

Prominent hepatic ductular reaction induced by *Oschmarinella macrorchis* in a Hubbs' beaked whale *Mesoplodon carlhubbsi*, with biological notes

Shotaro Nakagun*, Akira Shiozaki, Mari Ochiai, Ayaka Matsuda, Yuko Tajima, Takashi Matsuishi, Kenichi Watanabe, Noriyuki Horiuchi, Yoshiyasu Kobayashi

*Corresponding author: snakagun@gmail.com

Diseases of Aquatic Organisms 127: 177–192 (2018)

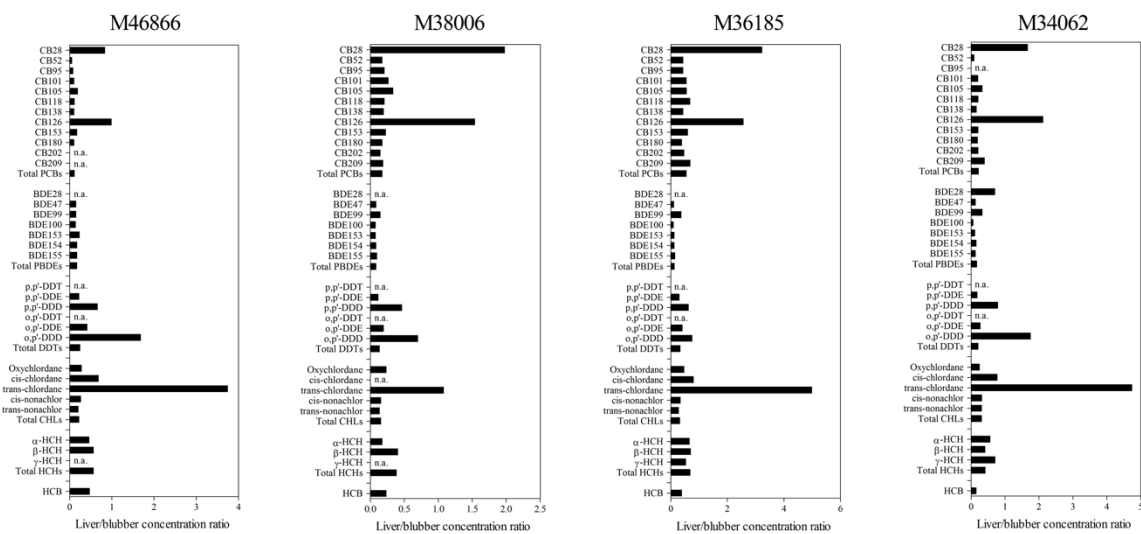


Fig. S1. Liver to blubber concentration ratios of polychlorinated biphenyls (PCBs), polybrominated diphenyl ether (PBDE), dichlorodiphenyltrichloroethane and its related compounds (DDTs), chlordanes (CHLs), hexachlorocyclohexanes (HCHs) and hexachlorobenzene (HCB) in 4 male *Mesoplodon carlhubbsi*.

Table S1. List of primers used for the amplification and sequencing of mitochondrial DNA NADH dehydrogenase subunit 3 (mtND3), 18S ribosomal RNA (rRNA) and 28S rRNA trematode genes.

	Use	Primer sequence (5' – 3')	Reference
mtND3			
ND3F	Amplifying/Sequencing	GCT TAA TTK KTA AAG CYT TGR ATT CTT ACT	Fernández et al. 1998
ND3-4	Amplifying/Sequencing	CTA CTA GTC CCA CTC AAC RTA ACC YT	Fernández et al. 2000
18S rRNA			
Worm A	Amplifying/Sequencing	GCG AAT GGC TCA TTA AAT CAG	Littlewood & Olson 2001
Worm B	Amplifying/Sequencing	ACG GAA ACC TTG TTA CGA CT	Littlewood & Olson 2001
N600	Sequencing	CTG CTG GCA CCA GAC TTG	this study
N600	Sequencing	CAA GTC TGG TGC CAG CAG	this study
NF1200	Sequencing	TTG CAA CCA TAC TTC CCC CG	this study
Tet1100	Sequencing	CGA AGA CGA TCA GAT ACC G	Caira et al. 2014
Tet1420	Sequencing	TAA CCA GAC AAA TCG CTC C	Caira et al. 2014
NL1300	Sequencing	CCT GCG GCT TAA TTC GAC TC	this study
28S rRNA			
CLF28A	Amplifying/Sequencing	AGT AAC GGC GAG TGA ACA GG	this study
CLF28B	Amplifying/Sequencing	GCA CTG GTC CGA AGA CTA TG	this study
iCLF28C	Sequencing	AGC TGA TTA CAC CCG AAG GC	this study
iCLF28D	Sequencing	GTT GTG CGC TTC GGA TGT TC	this study

Table S2. Biological data of 4 male *Mesoplodon carlhubbsi* specimens used for contaminant assessment.

Field ID	Sex	Body Length (cm)	Extent of Decomposition	Date Stranded	Location	Coordinates
M46866	M	493	Mild	20150415	Hirau, Samani, Hokkaido	42°07'21"N, 142°56'56"E
M38006	M	510	Severe	20110531	Uchiura, Yakumo, Hokkaido	42°14'38"N, 140°17'45"E
M36185	M	486	Severe	20091021	Haneda Airport, Ota, Tokyo	35°33'00"N, 139°48'00"E
M34062	M	522	Mild	20051022	Yamanishi, Ninomiya, Kanagawa	35°17'16"N, 139°14'17"E

LITERATURE CITED

- Caira JN, Jensen K, Waeschenbach A, Olson PD, Littlewood DTJ (2014) Orders out of chaos – molecular phylogenetics reveals the complexity of shark and stingray tapeworm relationships. *Int J Parasitol* 44:55-73
- Fernández M, Aznar FJ, Lattore A, Raga JA (1998) Molecular phylogeny of the families Campulidae and Nasitrematidae (Trematoda) based on mtDNA sequence comparison. *Int J Parasitol* 28:767-775
- Fernández M, Aznar FJ, Raga JA, Lattore A (2000) The origin of *Lecithodesmus* (Digenea: Campulidae) based on ND3 gene comparison. *J Parasitol* 86:850-852
- Littlewood DTJ, Olson PD (2001) Small subunit rDNA and the Platyhelminthes: signal, noise, conflict and compromise. In: Littlewood DTJ, Bray RA (eds) *Interrelationships of the Platyhelminthes*. Taylor & Francis, London, p 262-278