



Report on genetic identification of unknown dolphin tissue sample T022417 (Fauna lab) T01763 (Marine)

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The tissue sample (T022417), suspected to be a Fraser's dolphin (*Lagenodelphis hosei*) was collected from an animal stranded in the Northern Territory and received from Kelly Waples in July 2025. The sample was confirmed via sequencing analysis to be a Fraser's dolphin.

DNA was extracted from the tissue sample using a TNES extraction method. The Displacement Loop primers Delph-D-Loop Forward /Delph-H00034 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. Forward sequence data was edited using the Geneious sequence alignment editor although there appeared to be slippage present in the Reverse sequence and this was not assessed further.

The sequenced (Forward primer only) region produced a clean sequence read of 520bp. 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 101 sequences of Delphinidae (marine dolphins). There were 97 significant alignments to *Lagenodelphis hosei* (Fraser's dolphin), 2 significant alignments to *Tursiops truncatus* (common bottlenose dolphin), and 2 significant alignments to *Stenella longirostris* (spinner dolphin, Fig 1). Of the sequences producing significant alignment, the top 54 with the highest Maximum Scores, highest Total Scores, highest Query Coverages, lowest E values, and highest Percent Identities were from *L. hosei* (Fig 2).

100 sequences selected ?				
Organism	Blast Name	Score	Number of Hits	Description
Delphinidae	whales & dolphins		101	
• <i>Lagenodelphis hosei</i>	whales & dolphins	893	97	Lagenodelphis hosei hits
• <i>Tursiops truncatus</i>	whales & dolphins	854	2	Tursiops truncatus hits
• <i>Stenella longirostris</i>	whales & dolphins	824	2	Stenella longirostris hits

Figure 1. Number of significant alignments (Hits) for tissue sample T022417.

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	Lagenodelphis hosei voucher JHT0303 tRNA-Pro ...	Lagenodelphis hosei	893	893	100%	0.0	97.69%	777	MN268673.1
<input type="checkbox"/>	Lagenodelphis hosei voucher ZZ20018 tRNA-Pro ...	Lagenodelphis hosei	887	887	100%	0.0	97.50%	777	MN268633.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00561 tRNA-Pro ...	Lagenodelphis hosei	887	887	100%	0.0	97.50%	777	MN268632.1
<input type="checkbox"/>	Lagenodelphis hosei voucher WFP0778/SUML006 ...	Lagenodelphis hosei	881	881	100%	0.0	97.31%	777	MN268646.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00572 tRNA-Pro ...	Lagenodelphis hosei	881	881	100%	0.0	97.31%	777	MN268590.1
<input type="checkbox"/>	Lagenodelphis hosei voucher KH20120329 tRNA- ...	Lagenodelphis hosei	881	881	100%	0.0	97.31%	777	MN268672.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00567 tRNA-Pro ...	Lagenodelphis hosei	881	881	100%	0.0	97.31%	777	MN268591.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00544 tRNA-Pro ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268602.1
<input type="checkbox"/>	Lagenodelphis hosei voucher CY0108 tRNA-Pro g ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268586.1
<input type="checkbox"/>	Lagenodelphis hosei voucher ST2005 tRNA-Pro g ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268661.1
<input type="checkbox"/>	Lagenodelphis hosei voucher TD20100707 tRNA- ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268589.1
<input type="checkbox"/>	Lagenodelphis hosei voucher ST041012-5 tRNA-P ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268663.1
<input type="checkbox"/>	Lagenodelphis hosei voucher ST041012-1 tRNA-P ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268662.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU2001014 tRNA-P ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268587.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00575 tRNA-Pro ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268585.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00571 tRNA-Pro ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268584.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU2000026 tRNA-P ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268660.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00568 tRNA-Pro ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268583.1
<input type="checkbox"/>	Lagenodelphis hosei voucher TD20090526 tRNA- ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	778	MN268670.1
<input type="checkbox"/>	Lagenodelphis hosei voucher ST20051215 tRNA- ...	Lagenodelphis hosei	876	876	100%	0.0	97.12%	777	MN268588.1
<input type="checkbox"/>	Lagenodelphis hosei voucher PS-02 tRNA-Pro gen ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	778	MN268648.1
<input type="checkbox"/>	Lagenodelphis hosei voucher DSJ021104.03 tRNA ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268675.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00550 tRNA-Pro ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268614.1
<input type="checkbox"/>	Lagenodelphis hosei voucher ST041022-1 tRNA-P ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268653.1
<input type="checkbox"/>	Lagenodelphis hosei voucher PT2001001 tRNA-Pr ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268654.1
<input type="checkbox"/>	Lagenodelphis hosei voucher NEPST842 tRNA-Pr ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268650.1
<input type="checkbox"/>	Lagenodelphis hosei voucher STNA (01) tRNA-Pro ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	778	MN268647.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00576 tRNA-Pro ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268640.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU2000027 tRNA-P ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268652.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU20130706 tRNA- ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268657.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU9809 tRNA-Pro g ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268656.1
<input type="checkbox"/>	Lagenodelphis hosei voucher DD2000001 tRNA-P ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268659.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU2000045 tRNA-P ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268655.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00586 tRNA-Pro ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268651.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00555 tRNA-Pro ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268620.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU2001017 tRNA-P ...	Lagenodelphis hosei	870	870	100%	0.0	96.92%	777	MN268666.1
<input type="checkbox"/>	Lagenodelphis hosei voucher HU2000030 tRNA-P ...	Lagenodelphis hosei	865	865	100%	0.0	96.73%	777	MN268664.1
<input type="checkbox"/>	Lagenodelphis hosei voucher GL20050322 tRNA- ...	Lagenodelphis hosei	865	865	100%	0.0	96.73%	777	MN268626.1
<input type="checkbox"/>	Lagenodelphis hosei voucher CK9713 tRNA-Pro g ...	Lagenodelphis hosei	865	865	100%	0.0	96.73%	777	MN268628.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00545 tRNA-Pro ...	Lagenodelphis hosei	865	865	100%	0.0	96.73%	777	MN268603.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00574 tRNA-Pro ...	Lagenodelphis hosei	865	865	100%	0.0	96.73%	777	MN268605.1
<input type="checkbox"/>	Lagenodelphis hosei voucher EW00584 tRNA-Pro ...	Lagenodelphis hosei	865	865	100%	0.0	96.73%	777	MN268644.1

Figure 2. Sequences producing significant alignments for tissue sample T022417.

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

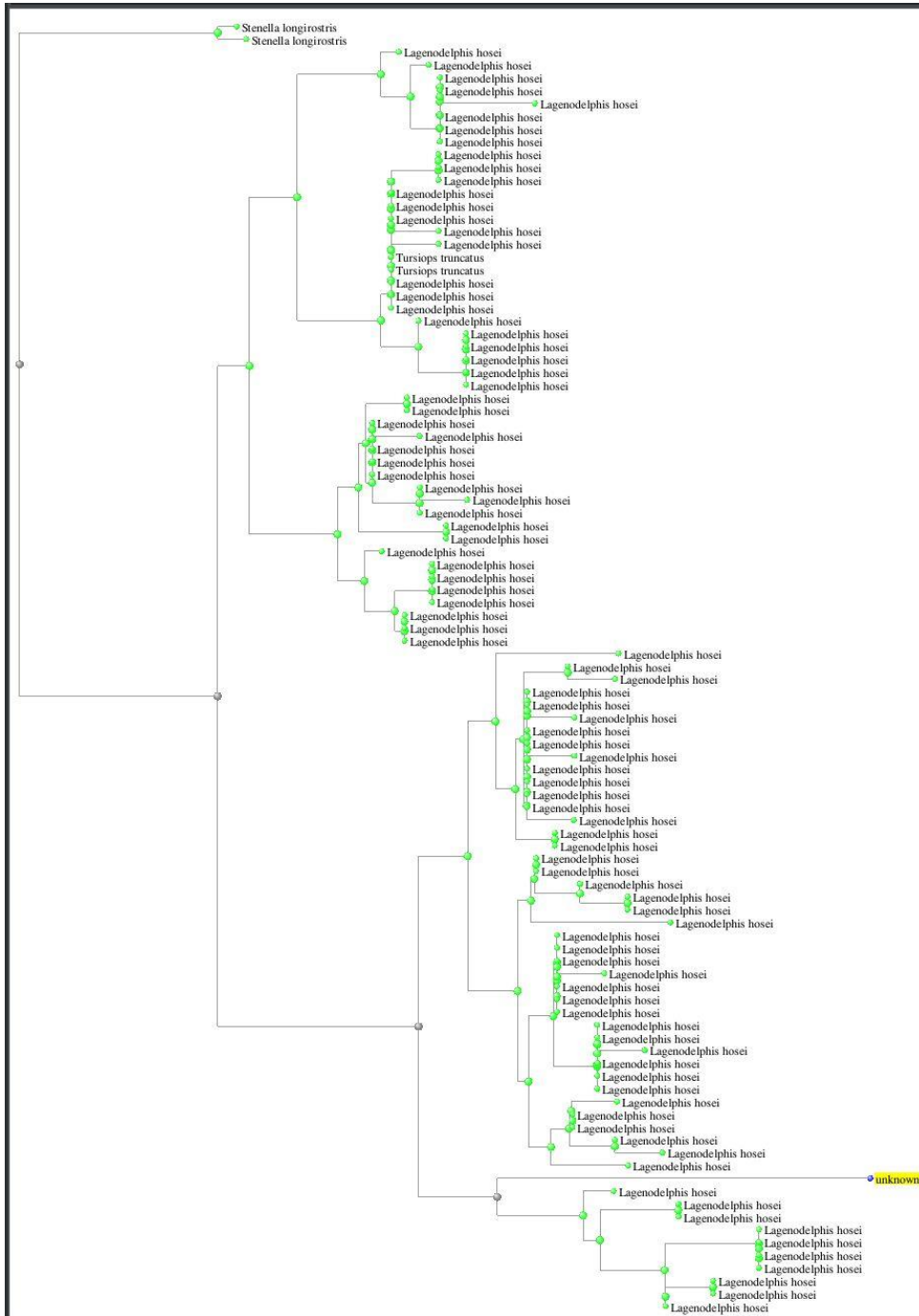


Figure 3. Yellow indicates the queried (sample) region. Green are GenBank sequence accessions with significant sequence alignment.

Conclusion

T022417 has the greatest sequence alignment with and is identified as a Fraser's dolphin *Lagenodelphis hosei*.