON652898.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1685	1685	100%	0.0	98.74%	16389	ON652894.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1685	1685	100%	0.0	98.74%	16389	ON652892.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1685	1685	100%	0.0	98.74%	16389	ON652891.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1685	1685	100%	0.0	98.74%	16389	ON652884.1
☑	Peponocephala electra voucher SWFSC:74906 mi...	Pepono...	1679	1679	100%	0.0	98.63%	16388	JF289176.1
☑	Peponocephala electra mitochondrion, complete g...	Pepono...	1679	1679	100%	0.0	98.63%	16388	NC_019589.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1679	1679	100%	0.0	98.63%	16389	ON652890.1
☑	Peponocephala electra haplotype 42 tRNA-Pro ge...	Pepono...	1676	1676	96%	0.0	99.78%	961	KT223089.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1674	1674	100%	0.0	98.52%	16389	ON652897.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1674	1674	100%	0.0	98.52%	16389	ON652883.1
☑	Peponocephala electra isolate SWFSC_MMASTR...	Pepono...	1674	1674	100%	0.0	98.52%	16389	ON652887.1
☑	Peponocephala electra haplotype 2 tRNA-Pro gen...	Pepono...	1670	1670	96%	0.0	99.67%	961	KT223049.1
☑	Peponocephala electra haplotype 14 tRNA-Pro ge...	Pepono...	1664	1664	96%	0.0	99.56%	961	KT223061.1
☑	Peponocephala electra haplotype 5 tRNA-Pro gen...	Pepono...	1664	1664	96%	0.0	99.56%	961	KT223052.1
☑	Peponocephala electra haplotype 12 tRNA-Pro ge...	Pepono...	1664	1664	96%	0.0	99.56%	961	KT223059.1
☑	Peponocephala electra haplotype 30 tRNA-Pro ge...	Pepono...	1664	1664	96%	0.0	99.56%	961	KT223077.1
☑	Peponocephala electra haplotype 24 tRNA-Pro ge...	Pepono...	1664	1664	96%	0.0	99.56%	961	KT223071.1
☑	Peponocephala electra haplotype 33 tRNA-Pro ge...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223080.1
☑	Peponocephala electra haplotype 9 tRNA-Pro gen...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223056.1
☑	Peponocephala electra haplotype 18 tRNA-Pro ge...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223065.1
☑	Peponocephala electra haplotype 29 tRNA-Pro ge...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223076.1
☑	Peponocephala electra haplotype 28 tRNA-Pro ge...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223075.1
☑	Peponocephala electra haplotype 19 tRNA-Pro ge...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223066.1
☑	Peponocephala electra haplotype 41 tRNA-Pro ge...	Pepono...	1659	1659	96%	0.0	99.45%	961	KT223088.1
☑	Peponocephala electra haplotype 35 tRNA-Pro ge...	Pepono...	1653	1653	96%	0.0	99.34%	961	KT223082.1
☑	Peponocephala electra haplotype 4 tRNA-Pro gen...	Pepono...	1653	1653	96%	0.0	99.34%	961	KT223051.1
☑	Peponocephala electra haplotype 34 tRNA-Pro ge...	Pepono...	1653	1653	96%	0.0	99.34%	961	KT223081.1
☑	Peponocephala electra haplotype 38 tRNA-Pro ge...	Pepono...	1653	1653	96%	0.0	99.34%	961	KT223085.1

Figure 2. Sequences producing significant alignments for tissue sample T18827.

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

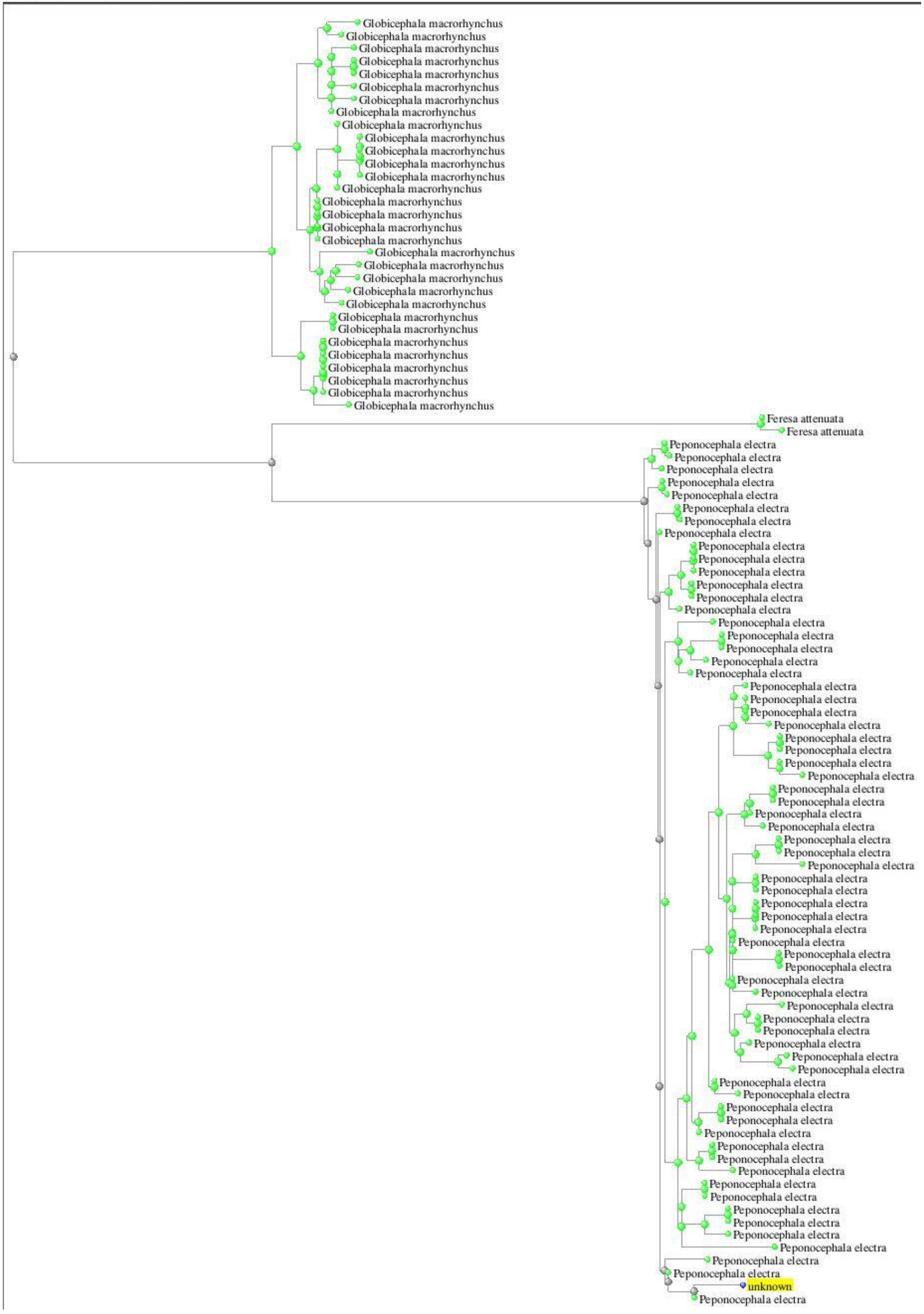


Figure 3. Yellow indicates the queried (sample) region. Green are GenBank sequence accessions with significant sequence alignment.

Conclusion

T18827 has the greatest sequence alignment with and is identified as a Melon headed whale, *P. electra*.