
GENETIC ANALYSIS OF A *KOGIA SP.* SKIN SAMPLE COLLECTED IN SAMOA IN 2005

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Summary

A cetacean stranded in Samoa in early March 2005 and an examination of its morphological characters identified it as a *Kogia sp.* A skin sample was collected from this specimen, which was processed for genetic analysis. Amplification of the sex Y chromosome gene *sry* confirmed the visual identification of the specimen as a male. The partial sequencing of the mitochondrial DNA control region analysis identified it as dwarf sperm whale *Kogia sima*. This is the first record of this species in Samoan waters. A comparison with sequences from three other specimens sampled in Australia and South Africa showed that none of them shared the same haplotype. The opportune sampling of the specimen proved that the genetic sampling protocol currently in practice by the Ministry of Natural Resources, Environment & Meteorology can provide significant information on the cetacean diversity around the Samoan islands.

Introduction

Surveys have been conducted around the islands of Samoa in recent years to establish the current cetacean diversity. Nine species have been recorded:

sperm whale (*Physeter macrocephalus*), humpback whale (*Megaptera novaeangliae*), minke whale (*Balaenoptera* sp.)¹, false killer whale (*Pseudorca crassidens*), spinner dolphin (*Stenella longirostris*), short-finned pilot whale (*Globicephala macrorhynchus*), bottlenose dolphin (*Tursiops truncatus*), beaked whale (*Mesoplodon* sp.) and rough-toothed dolphin (*Steno bredanensis*, Paton et al. 2002; Walsh & Paton 2003).

In this report we present the results of the genetic analysis of a skin sample collected from a stranded *Kogia* sp. found in the Upolu island of Samoa. Because the external examination did not assigned it unequivocally to any of the two species of the genus *Kogia*, that is the dwarf sperm whale *K. sima*² or the pygmy sperm whale *K. breviceps*, the analysis was focused on the species identification based on molecular markers.

Materials and Methods

Stranding data collection

Stranding data was collected following the “Samoa’s Cetacean Stranding Report” recently designed by the Division of Environment & Conservation of the Ministry of Natural Resources, Environment & Meteorology.

Collection of skin samples

Biopsy skin samples were collected from behind the dorsal fin and from the fluke. Sterilised forceps and blades were used, as well as surgical gloves to avoid contamination. Two tubes with 70% ethanol and three with 99% ethanol were used to store the samples.

¹ The minke whale may be distributed in Samoan waters, based on Japanese sighting surveys between 1976 and 1987 (Kasamatsu et al. 1995). The distinction between the two southern hemisphere minke whales, Antarctic minke whale *B. bonaerensis* or Dwarf minke whale *B. acutorostrata* sp (Best 1985; Arnold et al. 1987) was made posterior to the surveys analyzed, thus it is no clear if that distinction in recording each form was effectively achieved during the surveys, despite Kasamatsu et al. (1995) stated “only the more abundant ‘dark-shoulder’ form was considered in this study”.

² It is necessary to note that a recent review of cetacean systematics corrected the specific name from *K. simus* to *K. sima* (Rice 1998).

Genetic analysis

DNA was extracted from one of the samples stored with 70% ethanol. A small portion of skin sample was extracted using a standard phenol/chloroform protocol (Davis et al. (1986) as modified by Baker et al. (1993)).

The sex was identified by amplification of sex specific markers following Gilson et al. (1998). This protocol amplifies a fragment of 224 base pairs (bp) long from the *sry* gene located on the Y chromosome via the Polymerase Chain Reaction (PCR, Saiki et al. 1988). As an internal positive control against amplification failure, the homologous *ZFY/ZFX* region of 445 bp is amplified to show that the lack of the amplified segment is not due to an amplification failure. Thus, in males two bands of 224 and 445 bp are observed and in females just one of 445 bp.

The mitochondrial DNA (mtDNA) is a circular, non-recombining genome that is maternally inherited (Wilson et al. 1985). Because of its small effective population size and its rapid rate of evolution compared to nuclear DNA (Brown et al. 1986) this molecular marker has been widely used in phylogenetic and population genetic analysis. Within the mtDNA, the control region or D-loop is the most rapidly evolving in most vertebrates and as such is the most commonly used segment for population analysis (Moritz et al. 1987).

Symmetrical amplification of the mtDNA control region, proximal to the tPro RNA gene, was performed via PCR. An 800 bp portion of the mtDNA control region was amplified using the primers light-strand tPro-whale Dlp-1.5 (Dalebout et al. 1998) and heavy strand Dlp-8G (Pichler et al. 2001). Amplification and subsequent cycle sequencing were improved by the addition of an M13 sequence to the 5' end of the tPro-whale Dlp-1.5. The amplicon was electrophoresed on a 1.6% agarose gel, stained with ethidium bromide and visualized under UV light.

The PCR product was then sequenced with BigDye™ terminator chemistry (ABI vs 3.1) on an ABI3100 DNA sequencer (Applied Biosystem). The

sequence was aligned and edited using the program Sequencher™ (version 4.1.2, Genes Codes Co.).

The species identity was revealed by the comparison of the Samoan specimen with the data base of *DNA-surveillance* (<http://www.dna-surveillance.auckland.ac.nz>, Baker et al. 2003; Ross et al. 2003). This web-based software, developed for molecular taxonomy of cetaceans, compares the sequence of interest with an extensive data set of validated cetacean species.

A comparison with three other *K. sima* sequences from specimens sampled in Australia and South Africa (Plön 2004) was performed using MacClade software (Maddison & Maddison 2000) to identify identical sequences (haplotypes). A phylogenetic reconstruction was performed using PAUP* (Swofford 2000).

Results

Stranding data collection

In early March a Peace Corps Volunteer and caretaker reported the stranding of a whale in Lotofaga, Safata (Figure 1). Officers of the Division of Environment & Conservation of the Ministry of Natural Resources, Environment & Meteorology of Samoa visited the location and examined the specimen (Figure 2). Standard data were collected (Figure 3).

Sex identification

The sex of the specimen was identified in the field as a male, based on the relative distance between the anus and the genital slit (Juney Ward, 5th March 2005; Figure 4).

The genetic analysis confirmed the field identification when the band of the Sry gene was amplified (Figure 5).

Species identification

The photographic evidence indicated that the stranded specimen was possibly a dwarf sperm whale *K. sima*, based mainly on the location and shape of the dorsal fin (Ross 1979; Ross 1984).

The subsequent comparison of the specimen sequence of mitochondrial DNA control region (Figure 6) in the data base of the web-based program *DNA-surveillance* confirmed the earlier photographic identification (Figure 7), by means of a phylogenetic method (tree).

Another method for genetic species identification is the measure of evolutionary distance. This distance was calculated between the Samoan specimen and each species sequence used in *DNA-surveillance* (Table 1). The closest distance was with the dwarf sperm whale.

After the morphological and genetic species identification, the sample was coded as *Ksi05Sa01* for archiving purposes.

Comparison with other *K. sima* specimens

A comparison of the control region mtDNA sequence of the Samoan specimen with four other *K. sima* specimens from Australia and South Africa (Table 2) revealed no shared haplotypes (Figure 8). A Neighbour-joining phylogenetic reconstruction revealed a closer relationship between the Samoan and the South African specimen (KsiSFRI 2000/04).

Discussion

An early morphological examination based on photographs identified the specimen stranded in Lotofaga as a male dwarf sperm whale. However, due to the potential difficulty in unambiguously identifying the species in the genus *Kogia* (McAlpine 2002; Plön 2004), it was necessary to utilize molecular methods to confirm the species and sex identification.

This is the first record of the species in Samoan waters and the third for the eastern South Pacific region, where previous records occurred in New Caledonia and French Polynesia (SPWRC 2004). This raises the current list of cetaceans recorded in Samoan waters to ten (Table 3).

The genetic relationship of *K. sima* among different populations it has been only recently examined (Chivers et al. 2004). It has been postulated that genetic differentiation occurs between Atlantic and Indo-Pacific *K. sima* specimens, which may lead to the recognition of a third *Kogia* species. The

reduced number *K. sima* specimens in our study (all from the Indo-Pacific region) and the unavailability to compare with Chivers et al. (2004) data set, prevents further population analysis. However, it was interesting to note the closest relationship of the Samoan specimen was not observed with the geographically closest individuals (Australia). A wider and extensive sampling and the inclusion of other sampled specimens analyzed on population genetic analyses (Chivers et al. 2004; Plön 2004) would allow in the future to test the hypothesis of speciation by Chivers et al. (2004).

It is recommended that collection of genetic material be continued in Samoa, as this type of study has proved (this report and also see Olavarría et al. 2004) to be a significant contribution to the cetacean biodiversity survey that is currently undertaken by the Ministry of Natural Resources and Environment of Samoa.

Acknowledgements

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Bibliographic References

Arnold, P.; Marsh, H.; Heinsohn, G. 1987: The occurrence of two forms of minke whales in east Australian waters with a description of external

- characters and skeleton of the diminutive or dwarf form. *Scientific Report of the Whales Research Institute* 38: 1-46.
- Baker, C. S.; Dalebout, M. L.; Lavery, S.; Ross, H. A. 2003: www.DNA-surveillance: applied molecular taxonomy for species conservation and discovery. *Trends in Ecology & Evolution* 18: 271-272.
- Baker, C. S.; Gilbert, D. A.; Weinrich, M. T.; Lambertsen, R. H.; Calambokidis, J.; McArdle, B.; Chambers, G. K.; O'Brien, S. J. 1993: Population characteristics of DNA fingerprints in humpback whales (*Megaptera novaeangliae*). *The Journal of Heredity* 84: 281-290.
- Best, P. B. 1985: External characteristics of southern minke whales and the existence of a diminutive form. *Scientific Report of the Whales Research Institute* 36: 1-33.
- Brown, G. G.; Gadeleta, G.; Pepe, G.; Saccone, C.; Sbisà, E. 1986: Structural conservation and variation in the D-loop containing region of vertebrate mitochondrial DNA. *Journal of Molecular Biology* 192: 503-511.
- Chivers, S. J.; Le Duc, R. G.; Robertson, K. M.; Barros, N. B.; Dizon, A. E. 2004: Large inter-ocean genetic differences within *Kogia sima* indicate long-term isolation and possibly a second species. Cetacean systematics approaches in genetics, morphology, & behavior. La Jolla, CA, USA.
- Dalebout, M. L.; Van Helden, A.; Van Waerebeek, K.; Baker, C. S. 1998: Molecular genetic identification of southern hemisphere beaked whales (Cetacea: Ziphiidae). *Molecular Ecology* 7: 687-695.
- Davis, L. G.; Dibner, M. D.; Battey, J. F. 1986: Basic methods in molecular biology. Elsevier Science Publishing Co.
- Gilson, A.; Syvanen, M.; Levine, K.; Banks, J. 1998: Deer gender determination by Polymerase Chain Reaction: validation study and application to tissues, bloodstains and hair forensic samples from California. *California Fish and Game* 84: 159-169.
- Kasamatsu, F.; Nishiwaki, S.; Ishikawa, H. 1995: Breeding areas and southbound migrations of southern minke whales *Balaenoptera acutorostrata*. *Marine Ecology Progress Series* 119: 1-10.
- Kimura, M. 1980: A simple method for estimating rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16: 111-120.
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- Maddison, D. R.; Maddison, W. P. 2000: MacClade: Analysis of phylogeny and character evolution. Sunderland, Massachusetts, Sinauer Associates, Inc.
- McAlpine, D. F. 2002: Pygmy and Dwarf sperm whales. *In*: Perrin, W. F.; Wursig, B.; Thewissen, J. G. M. ed. Encyclopedia of marine mammals. Sydney, Academic Press. Pp. 1007-1008.
- Moritz, C.; Dowling, T. E.; Brown, W. M. 1987: Evolution of animal mitochondrial DNA: relevance for population biology and systematics. *Annual Review of Ecology and Systematics* 18: 269-292.
- Olavarría, C.; Oremus, M.; Pinto, G. d. T.; Steel, D.; Paton, D.; Baker, C. S. 2004: Genetic identification of small cetaceans from the waters of Samoa, South Pacific. Report SC/56/SM25 to the Scientific Committee of the International Whaling Commission.
- Paton, D. A.; Gibbs, N.; Childerhouse, S. J.; Noad, M. J. 2002: South Pacific Island Whale and Dolphin Program, Stage 1, Independent Samoa 2001, Draft Report for Comment. Southern Cross Centre for Whale Research, Southern Cross University. 73 plus annexes.
- Pichler, F. B.; Robineau, D.; Goodall, R. N. P.; Meyer, M. A.; Olavarría, C.; Baker, C. S. 2001: Origin and radiation of Southern Hemisphere coastal dolphins (genus *Cephalorhynchus*). *Molecular Ecology* 10: 2215-2223.
- Plön, S. 2004: The status and natural history of pygmy (*Kogia breviceps*) and dwarf (*K. sima*) sperm whales off Southern Africa. Department of Zoology & Entomology. Grahamstown, South Africa, Rhodes University.
- Rice, D. W. 1998: Marine mammals of the world: systematics and distribution. Lawrence, KS, Society for Marine Mammalogy.
- Ross, G. J. B. 1979: Records of pygmy and dwarf sperm whales, genus *Kogia*, from southern Africa, with biological notes and some comparisons. *Annals of the Cape Provincial Museums, Natural History* 11: 259-327.
- Ross, G. J. B. 1984: The smaller cetaceans of the south east coast of southern Africa. *Annals of the Cape Provincial Museums, Natural History* 15: 173-410.
- Ross, H. A.; Lento, G. M.; Dalebout, M. L.; Goode, M.; Ewing, G.; McLaren, P.; Rodrigo, A. G.; Lavery, S.; Baker, C. S. 2003: DNA surveillance: web-
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- based molecular identification of whales, dolphins and porpoises. *The Journal of Heredity* 94: 111–114.
- Saiki, R. K.; Gelfand, D. H.; Stoffel, S.; Scharf, S. J.; Higuchi, R.; Horn, G. T.; Mullis, K. B.; Erlich, H. A. 1988: Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. *Science* 239: 487-491.
- SPWRC 2004: Report of the Annual Meeting of the South Pacific Whale Research Consortium: 2-6 April 2004, Byron Bay, NSW, Australia. Report SC/56/SH7 to the Scientific Committee of the International Whaling Commission.
- Swofford, D. L. 2000: PAUP*: Phylogenetic Analysis Using Parsimony (*and Other Methods). Sunderland, MA, Sinauer Associates.
- Walsh, S. A.; Paton, D. A. 2003: Preliminary report on the survey of whales and dolphins in Samoa during September 2003. Southern Cross University Whale Research Centre. 7.
- Wilson, A. C.; Cann, R. L.; Carr, S. M.; George, M.; Gyllenstein, U. B.; Helm-Bychowski, K. M.; Higuchi, R. G.; Palumbi, S. R.; Pragger, E. M.; Sage, R. D.; Stoneking, M. 1985: Mitochondrial DNA and two perspectives on evolutionary genetics. *Biological Journal of the Linnean Society* 26: 375-400.
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Figure 1. The approximated location of the stranding, in Lotofaga, Safata, Upolu island, is indicated by a red dot.






Figure 2 A, B, C. Dwarf sperm whale when stranded in Lotofaga (Photographs: Marc Barr).



MINISTRY OF NATURAL RESOURCES, ENVIRONMENT
& METEOROLOGY
Division of Environment & Conservation



SAMOA'S WHALE & DOLPHIN STRANDING REPORT

ID #: Ksi01Sa05str

1. Observer(s) Name	Contact	Date	Time Cetacean found	Examiner
Mac Barr + Mulina Petelo	macbarr@hotmail.com	03/03/05	9:00 am	June Ward

2. LOCATION OF STRANDING

Village: Lotofaga, Safata GPS Coordinates:
 Latitude: n/a Longitude: n/a

Description of location:
Stranded whale was found on accessible sandy beach @ Lotofaga MPA center, close to sea.

3. CETACEAN INFORMATION

<p>Species: <u>Possible</u> Common Name: <u>Rhymy sperm/Dwarf whale</u> Scientific: <u>Kogia sp.</u> Sex: <u>male</u> Estimated Length(s): <u>1.5-2m</u></p>	<p>Estimated Age Class: (please tick)</p> <p>Adult <input checked="" type="checkbox"/> Sub-adult <input checked="" type="checkbox"/> Calf <input type="checkbox"/> Unknown <input type="checkbox"/></p>																
<p>Event Type:</p> <table style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 30%;">Entanglement</td> <td style="width: 10%;"><input type="checkbox"/></td> <td style="width: 30%;">Dead/Ashore</td> <td style="width: 10%;"><input checked="" type="checkbox"/></td> </tr> <tr> <td>Possible shooting</td> <td><input type="checkbox"/></td> <td>Dead/Floating</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Vessel strike</td> <td><input type="checkbox"/></td> <td>Injured</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Illness</td> <td><input type="checkbox"/></td> <td>Unknown</td> <td><input type="checkbox"/></td> </tr> </table>	Entanglement	<input type="checkbox"/>	Dead/Ashore	<input checked="" type="checkbox"/>	Possible shooting	<input type="checkbox"/>	Dead/Floating	<input type="checkbox"/>	Vessel strike	<input type="checkbox"/>	Injured	<input type="checkbox"/>	Illness	<input type="checkbox"/>	Unknown	<input type="checkbox"/>	<p># of Stranded Animals:</p> <p>Single stranding <input checked="" type="checkbox"/> Mass stranding <input type="checkbox"/> # of dead animals <u>1</u> # of alive animals _____</p>
Entanglement	<input type="checkbox"/>	Dead/Ashore	<input checked="" type="checkbox"/>														
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Illness	<input type="checkbox"/>	Unknown	<input type="checkbox"/>														

Appearance of cetacean(s): skin colour & markings, public & canine disturbances
colouration of whale was white (found 1 day after report was made), had cuts on the body possibly made during stranding on reef. Whale was eaten by dogs, people removed fluke.

4. CONDITION OF CETACEAN

If dead, state of carcass(es):

Fresh	<input checked="" type="checkbox"/>	Advanced decomposition	<input type="checkbox"/>	Unknown	<input type="checkbox"/>
Moderate decomposition	<input type="checkbox"/>	Mummified/Skeletal	<input type="checkbox"/>		

If alive, state:
 The nature of wounds & location:
n/a

Whether cetacean(s) were released:
no

5. COMMENTS

whale was reported by Safata PCV + care-taker. Found dead ashore on sandy beach. Tissue samples collected the ff. day. Dogs ate whale carcass + fluke was cut off. Head of whale was removed + buried to be dug up later for mouth region. Carcass was buried by local people. Tissue samples store in 99.9% + 70% ethanol for analysis @ Uni of Auckland by Carlos Olvarria.

Figure 3. Stranding data sheet of the dwarf sperm whale stranded in Lotofaga.



Figure 4. Ventral view of the dwarf sperm whale stranded in Lotofaga, showing the relative distance between anus and genital slit used for sex identification on the field (Photograph: Marc Barr).

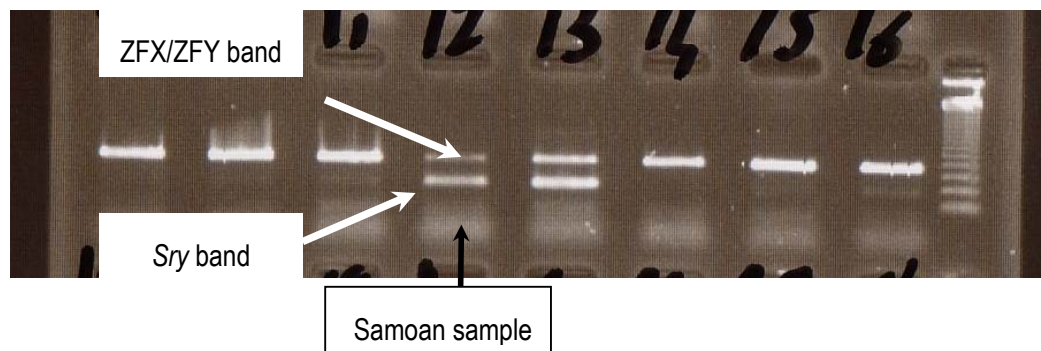


Figure 5. Sex identification of dwarf sperm whale stranded in Lotofaga, showing amplified band of the *Sry* gen, which identified it as a male.

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1  CCTTGAAAGG GCTTTATTGT AAGTAATCAC AAACCCCTAG TGCCATGTCA
51  GTATTAAAAT TAATCCACCC AATTACATTC TCATGTTGAA AAAACCATGC
101 AAATATATGT CCCATTTCAA TAAATAGCGT TCTCCTCGTA GATGCATGTA
151 TATACATGCT ATGTATAATA GTGCATTCAA TTATTTTCCC CACGAGAAGT
201 TAAAGCTCGT ATTGAATTCT ATTAATTTTA CATATTACAT AATATTATTG
251 GTCGTACATA AAACATACTG TTAAATCAGT CCCAGCCCCT TAATATGATG
301 GCCGCTCCAT TAGATCACGA GCTTAATCAC CATGCCGCGT GAAACCAGCA
351 ACCCGCTCGG CTGGGATCCC CCTCCTCGCA CCGGGCCCAT CAATTGTGGG
401 GGTAGCTATT TAATGCCTTT TACAATACAT CTGGTTCTTA CTTCAGGGCC
451 ATTTTCATCT AAAATCGCCC ACTCGTTCCC CTTAAATAAG ACATCTCGAT
501 GGATTAGTTA CATTGTGGTC TCTTAATCTG GTCACGGGTG GTTTTTTCATG
551 CCTCTGGTAT CTTTTTTTTT GGGGGGGGGG ATTTGCACCG ACTCCCCTAT
601 GGCCGACGGG GCGGCCCCGC CGCAGTCAGA GTTGGTCTTA GCTGGACTTG
651 TGTGTATTTT TGATCGGGCA ACTCTCCTAG TCCCTACTTA AATTAATGAT
701 CGTAAGACAT AATTAATTAA TGGTTACCGG

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Figure 6. Sequence of the mitochondrial control region of the dwarf sperm whale stranded in Lotofaga.

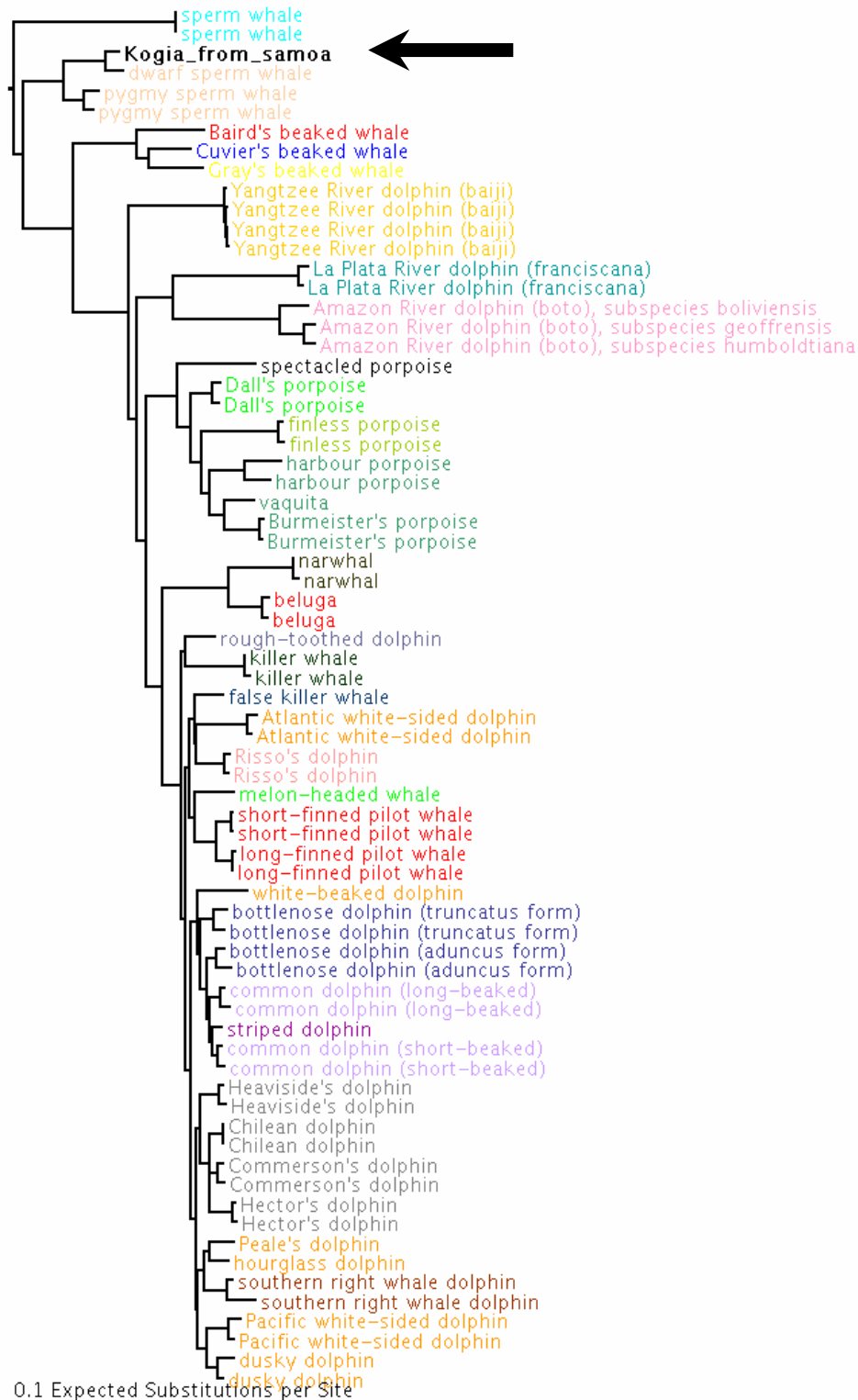


Figure 7. Phylogenetic reconstruction of odontocete species, including the dwarf sperm whale stranded in Lotofaga (see arrow), showing the closest relationship with a reference sequence of a dwarf sperm whale.

	7	35	107	249	268	279	404	456	457
KsiTASPWW2	G	C	C	G	C	T	C	C	C
Ksi05Sa01	.	T	T	.	G	C	.	T	.
KsiSAM99.260	A	T	.	A	A	.	T	.	.
KsiSFRI 2000/04	.	T	.	A	G	C	.	.	T

Figure 8. Variable sites in the control region mtDNA sequences of *Kogia sima*. Dots (.) indicate similar nucleotide as the top sequence KsiTASPWW2.

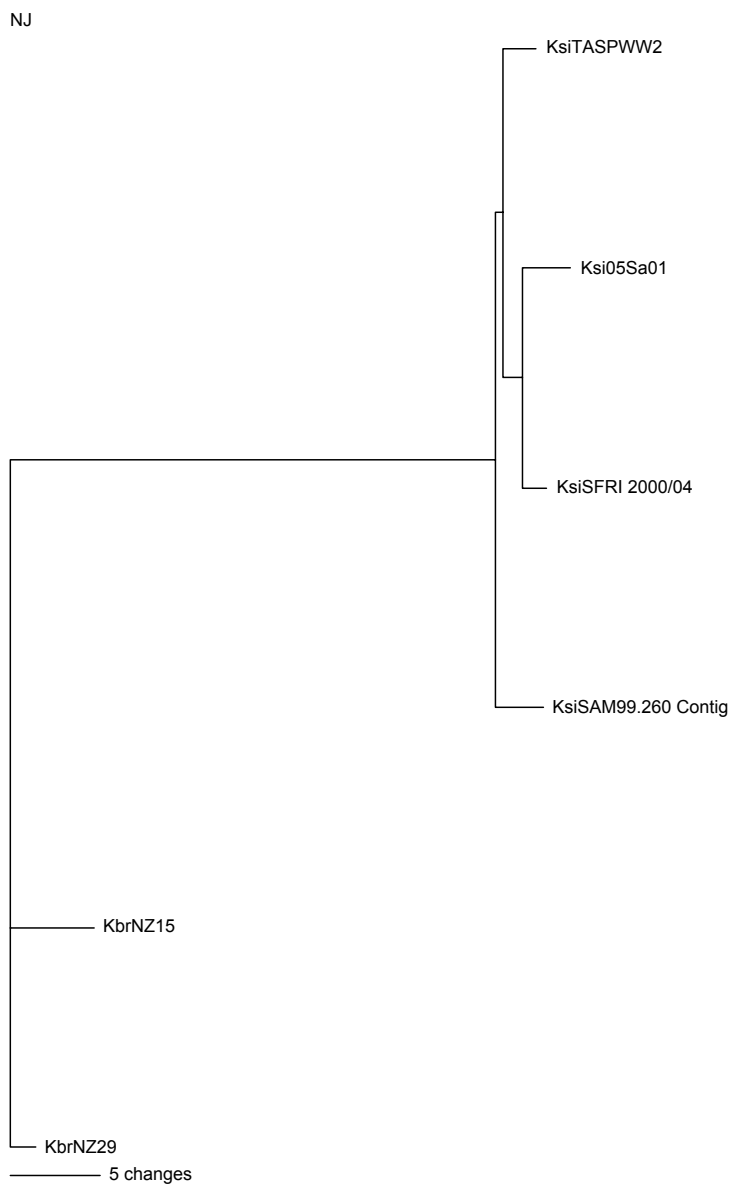


Figure 9. Neighbour-joining phylogenetic reconstruction of *Kogia sima* control region mtDNA haplotypes, under Kimura 2-parameter model of multiple substitutions (Kimura 1980).

Table 1. Evolutionary distance between Samoan specimen and some of the odontocete species from DNA-surveillance data base.

ID	Common Name	Distance
KsiTASPWW2	dwarf sperm whale	0.034
KbreNZ01SP	pygmy sperm whale	0.104
CeutC6.FP	Chilean dolphin	0.127
PmacEP4.DW	sperm whale	0.279
CheavMH.FP	Heaviside's dolphin	0.286
BbaSW4965	Baird's beaked whale	0.286
CheavMA.FP	Heaviside's dolphin	0.291
CcomL2.FP	Commerson's dolphin	0.293
CeutH1.FP	Chilean dolphin	0.3
SbreFP1.MP	rough-toothed dolphin	0.303
ZcaNZ11.MD	Cuvier's beaked whale	0.304
TtruT2.JW	bottlenose dolphin (truncatus form)	0.306
LobsNZW1AH	dusky dolphin	0.307
TaduA1.JW	bottlenose dolphin (aduncus form)	0.308
LobINP1.FC	Pacific white-sided dolphin	0.313
LobsPE2.FC	dusky dolphin	0.316
CheBP03D	Hector's dolphin	0.321
PeleFP1.MP	melon-headed whale	0.323
MgrNZ05.MD	Gray's beaked whale	0.323
GmacCA2.LS	short-finned pilot whale	0.328
PdalNP9.PR	Dall's porpoise	0.329
LperNZ4.FP	southern right whale dolphin	0.33
GmacAT1.LS	short-finned pilot whale	0.332
PcraNZ1.MD	false killer whale	0.333
LvexC8.SL	Yangtze River dolphin (baiji)	0.334
LobINP8.FC	Pacific white-sided dolphin	0.335
GmeINZ01MD	long-finned pilot whale	0.335
LacuNF6.FC	Atlantic white-sided dolphin	0.336
DdelCA7.PR	common dolphin (short-beaked)	0.336
PdalNP2.PR	Dall's porpoise	0.336
LvexD9.SL	Yangtze River dolphin (baiji)	0.338
DdelCA6.PR	common dolphin (short-beaked)	0.34
LacuNF7.FC	Atlantic white-sided dolphin	0.341
DcapCA4.PR	common dolphin (long-beaked)	0.342
AdioTF5.PR	Spectacled porpoise	0.345
ScoeMD1.AV	striped dolphin	0.346
PsinCA3.PR	Vaquita	0.348
PphoNP0.PR	harbour porpoise	0.353
GgriNZ1.MD	Risso's dolphin	0.355
DleuAR7.WL	Beluga	0.356
PspiPE7.PR	Burmeister's porpoise	0.365
PphoNP5.PR	harbour porpoise	0.376
LcruMG2.FP	hourglass dolphin	0.382
OorcNP9.RH	killer whale	0.385
LalbNA5.FC	white-beaked dolphin	0.39
LausMG2.FP	Peale's dolphin	0.4

Table 2. *K. sima* data for other specimens from which mtDNA control region sequences were available and compared with the Samoan specimen.

Code	Sex	Location	Date	Collected by	Source
KsiSFRI 2000/04	F	32°47'S; 18°10'E St. Helena Bay, West coast, South Africa	05-May-02	M Meyer	(Plön 2004)
KsiSAM99.260	F	200m N of Largs Bay Jetty, Darwin, Australia	27-Nov-99	C Kemper	(Plön 2004)
KsiTASPWW2	F	43°27'S; 147°15'E Cloudy Bay, Bruny Island, Tasmania, Australia	16-Nov-92	K Evans	(Plön 2004)

Table 3. Updated list of recorded cetaceans for Samoan waters, July 2005

Common	Species
Humpback whale	<i>Megaptera novaeangliae</i>
Minke whale ³	<i>Balaenoptera sp</i>
Sperm whale	<i>Physeter macrocephalus</i>
False killer whale	<i>Pseudorca crassidens</i>
Short-finned pilot whale	<i>Globicephala macrorhynchus</i>
Beaked whale sp.	<i>Mesoplodon sp.</i>
Dwarf sperm whale	<i>Kogia sima</i>
Bottlenose dolphin	<i>Tursiops truncatus</i>
Rough-toothed dolphin	<i>Steno bredanensis</i>
Spinner dolphin	<i>Stenella longirostris</i>

³ see footnote 1 regarding the positively species identification of southern hemisphere minke whales in Samoan waters.