GOVERNMENT OF
WESTERN AUSTRALIA

Department of **Biodiversity,**
**Conservation and Attractions**

Biodiversity and
Conservation Science

# Report on genetic identification of unknown whale tissue sample T018826 (Fauna lab) T01692 (Marine)

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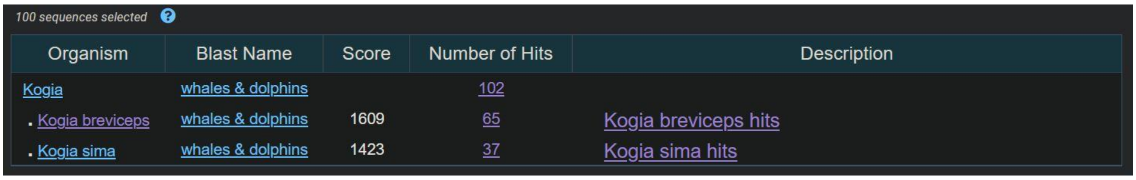
The tissue sample (T018826), suspected to be a pygmy sperm whale (*Kogia breviceps*) or dwarf sperm whale (*Kogia sima*) was collected from a stranding at Eight Mile beach (22/11/2024) and received from Kelly Waples in Jan 2025.

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 905bp. 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 65 significant alignments to the pygmy sperm whale *Kogia breviceps*, and 37 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 65 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 | 1609 | 65 | Kogia breviceps hits |
| . Kogia sima | whales & dolphins | 1423 | 37 | Kogia sima hits |

Figure 1. Number of significant alignments (Hits) for tissue sample T018826.

| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|---|---|---|---|---|---|---|---|---|
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1609 | 1609 | 100% | 0.0 | 98.78% | 940 | LC741095.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1604 | 1604 | 100% | 0.0 | 98.67% | 940 | LC741094.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1604 | 1604 | 100% | 0.0 | 98.67% | 940 | LC741109.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1592 | 1592 | 100% | 0.0 | 98.45% | 940 | LC741107.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1592 | 1592 | 100% | 0.0 | 98.45% | 940 | LC741096.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1587 | 1587 | 100% | 0.0 | 98.34% | 940 | LC741106.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1587 | 1587 | 100% | 0.0 | 98.34% | 940 | LC741097.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1587 | 1587 | 100% | 0.0 | 98.34% | 940 | LC741108.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1581 | 1581 | 100% | 0.0 | 98.23% | 940 | LC741110.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1581 | 1581 | 100% | 0.0 | 98.23% | 940 | LC741098.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1581 | 1581 | 100% | 0.0 | 98.23% | 940 | LC741119.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741115.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741116.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741092.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741100.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741093.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741105.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741104.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | LC741117.1 |
| ☑ | K.breviceps mitochondrial DNA control region | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 940 | X72201.1 |
| ☑ | Kogia breviceps mitochondrion, complete genome | Kogia br… | 1576 | 1576 | 100% | 0.0 | 98.12% | 16406 | NC_005272.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1570 | 1570 | 100% | 0.0 | 98.01% | 940 | LC741099.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1565 | 1565 | 100% | 0.0 | 97.90% | 940 | LC741120.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1565 | 1565 | 100% | 0.0 | 97.90% | 940 | LC741118.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1559 | 1559 | 100% | 0.0 | 97.79% | 940 | LC741101.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1559 | 1559 | 100% | 0.0 | 97.79% | 940 | LC741121.1 |
| ☑ | Kogia breviceps isolate 2014072602 tRNA-Pro gene… | Kogia br… | 1555 | 1555 | 99% | 0.0 | 97.89% | 990 | KY542109.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1554 | 1554 | 100% | 0.0 | 97.68% | 940 | LC741114.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1554 | 1554 | 100% | 0.0 | 97.68% | 940 | LC741102.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1554 | 1554 | 100% | 0.0 | 97.68% | 940 | LC741113.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1548 | 1548 | 100% | 0.0 | 97.57% | 940 | LC741112.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1548 | 1548 | 100% | 0.0 | 97.57% | 940 | LC741103.1 |
| ☑ | Kogia breviceps mitochondrial DNA, control region,… | Kogia br… | 1539 | 1539 | 100% | 0.0 | 97.35% | 941 | LC741111.1 |
| ☑ | Kogia breviceps isolate 20120412 tRNA-Pro gene a… | Kogia br… | 1513 | 1513 | 97% | 0.0 | 97.83% | 941 | KY542108.1 |
| ☑ | Kogia sima mitochondrial DNA, control region, haplo… | Kogia si… | 1423 | 1423 | 100% | 0.0 | 95.04% | 941 | LC741091.1 |
| ☑ | Kogia sima mitochondrial DNA, control region, haplo… | Kogia si… | 1410 | 1410 | 100% | 0.0 | 94.81% | 940 | LC741065.1 |
| ☑ | Kogia sima mitochondrial DNA, control region, haplo… | Kogia si… | 1406 | 1406 | 100% | 0.0 | 94.71% | 941 | LC741059.1 |
| ☑ | Kogia sima mitochondrial DNA, control region, haplo… | Kogia si… | 1400 | 1400 | 100% | 0.0 | 94.60% | 941 | LC741058.1 |
| ☑ | Kogia sima mitochondrial DNA, control region, haplo… | Kogia si… | 1400 | 1400 | 100% | 0.0 | 94.60% | 941 | LC741063.1 |
| ☑ | Kogia sima mitochondrial DNA, control region, haplo… | Kogia si… | 1400 | 1400 | 100% | 0.0 | 94.60% | 941 | LC741073.1 |

Figure 2. Sequences producing significant alignments for tissue sample T18826.

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

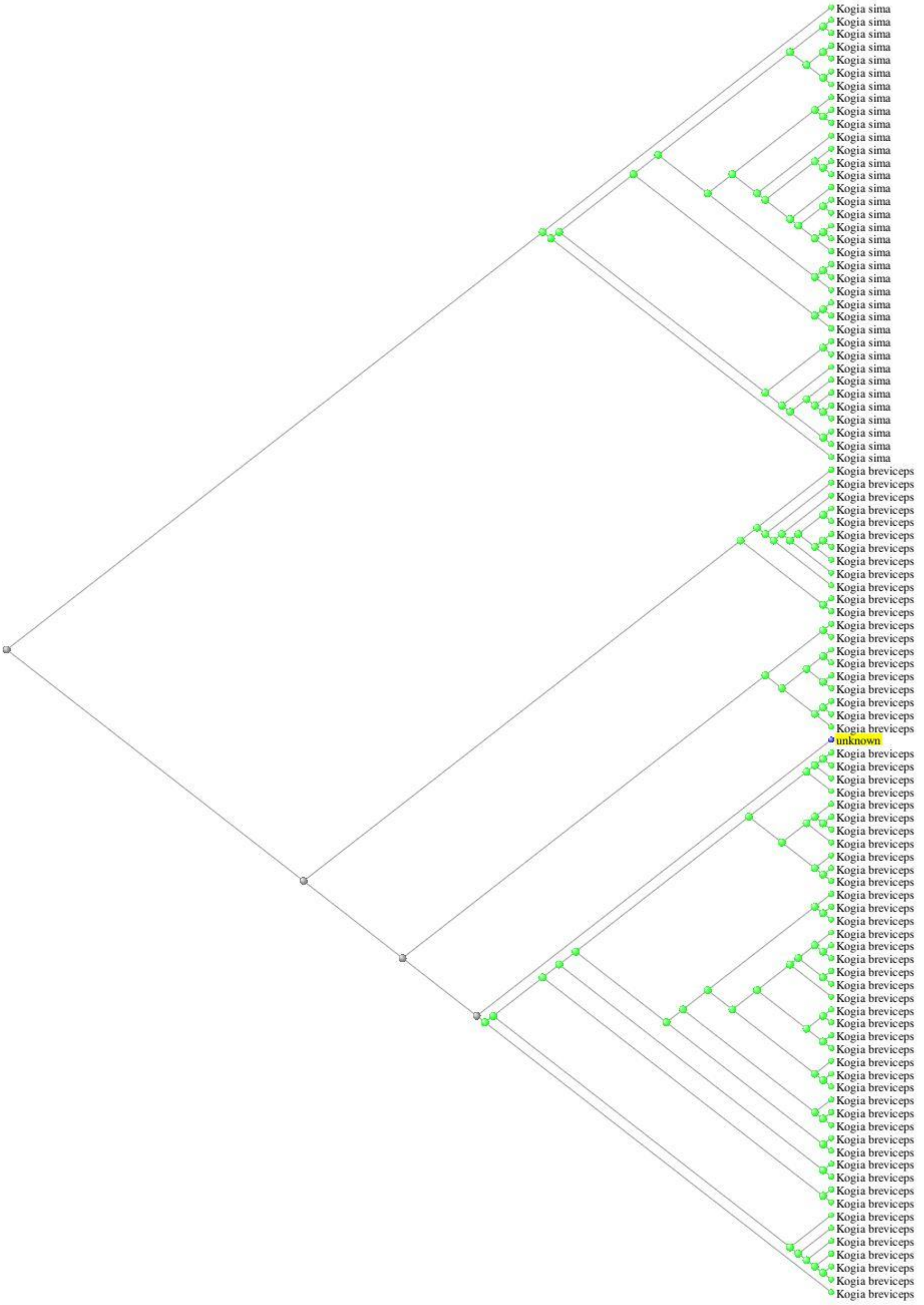


Figure 3. Yellow indicates the queried (sample) region. Green are GenBank sequence accessions with significant sequence alignment.

Conclusion

T18826 has the greatest sequence alignment with and is identified as a pygmy sperm whale *K. breviceps*.