


Report on genetic identification of unknown whale tissue sample T15991

MA Millar 1/11/2023

The tissue and blubber sample (T15991), suspected to be a pygmy sperm whale (*Kogia breviceps*) or dwarf sperm whale (*Kogia sima*) was collected from circus beach Walpole (20/9/2023) and received from Kelly Waples 23/10/2023.

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 963bp. 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 34 with the highest Maximum Scores, highest Total Scores, highest Query Coverages, lowest E values, and highest Percent Identities were from *K. breviceps* (Fig 2).

Organism	Blast Name	Score	Number of Hits	Description
Kogia	whales & dolphins		102	
• Kogia breviceps	whales & dolphins	1681	66	Kogia breviceps hits
• Kogia sima	whales & dolphins	1443	36	Kogia sima hits

Figure 1. Number of significant alignments (Hits) for tissue sample T15991.

Sequences producing significant alignments										Download ▾
										Select columns ▾
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										?
<input checked="" type="checkbox"/> 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	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1681	1681	97%	0.0	98.94%	940	LC741113.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1676	1676	97%	0.0	98.83%	940	LC741112.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1670	1670	97%	0.0	98.72%	940	LC741114.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1664	1664	97%	0.0	98.62%	940	LC741107.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1659	1659	97%	0.0	98.51%	940	LC741104.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1659	1659	97%	0.0	98.51%	940	LC741105.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1659	1659	97%	0.0	98.51%	940	LC741106.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1659	1659	97%	0.0	98.51%	940	LC741108.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1659	1659	97%	0.0	98.51%	940	LC741117.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1653	1653	97%	0.0	98.41%	941	LC741111.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1653	1653	97%	0.0	98.40%	940	LC741119.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1648	1648	97%	0.0	98.30%	940	LC741110.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1648	1648	97%	0.0	98.30%	940	LC741116.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1648	1648	97%	0.0	98.30%	940	LC741118.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1648	1648	97%	0.0	98.30%	940	LC741120.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1648	1648	97%	0.0	98.40%	940	LC741121.1	
<input checked="" type="checkbox"/>	Kogia breviceps isolate 20120412 tRNA-Pro gen...	Kogia br...	1644	1644	96%	0.0	98.70%	941	KY542108.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1642	1642	97%	0.0	98.19%	940	LC741094.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1642	1642	97%	0.0	98.19%	940	LC741101.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1642	1642	97%	0.0	98.19%	940	LC741103.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1642	1642	97%	0.0	98.19%	940	LC741109.1	
<input checked="" type="checkbox"/>	Kogia breviceps isolate 2014072602 tRNA-Pro g...	Kogia br...	1642	1642	98%	0.0	97.89%	990	KY542109.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1637	1637	97%	0.0	98.09%	940	LC741095.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1637	1637	97%	0.0	98.09%	940	LC741102.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrion, complete genome	Kogia br...	1629	1629	99%	0.0	97.30%	16406	NC_005272.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1626	1626	97%	0.0	97.87%	940	LC741092.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1626	1626	97%	0.0	97.87%	940	LC741093.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1626	1626	97%	0.0	97.87%	940	LC741115.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1620	1620	97%	0.0	97.77%	940	LC741096.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1615	1615	97%	0.0	97.66%	940	LC741098.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1615	1615	97%	0.0	97.66%	940	LC741100.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1609	1609	97%	0.0	97.55%	940	LC741099.1	
<input checked="" type="checkbox"/>	Kogia breviceps mitochondrial DNA, control regio...	Kogia br...	1604	1604	97%	0.0	97.45%	940	LC741097.1	
<input checked="" type="checkbox"/>	K breviceps mitochondrial DNA control region	Kogia br...	1592	1592	97%	0.0	97.24%	940	X72201.1	
<input checked="" type="checkbox"/>	Kogia sima mitochondrial DNA, control region, ha...	Kogia si...	1443	1443	97%	0.0	94.37%	940	LC741083.1	
<input checked="" type="checkbox"/>	Kogia sima mitochondrial DNA, control region, ha...	Kogia si...	1432	1432	97%	0.0	94.16%	941	LC741084.1	
<input checked="" type="checkbox"/>	Kogia sima mitochondrial DNA, control region, ha...	Kogia si...	1432	1432	97%	0.0	94.16%	941	LC741091.1	
<input checked="" type="checkbox"/>	Kogia sima mitochondrial DNA, control region, ha...	Kogia si...	1426	1426	97%	0.0	94.07%	941	LC741090.1	

Figure 2. Sequences producing significant alignments for tissue sample T15991.

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

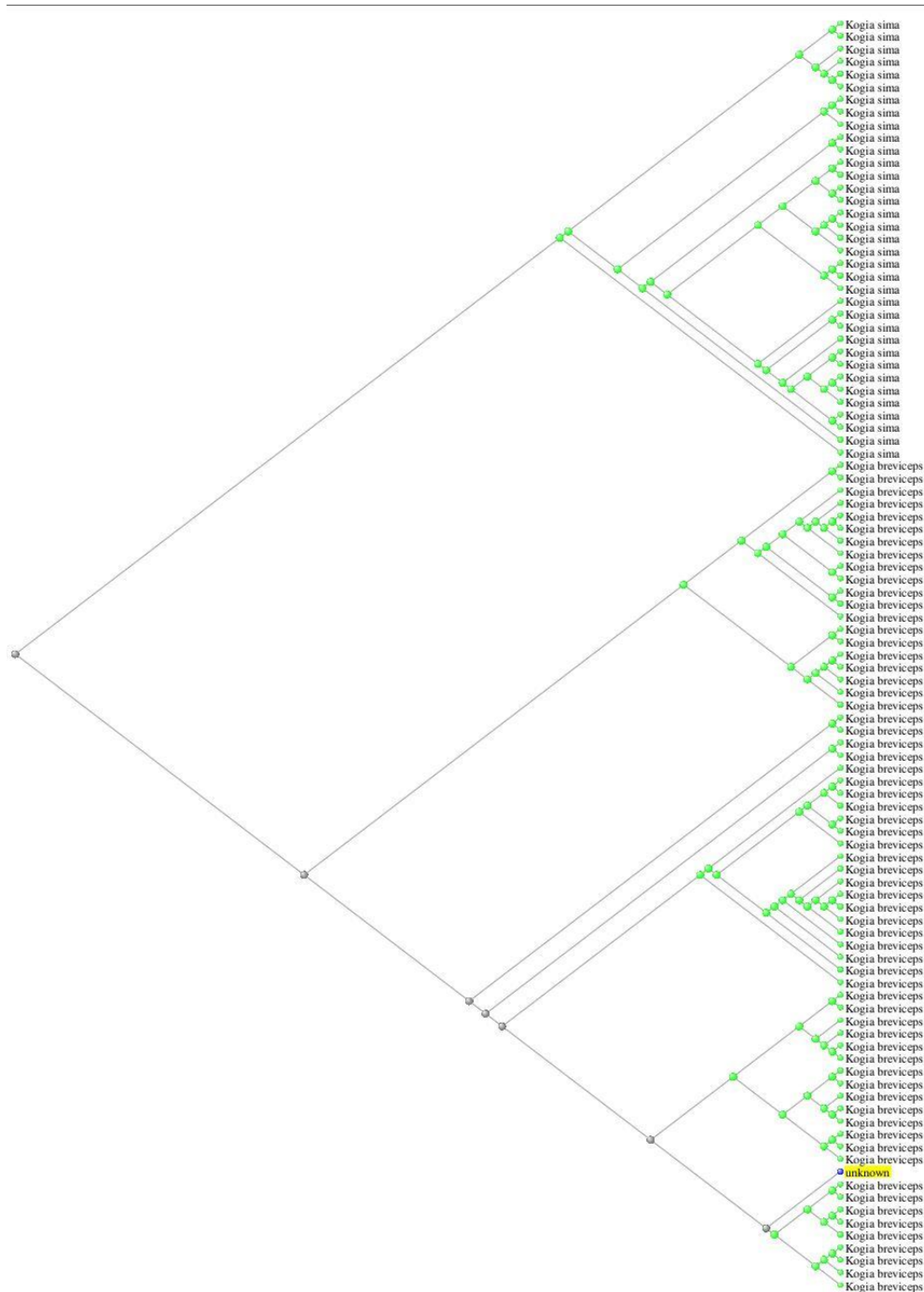


Figure 3. Yellow indicates the queried (sample) region. Green are GenBank sequence accessions with significant sequence alignment.

Conclusion



Department of **Biodiversity,
Conservation and Attractions**



**Biodiversity and
Conservation Science**

T15991 has the greatest sequence alignment with and is identified as a pygmy sperm whale *K. breviceps*.