GOVERNMENT OF
WESTERN AUSTRALIA

Department of **Biodiversity,**
Conservation and Attractions

Biodiversity and
Conservation Science

Report on genetic identification of unknown whale tissue sample T018380 (Fauna lab) T01245 (Marine)

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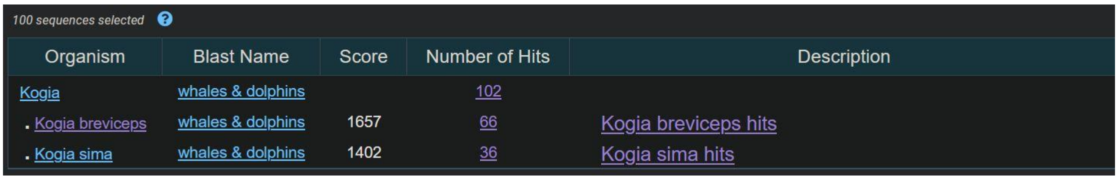
The tissue r sample (T018380), suspected to be a pygmy sperm whale (*Kogia breviceps*) or dwarf sperm whale (*Kogia sima*) was collected from an animal euthanised at Floreat beach (20/10/2024) and received from Kelly Waples in Jan 2025.

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 952bp. This sequence region was queried using the blastn suite (megablast) for highly similar sequences (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

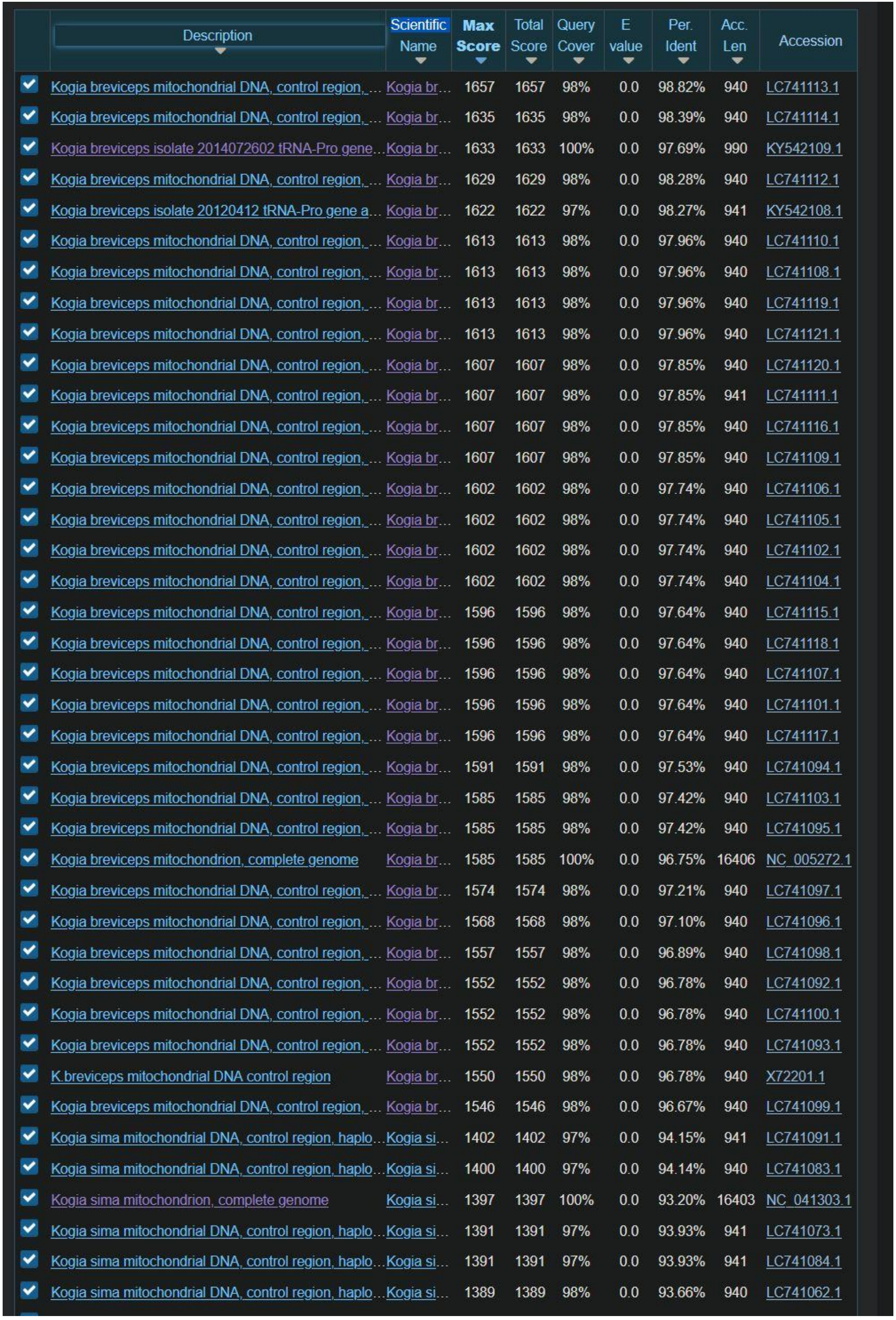
The queried sequence was significantly aligned to 102 sequences of *Kogia*, a genus of toothed whales. There were 66 significant alignments to the pygmy sperm whale *Kogia breviceps*, and 36 significant alignments with *Kogia sima* (Fig 1), the dwarf sperm whale, which was synonymous with the pygmy sperm whale until 1998. Of the sequences producing significant alignment, the top 66 with the highest Maximum Scores, highest Total Scores, highest Query Coverages, lowest E values, and highest Percent Identities were from *K. breviceps* (Fig 2).



100 sequences selected

Organism	Blast Name	Score	Number of Hits	Description
Kogia	whales & dolphins		102	
. Kogia breviceps	whales & dolphins	1657	66	Kogia breviceps hits
. Kogia sima	whales & dolphins	1402	36	Kogia sima hits

Figure 1. Number of significant alignments (Hits) for tissue sample T018380.



	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1657	1657	98%	0.0	98.82%	940	LC741113.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1635	1635	98%	0.0	98.39%	940	LC741114.1
☑	Kogia breviceps isolate 2014072602 tRNA-Pro gene...	Kogia br...	1633	1633	100%	0.0	97.69%	990	KY542109.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1629	1629	98%	0.0	98.28%	940	LC741112.1
☑	Kogia breviceps isolate 20120412 tRNA-Pro gene a...	Kogia br...	1622	1622	97%	0.0	98.27%	941	KY542108.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1613	1613	98%	0.0	97.96%	940	LC741110.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1613	1613	98%	0.0	97.96%	940	LC741108.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1613	1613	98%	0.0	97.96%	940	LC741119.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1613	1613	98%	0.0	97.96%	940	LC741121.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1607	1607	98%	0.0	97.85%	940	LC741120.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1607	1607	98%	0.0	97.85%	941	LC741111.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1607	1607	98%	0.0	97.85%	940	LC741116.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1607	1607	98%	0.0	97.85%	940	LC741109.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1602	1602	98%	0.0	97.74%	940	LC741106.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1602	1602	98%	0.0	97.74%	940	LC741105.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1602	1602	98%	0.0	97.74%	940	LC741102.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1602	1602	98%	0.0	97.74%	940	LC741104.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1596	1596	98%	0.0	97.64%	940	LC741115.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1596	1596	98%	0.0	97.64%	940	LC741118.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1596	1596	98%	0.0	97.64%	940	LC741107.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1596	1596	98%	0.0	97.64%	940	LC741101.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1596	1596	98%	0.0	97.64%	940	LC741117.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1591	1591	98%	0.0	97.53%	940	LC741094.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1585	1585	98%	0.0	97.42%	940	LC741103.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1585	1585	98%	0.0	97.42%	940	LC741095.1
☑	Kogia breviceps mitochondrion, complete genome	Kogia br...	1585	1585	100%	0.0	96.75%	16406	NC_005272.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1574	1574	98%	0.0	97.21%	940	LC741097.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1568	1568	98%	0.0	97.10%	940	LC741096.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1557	1557	98%	0.0	96.89%	940	LC741098.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1552	1552	98%	0.0	96.78%	940	LC741092.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1552	1552	98%	0.0	96.78%	940	LC741100.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1552	1552	98%	0.0	96.78%	940	LC741093.1
☑	K.breviceps mitochondrial DNA control region	Kogia br...	1550	1550	98%	0.0	96.78%	940	X72201.1
☑	Kogia breviceps mitochondrial DNA, control region,...	Kogia br...	1546	1546	98%	0.0	96.67%	940	LC741099.1
☑	Kogia sima mitochondrial DNA, control region, haplo...	Kogia si...	1402	1402	97%	0.0	94.15%	941	LC741091.1
☑	Kogia sima mitochondrial DNA, control region, haplo...	Kogia si...	1400	1400	97%	0.0	94.14%	940	LC741083.1
☑	Kogia sima mitochondrion, complete genome	Kogia si...	1397	1397	100%	0.0	93.20%	16403	NC_041303.1
☑	Kogia sima mitochondrial DNA, control region, haplo...	Kogia si...	1391	1391	97%	0.0	93.93%	941	LC741073.1
☑	Kogia sima mitochondrial DNA, control region, haplo...	Kogia si...	1391	1391	97%	0.0	93.93%	941	LC741084.1
☑	Kogia sima mitochondrial DNA, control region, haplo...	Kogia si...	1389	1389	98%	0.0	93.66%	940	LC741062.1

Figure 2. Sequences producing significant alignments for tissue sample T18380.

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

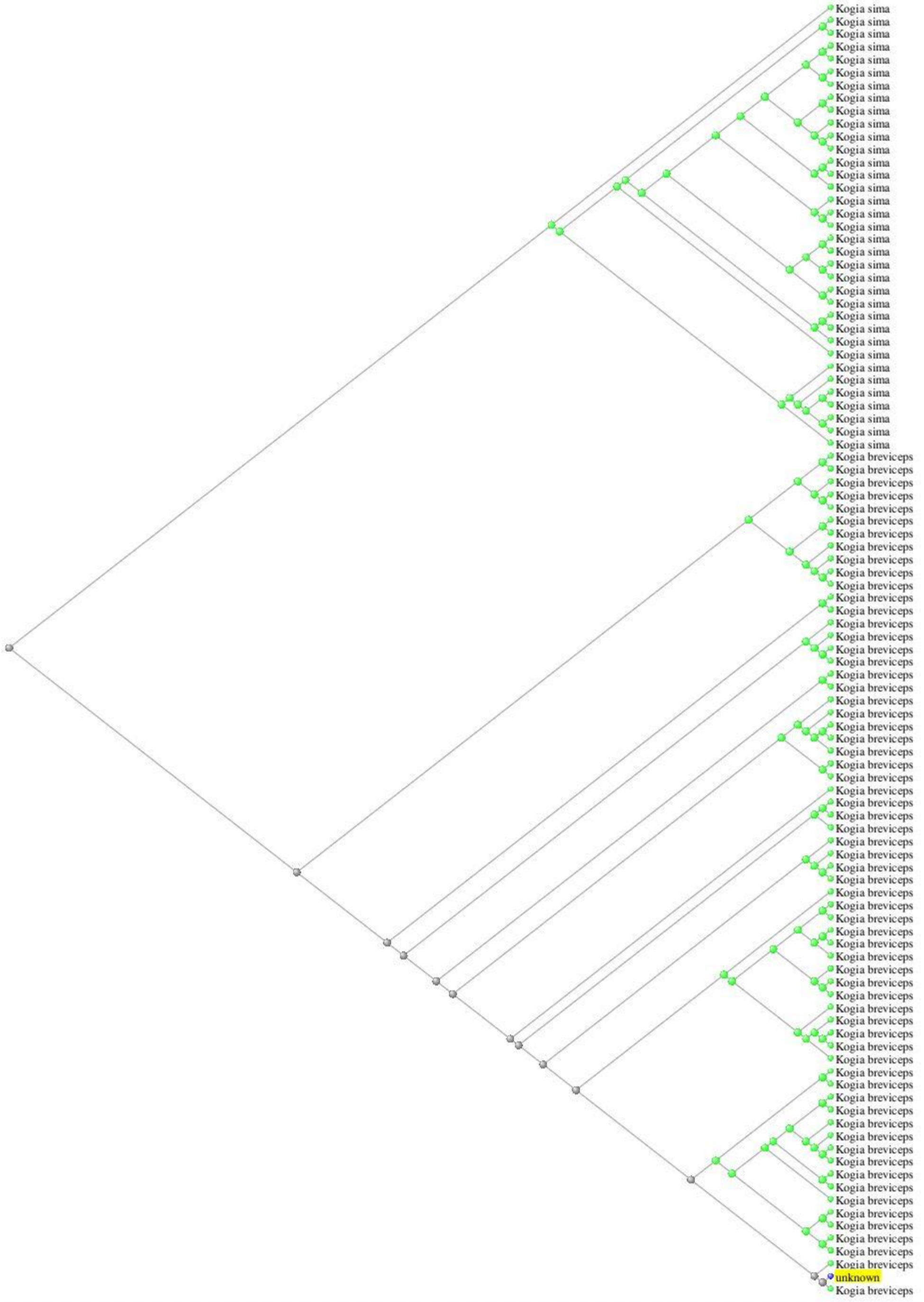


Figure 3. Yellow indicates the queried (sample) region. Green are GenBank sequence accessions with significant sequence alignment.

Conclusion

T18380 has the greatest sequence alignment with and is identified as a pygmy sperm whale *K. breviceps*.