

Molecular Identification of Stranded Cetaceans in Coastal China

Supplemental Material

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Supplemental Material

Supplemental Material 1. Percent identity values between sequences of the D-loop gene obtained in the present study for cetaceans numbered NJNU200210 and NJNU2012003, and DNA sequences from its respective congener available in the online database GenBank

Description	Max score	Total score	Query cover	E value	Ident.	Accession #
<i>Balaenoptera omurai</i> mitochondrial DNA, complete genome, isolate: NSMT-32992	1,683	1,683	100%	0.0	99%	AB201257.1
<i>B. omurai</i> mitochondrial DNA, complete genome, isolate: NSMT-32505	1,677	1,677	100%	0.0	99%	AB201256.1
<i>B. omurai</i> isolate Exmouth D-loop, complete sequence; mitochondrial	1,666	1,666	99%	0.0	99%	KT757371.1
<i>B. omurai</i> mitochondrial DNA, D-loop region, isolate: NSMT-M32505	1,661	1,661	99%	0.0	99%	AB116095.1
<i>B. omurai</i> mitochondrial DNA, D-loop region, isolate: NRIFSF7	1,650	1,650	99%	0.0	99%	AB116097.1
<i>Balaenoptera edeni</i> specimen-voucher NJNU0379 mitochondrial control region, partial sequence	1,650	1,650	99%	0.0	99%	AF398372.1
<i>B. omurai</i> mitochondrial DNA, D-loop region, isolate: NRIFSF1	1,644	1,644	99%	0.0	99%	AB116096.1
<i>B. edeni</i> mitochondrial DNA, complete genome, isolate: NSMT-33622	1,327	1,327	100%	0.0	93%	AB201258.1
<i>B. omurai</i> voucher MauBs_2013_11_03 tRNA-Tyr gene, partial sequence; tRNA-Pro gene, complete sequence; and D-loop, partial sequence; mitochondrial	1,328	1,328	78%	0.0	99%	KM233838.1
<i>Balaenoptera borealis</i> mitochondrial DNA, complete genome	1,303	1,303	100%	0.0	92%	AP006470.1
<i>B. borealis</i> isolate E91 mitochondrion, complete genome	1,291	1,291	100%	0.0	92%	MF409249.1
<i>B. borealis</i> isolate D27 mitochondrion, complete genome	1,291	1,291	100%	0.0	92%	MF409248.1
<i>B. borealis</i> voucher SEFSC: MMMGL: Bbor001 tRNA-Pro gene, partial sequence; D-loop, complete sequence; and tRNA-Phe gene, partial sequence; mitochondrial	1,291	1,291	100%	0.0	92%	KJ586813.1
<i>Balaenoptera brydei</i> mitochondrial DNA, complete genome	1,286	1,286	100%	0.0	92%	AP006469.1
<i>B. edeni</i> mitochondrial DNA, D-loop region, isolate: RMNH4003	1,280	1,280	98%	0.0	92%	AB116099.1
<i>B. brydei</i> mitochondrial DNA, complete genome, isolate: NSMT-33072	1,277	1,277	100%	0.0	92%	AB201259.1
<i>Balaenoptera musculus</i> mitochondrion, complete genome	1,271	1,271	100%	0.0	92%	MF409242.1

Due to the same BLAST results of NJNU200210 and NJNU2012003, here only are the results of NJNU200210 presented.

Supplemental Material 2. Percent identity values between sequences of the D-loop gene obtained in the present study for cetaceans numbered NJNU2010087 and NJNU2016059, and DNA sequences from its respective congener available in the online database GenBank

Description	Max score	Total score	Query cover	E value	Ident.	Accession #
<i>Balaenoptera edeni</i> mitochondrial DNA, complete genome, isolate: NSMT-33622	1,724	1,724	100%	0.0	100%	AB201258.1
<i>B. edeni</i> mitochondrial DNA, D-loop region, isolate: RMNH4003	1,650	1,650	97%	0.0	99%	AB116099.1
<i>B. edeni</i> voucher SEFSC: MMMGL: Bede001 tRNA-Pro gene, partial sequence; D-loop, complete sequence; and tRNA-Phe gene, partial sequence; mitochondrial	1,561	1,561	100%	0.0	97%	KJ586818.1
<i>B. edeni</i> voucher SEFSC: MMMGL: Bede004 tRNA-Pro gene, partial sequence; D-loop, complete sequence; and tRNA-Phe gene, partial sequence; mitochondrial	1,557	1,557	100%	0.0	97%	KJ586819.1
<i>B. edeni</i> voucher SEFSC: MMMGL: Bede005 tRNA-Pro gene, partial sequence; D-loop, complete sequence; and tRNA-Phe gene, partial sequence; mitochondrial	1,555	1,555	100%	0.0	97%	KJ586820.1
<i>Balaenoptera borealis</i> mitochondrial DNA, complete genome	1,555	1,555	100%	0.0	97%	AP006470.1
<i>B. borealis</i> isolate E91 mitochondrion, complete genome	1,553	1,553	100%	0.0	96%	MF409249.1
<i>B. borealis</i> isolate D27 mitochondrion, complete genome	1,553	1,553	100%	0.0	96%	MF409248.1
<i>B. borealis</i> voucher SEFSC: MMMGL: Bbor001 tRNA-Pro gene, partial sequence; D-loop, complete sequence; and tRNA-Phe gene, partial sequence; mitochondrial	1,553	1,553	100%	0.0	96%	KJ586813.1
<i>Balaenoptera brydei</i> mitochondrial DNA, complete genome, isolate: NSMT-33072	1,553	1,553	100%	0.0	96%	AB201259.1
<i>B. brydei</i> mitochondrial DNA, complete genome	1,515	1,515	100%	0.0	96%	AP006469.1
<i>B. brydei</i> mitochondrial DNA, D-loop region, isolate: 77N62	1,502	1,502	97%	0.0	96%	AB116098.1
<i>Balaenoptera physalus</i> mitochondrion, complete genome	1,367	1,367	100%	0.0	93%	MF409243.1
<i>B. physalus</i> control region, complete sequence; mitochondrial	1,367	1,367	100%	0.0	93%	AY582748.1
<i>Balaenoptera omurai</i> mitochondrial DNA, complete genome, isolate: NSMT-32505	1,363	1,363	100%	0.0	93%	AB201256.1
<i>Balaenoptera musculus</i> mitochondrion, complete genome	1,358	1,358	100%	0.0	93%	MF409242.1

Due to the same BLAST results of NJNU2016059 and NJNU2010087, here only are the results of NJNU2016059 presented.

Supplemental Material 3. Percent identity values between sequences of the D-loop gene obtained in the present study for cetaceans numbered NJNU2010088 and DNA sequences from its respective congener available in the online database GenBank

Description	Max score	Total score	Query cover	E value	Ident.	Accession #
<i>Mesoplodon densirostris</i> isolate SWFSC ID z0094563 mitochondrion, complete genome	1,474	1,474	100%	0.0	99%	KF032878.2
<i>M. densirostris</i> isolate SWFSC ID z0079840 mitochondrion, partial genome	1,474	1,474	100%	0.0	99%	KF032877.2
<i>M. densirostris</i> isolate SWFSC ID z0079839 mitochondrion, complete genome	1,474	1,474	100%	0.0	99%	KF032876.2
<i>M. densirostris</i> isolate SWFSC ID z0079824 mitochondrion, partial genome	1,474	1,474	100%	0.0	99%	KF032872.2
<i>M. densirostris</i> isolate SWFSC ID z0008681 mitochondrion, complete genome	1,474	1,474	100%	0.0	99%	KF032871.2
<i>M. densirostris</i> isolate SWFSC ID z0050723 mitochondrion, partial genome	1,474	1,474	100%	0.0	99%	KF032864.2
<i>M. densirostris</i> isolate SWFSC ID z0009110 mitochondrion, complete genome	1,474	1,474	100%	0.0	99%	KF032861.2
<i>M. densirostris</i> isolate SWFSC ID z0004010 mitochondrion, complete genome	1,474	1,474	100%	0.0	99%	KF032860.2
<i>M. densirostris</i> isolate SWFSC ID z0074263 mitochondrion, partial genome	1,472	1,472	99%	0.0	99%	KF032869.2
<i>M. densirostris</i> isolate SWFSC ID z0074425 mitochondrion, complete genome	1,469	1,469	100%	0.0	99%	KF032868.2
<i>M. densirostris</i> isolate SWFSC ID z0074424 mitochondrion, complete genome	1,469	1,469	100%	0.0	99%	KF032867.2
<i>M. densirostris</i> isolate SWFSC ID z0033737 mitochondrion, complete genome	1,469	1,469	100%	0.0	99%	KF032863.2
<i>M. densirostris</i> isolate SWFSC ID z0074264 mitochondrion, complete genome	1,463	1,463	99%	0.0	99%	KF032870.2
<i>M. densirostris</i> isolate SWFSC ID z0079838 mitochondrion, partial genome	1,441	1,441	100%	0.0	99%	KF032875.2
<i>M. densirostris</i> isolate SWFSC ID z0079837 mitochondrion, partial genome	1,437	1,437	98%	0.0	99%	KF032874.2
<i>Mesoplodon grayi</i> voucher Mgr159 mitochondrion, complete genome	1,325	1,325	99%	0.0	97%	KF981442.1
<i>Mesoplodon stejnegeri</i> voucher CRI000090 mitochondrion, complete genome	1,321	1,321	99%	0.0	97%	NC036997.1
<i>M. stejnegeri</i> voucher CRI000090 mitochondrion, complete genome	1,321	1,321	99%	0.0	97%	MG000980.1
<i>Mesoplodon europaeus</i> isolate SWFSC ID z0074265 mitochondrion, complete genome	1,245	1,245	99%	0.0	95%	KC776694.2
<i>M. europaeus</i> isolate SWFSC ID z0094578 mitochondrion, complete genome	1,245	1,245	99%	0.0	95%	KC776695.1

Supplemental Material 4. Percent identity values between sequences of the Cytb gene obtained in the present study for cetaceans numbered NJNU200210 and NJNU2012003, and DNA sequences from its respective congener available in the online database GenBank

Description	Max score	Total score	Query cover	E value	Ident.	Accession #
<i>Balaenoptera omurai</i> mitochondrial DNA, complete genome, isolate: NSMT-32992	2,636	2,636	100%	0.0	100%	AB201257.1
<i>B. omurai</i> mitochondrial DNA, complete genome, isolate: NSMT-32505	2,614	2,614	100%	0.0	99%	AB201256.1
<i>Balaenoptera borealis</i> mitochondrial DNA, complete genome	2,058	2,058	99%	0.0	93%	AP006470.1
<i>B. borealis</i> isolate E91 mitochondrion, complete genome	2,052	2,052	99%	0.0	93%	MF409249.1
<i>B. borealis</i> isolate D27 mitochondrion, complete genome	2,052	2,052	99%	0.0	93%	MF409248.1
<i>B. omurai</i> voucher MauBs_2013_11_03 cytochrome b (Cytb) gene, partial cds; mitochondrial	2,043	2,043	77%	0.0	100%	KM233837.1
<i>Balaenoptera musculus</i> mitochondrion, complete genome	2,030	2,030	99%	0.0	92%	MF409242.1
<i>Balaenoptera edeni</i> mitochondrial DNA, complete genome, isolate: NSMT-33622	2,019	2,019	99%	0.0	92%	AB201258.1
<i>B. musculus</i> mitochondrial DNA complete genome	2,019	2,019	99%	0.0	92%	X72204.1
<i>Balaenoptera brydei</i> mitochondrial DNA, complete genome	1,991	1,991	99%	0.0	92%	AP006469.1
<i>B. brydei</i> mitochondrial DNA, complete genome, isolate: NSMT-33072	1,986	1,986	99%	0.0	92%	AB201259.1
<i>Balaenoptera physalus</i> isolate 79754 mitochondrion, complete genome	1,969	1,969	99%	0.0	92%	KC572824.1
<i>B. physalus</i> isolate 76902 mitochondrion, complete genome	1,969	1,969	99%	0.0	92%	KC572821.1
<i>B. physalus</i> isolate 37561 mitochondrion, complete genome	1,969	1,969	99%	0.0	92%	KC572741.1
<i>B. physalus</i> mitochondrion, complete genome	1,964	1,964	99%	0.0	92%	MF409243.1
<i>B. physalus</i> isolate 93840 mitochondrion, complete genome	1,964	1,964	99%	0.0	92%	KC572855.1
<i>B. physalus</i> isolate 91297 mitochondrion, complete genome	1,964	1,964	99%	0.0	92%	KC572835.1
<i>B. physalus</i> isolate 91295 mitochondrion, complete genome	1,964	1,964	99%	0.0	92%	KC572833.1
<i>B. physalus</i> isolate 88586 mitochondrion, complete genome	1,964	1,964	99%	0.0	92%	KC572829.1

Due to the same BLAST results of NJNU2012003 and NJNU200210, here only are the results of NJNU2012003 presented.

Supplemental Material 5. Percent identity values between sequences of the Cytb gene obtained in the present study for cetaceans numbered NJNU2010087, NJNU2016059, and NJNU2016059, and DNA sequences from its respective congener available in the online database GenBank

Description	Max score	Total score	Query cover	E value	Ident.	Accession #
<i>Balaenoptera edeni</i> mitochondrial DNA, complete genome, isolate: NSMT-33622	640	640	100%	1e-179	100%	AB201258.1
<i>B. edeni</i> voucher SEFSC: MMMGL: Bede007 cytochrome b (Cytb) gene, complete cds; mitochondrial	595	595	100%	3e-166	98%	KJ586849.1
<i>Balaenoptera borealis</i> isolate E91 mitochondrion, complete genome	579	579	100%	3e-161	97%	MF409249.1
<i>B. borealis</i> isolate D27 mitochondrion, complete genome	579	579	100%	3e-161	97%	MF409248.1
<i>B. borealis</i> mitochondrial DNA, complete genome	579	579	100%	3e-161	97%	AP006470.1
<i>B. borealis</i> mitochondrial gene for Cytb	579	579	100%	3e-161	97%	X75582.1
<i>Balaenoptera brydei</i> mitochondrial DNA, complete genome, isolate: NSMT-33072	562	562	100%	3e-156	96%	AB201259.1
<i>B. brydei</i> mitochondrial DNA, complete genome	562	562	100%	3e-156	96%	AP006469.1
<i>Eschrichtius robustus</i> voucher IPEE RAS: 2067 Cytb gene, partial cds; mitochondrial	503	503	99%	2e-138	93%	KJ865248.1
<i>Balaenoptera physalus</i> isolate 91302 mitochondrion, complete genome	503	503	99%	2e-138	93%	KC572839.1
<i>B. physalus</i> isolate 72987 mitochondrion, complete genome	503	503	99%	2e-138	93%	KC572800.1
<i>B. physalus</i> isolate 72984 mitochondrion, complete genome	503	503	99%	2e-138	93%	KC572797.1
<i>E. robustus</i> haplotype 6 Cytb gene, partial cds; mitochondrial	503	503	99%	2e-138	93%	EF165341.1
<i>E. robustus</i> mitochondrial DNA, complete genome	503	503	99%	2e-138	93%	AP006471.1
<i>Megaptera novaeangliae</i> voucher GOM9084 Cytb gene, complete cds; mitochondrial	497	497	99%	8e-137	93%	GQ353256.1
<i>M. novaeangliae</i> haplotype 3 Cytb gene, partial cds; mitochondrial	497	497	99%	8e-137	93%	EF165344.1
<i>M. novaeangliae</i> haplotype 2 Cytb gene, partial cds; mitochondrial	497	497	99%	8e-137	93%	EF165343.1

Due to the same BLAST results of NJNU2010087, NJNU2016059, and NJNU2016059, here only are the results of NJNU2010087 presented.