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Cetacean Population Studies

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PREFACE

The fifth volume of the *Cetacean Population Studies (CPOPS)* has finally been published. The considerable delay since the release of the previous volume is primarily due to a slowdown in my editorial work. This was influenced by personal health-related challenges, including partial visual impairment. Nevertheless, thanks to the steadfast commitment and collaborative efforts of the CPOPS editorial team at the secretariat—under the leadership of Dr. Gabriel Gomez—we are pleased to present this volume, which features a collection of high-quality contributions to the field.

This volume features valuable contributions such as rare sighting records of the extremely elusive pygmy right whale and new findings on whale lice parasitizing the bowhead whale.

Additionally, a comprehensive review on biological traits of a genetically identified stock of the common minke whale, as well as retrieval of biological data from a mass stranding event involving sperm whales, are included.

In any case, it is imperative that we strengthen our editorial structure promptly in order to ensure smoother progress in future.

December, 1, 2025

Hidehiro Kato, Ph. D.
Editor-in-Chief, Chairman,
Publication Committee for the Cetacean Population Studies

Foreword*

Remarkable evolution in cetacean studies in recent decades owes much to major journals that have made significant contribution to the development of modern cetology: Discovery Reports, published by the National Institute of Oceanography in the United Kingdom, and Norwegian Whaling Gazette in Norway, as well as The Scientific Reports of the Whales Research Institute in Japan.

The Scientific Reports of the Whales Research Institute was first published in 1948, a year after the Whales Research Institute was established. Aiming to share valuable research findings and scientific knowledge worldwide, the publication was formatted in English since its beginning, quite an ambitious attempt in Japan still recovering from the devastation of World War II.

Since its first publication, a total of 246 scientists contributed 419 scientific papers to The Scientific Reports of the Whales Research Institute. It is widely acknowledged and appreciated that these scientific papers were the foundation for the development of cetacean studies worldwide, and in today's terms, it was a research journal that had a significant impact factor, or high number of citations. Regrettably, however, The Scientific Reports of the Whales Research Institute was discontinued in 1988 with the 39th volume after the institute was reorganized into the Institute of Cetacean Research.

In the 30 years since then, various types of journals on cetacean studies have been published globally, each offering different perspectives on scientific research outcomes. As for Japan, no research journal matching The Scientific Reports of the Whales Research Institute in its quality has been published. It is probably because many domestic cetologists have sought to publish their papers in international research journals based outside Japan.

As the global environment surrounding the issue of whaling became increasingly complex, we have observed a shift in publishing policies among these journals, rejecting papers whose findings are based on specific research methods such as lethal sampling. Because of this, no small numbers of papers submitted by biological scientists using samples collected through lethal surveys, even just for some parts, have been denied proper reviews. While we agree that animal ethics should be given high priority when writing a research paper, if a paper, the research method of which is allowed under domestic and international rules, is rejected, it is a decision made beyond scientific judgment.

Our new journal for cetacean population studies intends to follow the scientific policy of The Scientific Reports of the Whales Research Institute, that is, to contribute to global development of cetacean studies. As long as submitted papers conform to scientifically-accepted animal ethics, we do not make distinctions based on research methods. At the same time, to maintain the journal's neutrality in the complex global environment surrounding whaling issues, the journal will be published from a newly organized committee, rather than as a bulletin type scientific report from a specific research institute. The title of the new journal will be Cetacean Population Studies to be abbreviated CPOPS, and we aim to keep our door wide-open for researchers worldwide, contribute to the scientific development of resource studies for marine mammals especially focusing on cetaceans, and nurture many aspiring scientists.

Seiji Ohsumi

Seiji Ohsumi[†], Ph. D.
December 31, 2018
Chairman
Publication Committee for the Cetacean Population Studies

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*Introductory declaration by the former Chairman of the Cetacean Population Studies Publication Committee on the occasion of the launching of this journal.

Full Paper

Pygmy right whale, Southern Ocean, 2004.

DOI https://doi.org/10.34331/cpops.2023-F-001 J-STAGE Advance published date: June 17, 2025

RARE SIGHTINGS OF THE PYGMY RIGHT WHALE (*CAPEREA MARGINATA*) DURING THE 2022/2023 JASS-A CRUISE IN THE SOUTHWESTERN PACIFIC

Yujin KIM*, Taiki KATSUMATA, Tatsuya ISODA and Koji MATSUOKA

Institute of Cetacean Research, 4–5 Toyomi-cho, Chuo-ku, Tokyo 104–0055, Japan
**Corresponding author: kim.cetacean@gmail.com*

Abstract

On 14 February 2023, during the 2022/2023 Japanese Abundance and Stock-structure Surveys in the Antarctic (JASS-A) cruises, two individual whales were sighted in the Southwestern Pacific. These whales were identified as pygmy right whales (*Caperea marginata*) by their prominently arched jawline, relatively narrow rostrum, dorsal fin located two-thirds of the way from the tip of the snout, and small body size. This species is one of the most mysterious whales, with few sightings at sea. Several measurements were taken from aerial videography using a small uncrewed aerial vehicle (UAV) for 9 min and 49 s. One individual swam slowly for 128.9 m in 53 s, with a swimming speed of 4.7 knots. A comparison of the external measurements of the whale in this study with those of whales reported to have a similar body length indicated no significant differences between photogrammetric and manual measurements. These sightings represent the second and third recorded occurrences of this species in the Southwestern Pacific, in highly pelagic waters near the northern boundary of the Subtropical Convergence Zone. This region is known for its high primary productivity, where whale prey species are concentrated.

Key words: Pygmy right whale, *Caperea marginata*, sighting survey, aerial videography, photogrammetry, JASS-A.

Introduction

The pygmy right whale (*Caperea marginata*, Grey 1846) is one of the smallest baleen whales. This species has been found only in the Southern Hemisphere and has rarely been observed at sea (Jefferson *et al.*, 2015). Fifteen sightings have been reported in the waters around Australia and New Zealand, while four sightings have been recorded off southern Africa (reviewed in Ross *et al.*, 1975; reviewed in Kemper, 2002; Gill *et al.*, 2008; reviewed in Kemper *et al.*, 2013). Reports of strandings, both live and dead, are more common. There have been 180 stranding reports from the Australia and New Zealand region, six from South Africa, and one from Chile (reviewed in Ross *et al.*, 1975; Cabrera *et al.*, 2005; reviewed in Kemper, 2002; reviewed in Kemper *et al.*, 2013). Stranded individuals have been used to study aspects of this species' biology, including external morphology, diet, osteology, genetics, and phylogeny (Ross *et al.*, 1975; Munday *et al.*, 1982; Sekiguchi *et al.*, 1992; Kemper, 2002; Bisconti, 2012; Fordyce and Marx, 2013; Tsai and Fordyce, 2014; Wolf *et al.*, 2023). Little is known about the life history of pygmy right whales in the wild due to the relative paucity of sightings at sea.

This paper reports two new sightings from the Southwestern Pacific recorded during the 2022/2023 Japanese Abundance and Stock-structure Surveys in the Antarctic (JASS-A) cruise. These new data are compared with previous records to expand information on this species' life history in the wild.

Author contributions were Kim: Conceptualization, visualization, validation, data curation. Katsumata: visualization, data curation, software. Isoda: Conceptualization, project administration, Matsuoka: data curation, supervision.

Materials and Methods

The JASS-A cruises began in 2019/2020 as a comprehensive effort to study large whales and ecosystem dynamics in the Indo-Pacific region of the Antarctic. These surveys utilized dedicated sighting methods and a range of non-lethal techniques to assess whale abundance, population trends, and stock-structure (Government of Japan, 2019a, 2019b, 2019c).

The 2022/2023 JASS-A cruises were conducted from 5 December 2022 to 14 March 2023 as the fourth year of surveys in the eight-year plan (Isoda *et al.*, 2023). The research area was set in Area VIE, south of 60°S, one of the areas managed by the International Whaling Commission (IWC). The sighting surveys were conducted by two research vessels: *Yushin-Maru No.2* (*YS2*) (747 GT) and *Yushin-Maru No.3* (*YS3*) (742 GT) (Fig. 1; Table 1). Both research vessels have a top barrel platform (TOP), an independent observer platform (IOP), and an upper bridge platform (UBP) (Fig. 1). Transit sighting surveys were conducted between Japan and the Antarctic research area using the Passing mode (NSP), with searching effort undertaken only when weather conditions were suitable for whale observations: visibility better than 1.5 nautical miles, wind speed less than 21 knots, and a searching vessel speed of 11.5 knots. During the searching effort, two primary observers on the TOP and two

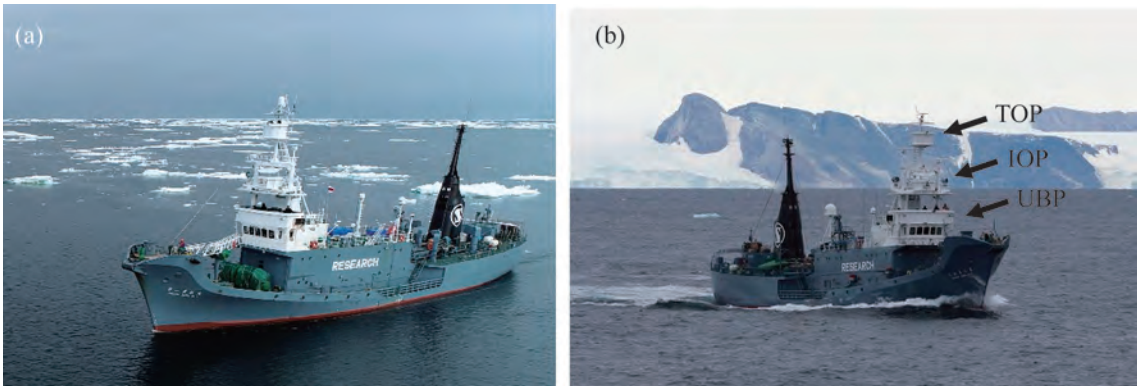

Fig. 1. Photographs of the two research vessels used in the 2022/2023 Japanese abundance and stock-structure surveys in the Antarctic (JASS-A) cruise (Isoda *et al.*, 2023). (a) *Yushin-Maru No.2*. (b) *Yushin-Maru No. 3*. From top to bottom: top barrel platform (TOP), independent observer platform (IOP), and upper bridge platform (UBP).

Table 1. Specifications of the research vessels used in the 2022/2023 Japanese abundance and stock-structure surveys in the Antarctic (JASS-A) cruise (Isoda *et al.*, 2023).

	Yushin-Maru No.2	*Yushin-Maru No.3*
Call sign	JPPV	7JCH
Length overall [m]	69.61	69.61
Molded breadth [m]	10.8	10.8
Gross tonnage [GT]	747	742
Top barrel height [m]	19.5	19.5
IO platform height [m]	13.5	13.5
Upper bridge height [m]	11.5	11.5
Bow height [m]	6.5	6.5
Engine power [PS/kW]	5,280/3,900	5,280/3,900

other primary observers (captain and helmsman) on the UBP conducted searches (IWC, 2008, 2012).

When a sighting was made, the whales were approached to determine their species, group size, and other observations. Species identification followed the guidelines used in the Southern Ocean Whale and Ecosystem Research (IWC-SOWER) survey (Matsuoka *et al.*, 2003; IWC, 2008, 2012). Depending on the progress of the survey, various experiments were conducted using the following non-lethal survey techniques: photo-identification, biopsy sampling, and satellite tagging (Isoda *et al.*, 2023).

Results

Sightings

On 14 February 2023, both *YS2* and *YS3* made whale sightings while conducting a transit survey from the research area to Japan (Fig. 2). A whale accompanied by a large number of seabirds was sighted by the top man of *YS2* at 43°59′S, 160°45′W, at 09:46 (UTC+13.0 h). Hereafter, this whale is referred to as #001 (Fig. 2 and Fig. 3). Weather conditions at the time were clear, with few clouds, a westerly wind of 4 knots, and a Beaufort sea state of 3. Visibility exceeded 7 nautical miles, with an air temperature of 19.0°C and a sea surface temperature (SST) of 16.4°C.

The second whale sighting occurred at 43°40′S, 161°26′W by *YS3* at 16:16 (UTC+12.0 h), only 35 nautical miles from the first sighting (Fig. 2). A single individual with a cued whale body was sighted. Hereafter, this whale is referred to as #002. Weather conditions at the time of the second sighting were also clear, with an east-northeast wind of 2 knots, a Beaufort sea state of 1, and visibility exceeding 7 nautical miles. The air temperature and SST were 21.3°C and 17.7°C, respectively.

Both vessels approached within 0.02 nautical miles of each sighting to observe external morphol-

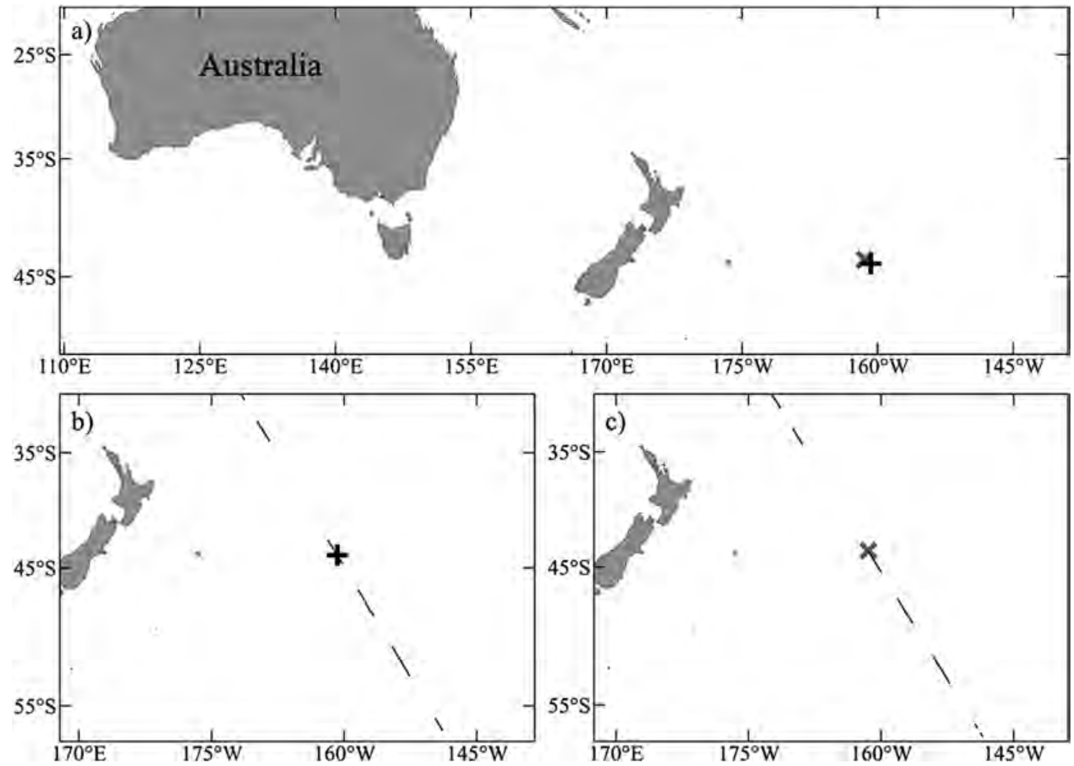

Fig. 2. The sighting locations of the pygmy right whales on 14 February 2023. (a) Wider area map. Black cross: location of whale (#001 sighted by *Yushin-Maru No. 2* (YS2). Gray cross: location of whale #002 sighted by *Yushin-Maru No.3* (YS3). (b) Search tracks (black lines) of YS2 and the sighting location of #001. (c) Search tracks of YS3 and the sighting location of #002.

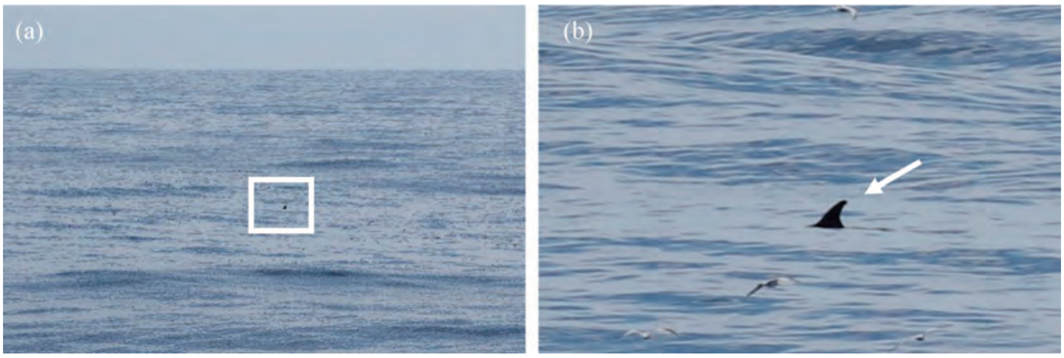

Fig. 3. Photographs of the pygmy right whale (#001). (a) Photograph during the approach of YS2 to the whale. Seabirds were seen around the whale. (b) A close-up of the white rectangular area in (a). The dorsal fin of the whale is clearly visible.

ogy and behavior for species identification. The individuals were identified as pygmy right whales (*C. marginata*) based on their prominent arched jawline, relatively narrow rostrum, dorsal fin located two-thirds of the way from the tip of the snout, and small body size.

Photo-identifications of #001 and #002 were taken using a Canon EOS 7D Mark II camera with a 100–400 mm image-stabilized lens and built-in GPS. Aerial observation and videography were also conducted for #002 using a small UAV. The DJI Inspire 2 was equipped with a Zenmuse X5S camera (DJI, China) featuring a Micro Four Thirds (Micro 4/3) sensor and an Olympus M. Zuiko Digital ED 14–42 mm f3.5–5.6 EZ lens (Olympus, Japan). The focal length of the UAV lens was fixed at 14 mm during flight. Additionally, the UAV was equipped with a laser rangefinder (Lightware SF11/C), GPS (Globalsat EM506), and an inertial measurement unit (IMU) (Pololu MiniIMU-9 v5) to collect data for photogrammetry (Dawson *et al.*, 2017). Whale #001 was observed for approximately 44 min, while whale #002 was observed for approximately 58 min after the initial sighting.

External morphology

Both whales were relatively small, with estimated body lengths of 5.8 m (#001) and 5.3 m (#002). These estimates were made by the boatswain of each vessel, an experienced and trained observer, and were agreed upon by the researchers and captains. The external morphology of the whales was observed from the head to the dorsal fin as they surfaced to breathe. Fig. 4 shows the heads of these whales. In the lateral head view, the rostrum displayed a dorsally arched jawline. This characteristic jawline curved upward from the tip of the rostrum to the front of the blowhole before curving downward. When the whales surfaced, the dorsal fin was visible simultaneously with the blowhole (Fig. 5). The dorsal fin was falcate, relatively narrow compared to its height, and its tip lacked a strong caudal curvature.

For the whale sighted by *YS3* (#002), aerial videography for photogrammetry was captured using a small UAV. From the aerial footage, four photographs were cropped in which the whale's body axis was straight as it surfaced to breathe (Fig. 5). These photographs were corrected for distortion caused by the wide-angle lens using the video editing software Defishr (Ver.1.0), and photogrammetry was conducted using MorphoMetriX (Ver.2.1.2) (Torres *et al.*, 2020). Seven external measurements, including body length, were taken by photogrammetry, based on previous studies (Mackintosh and Wheeler, 1929; Ohsumi, 1960; Amano and Miyazaki, 1993; Kim *et al.*, 2021) (Table 2): body length (*BL*), tip of snout to center of eyes (*TCE*), tip of snout to center of blowhole (*TCB*), tip of snout to anterior insertion of flipper (*TAF*), tip of snout to anterior insertion of dorsal fin (*TAD)*, total span of flukes (from left tip to right tip) (*TSF)*, and depth of flukes (anterior insertion to notch) (*DF*). Table 2 presents the mean measurements and the relative ratios of each body part to body length. The *BL* measured from the photographs was 5.6±0.2 m (mean±SD). The *TCE* measured 1.1±0.1 m, while the

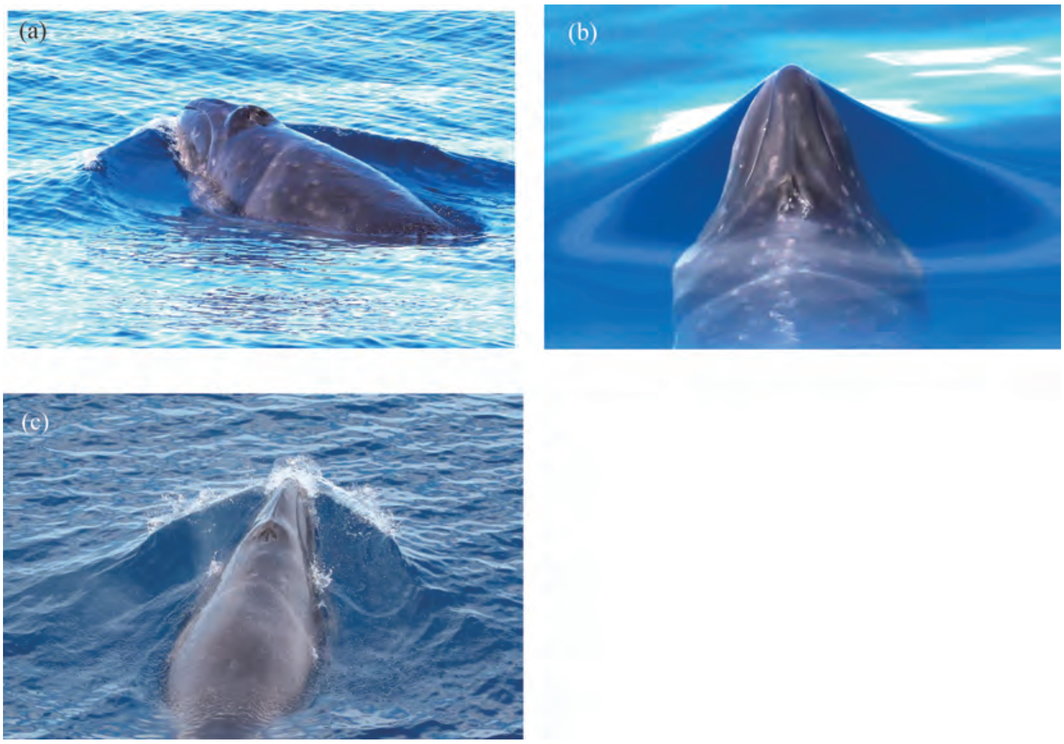

Fig. 4. Photographs of the heads of two pygmy right whales. (a) Lateral view of #001. (b) Dorsal view of #001. (c) Dorsal view of #002. The arched jawline and medially narrowing upper jaw are characteristic features. The chevron behind the blowhole is clearly visible, along with oval scars caused by cookie-cutter sharks (*Isistius* sp.). A single ridge and two slits in the blowhole were also observed.

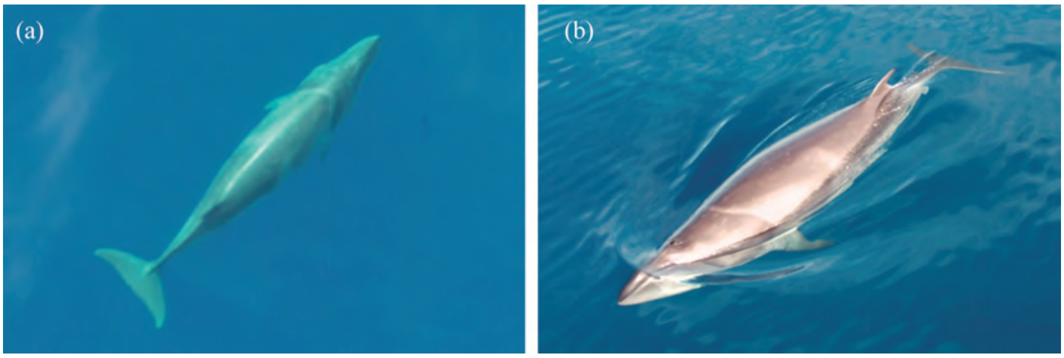

Fig. 5. Photographs of the pygmy right whale (#002) cropped from aerial videography taken using a small uncrewed aerial vehicle (UAV)). (a) Just before the whale surfaces to breathe. (b) The whale breaks the surface. The double chevrons are clearly visible. The blowhole and dorsal fin are on the surface simultaneously.

TCB measured 0.6±0.1 m. The *TAF* and *TAD* measurements were 1.9±0.0 m and 3.6±0.3 m, respectively. The two fluke measurements—*TSF* and *DF*—were 1.6±0.0 m and 0.5±0.0 m, respectively. The positions of each body part, based on the relative ratios of external measurements to body length, were as follows: The blowhole and eyes were positioned at 11.0±0.9% and 18.9±1.1% of the body length, respectively. The flippers were positioned from the tip of the snout (*TAD*) at 32.7±0.8%, approximately one-third of the body length. The dorsal fin was positioned at 64.6±2.5% of the body length, approximately two-thirds from the tip of the snout. The *TSF* measured 29.2±1.6% of the body length, while the *DF* measured 8.4±0.2%.

The coloration of the dorsal surface was generally dark gray, fading to light gray ventrally (Fig. 4 and Fig. 5). Two light gray bands, called chevrons, were observed on the lateral surface of the body and

Table 2. External measurements of the pygmy right whale (#002) obtained by photogrammetry. Measurement points were derived from previous studies (Mackintosh and Wheeler, 1929; Ohsumi, 1960; Amano and Miyazaki, 1993; Kim *et al.*, 2021). Ratios indicate the relative proportions of each body part to total body length. N denotes the number of aerial photographs used for each measurement.

	Measurement point	*N*	Measurement (m)		Ratio (%)	
			Range	Mean (SD)	Range	Mean (SD)
1	Body length (*BL*)	4	5.3–5.8	5.6 (0.2)	—	—
2	Tip of snout to center of eyes (*TCE*)	4	1.0–1.2	1.1 (0.1)	17.8–20.0	18.9 (1.1)
3	Tip of snout to center of blowhole (*TCB*)	4	0.5–0.7	0.6 (0.1)	10.0–12.2	11.0 (0.9)
4	Tip of snout to anterior insertion of flipper (*TAF*)	2	1.9–1.9	1.9 (0.0)	31.9–33.4	32.7 (0.8)
5	Tip of snout to anterior insertion of dorsal fin (*TAD*)	4	3.3–3.9	3.6 (0.3)	61.7–67.6	64.6 (2.5)
6	Total span of flukes (*TSF*)	4	1.6–1.7	1.6 (0.0)	27.2–31.3	29.2 (1.6)
7	Depth of flukes (*DF*)	4	0.5–0.5	0.5 (0.0)	8.1–8.7	8.4 (0.2)

were clearly distinguishable from the surrounding body color. The anterior chevrons swept dorsally from the flipper insertions on each side and met behind the blowhole. The posterior chevrons extended from the ends of the anterior chevrons, following a similar ventral-to-dorsal sweep but did not meet on the dorsal surface. There was a difference in brightness between the two chevrons, with the anterior chevron appearing brighter than the posterior one.

The body coloration of the flippers was light gray at the base and darkened toward the tip, though it remained lighter than the dorsal body coloration (Fig. 5). The coloration of the eyelids on both sides was the lightest of all observed body parts (Fig. 4). Dozens of pale gray oval scars, likely caused by cookie-cutter sharks (*Isistius* sp.), were observed on the dorsal surface (Fig. 4). No fresh scars were detected.

Behavioral observations

The whale's blow was small in width, low in height, and weak, making it difficult to detect from a distance. When surfacing, the tips of both jaws emerged first, followed by the blowhole and dorsal fin. Upon submerging, the whale did not arch its back or expose its flukes above the water.

The whale (#002) was observed from the air by a small UAV for 9 minutes and 49 s. During this time, six consecutive breaths followed by a single dive and resurfacing to breathe were recorded, providing insight into its respiratory rhythm. Surface time was defined as the period from when the whale surfaced to breathe until its exposed body parts disappeared below the surface. The interval between consecutive breaths was the time between the disappearance of the body below the surface and its reappearance. Dive time referred to the duration between consecutive breaths when the whale dived to a given depth, disappeared below the surface, and resurfaced. The whale spent 3–4 s at the surface. The shortest interval between six consecutive breaths was 22 s, while the longest was 53 seconds, with an average of 36 s. The dive time was recorded as 3 min and 5 s.

The whales normally swam calmly and slowly. When the vessels first approached, the whales were observed rolling and milling near the surface. However, as the vessels came within 30 m, the whales changed their swimming direction, seemingly attempting to move away. They also increased their swimming speed and began leaping out of the water. Once the vessels moved away, the whales resumed swimming at their natural speed and appeared to calm down. Initially, the whales swam slowly at approximately 4–5 knots, but as the ships approached, their speed increased to 7–8 knots. According to UAV video measurements, #002 moved 128.9 m in 53 s, maintaining a speed of 4.7 knots.

Based on external morphological characteristics, particularly the distinctive arched jawline, and behavioral observations, the whales sighted by *YS2* and *YS3* were identified as pygmy right whales. Additionally, a comparison of photographs of each individual revealed distinct bite marks from cookie-cutter sharks, confirming that the two whales were different individuals.

Discussion

Pygmy right whales are often confused at sea with Antarctic minke whales (*Balaenoptera bonaerensis*) due to their similar body shape (Ivashin *et al.*, 1972; Ross *et al.*, 1975; Jefferson *et al.*, 2015). The two pygmy right whales sighted in this study were identified by their arched jawline, relatively narrow rostrum, dorsal fin position, and small body size. As their name suggests, pygmy right whales exhibit a distinct dorsally arched jawline when viewed laterally, similar to right whales (*Eubalaena* sp.), whereas the jawline of Antarctic minke whales is relatively flat (Jefferson *et al.*, 2015). In dorsal view, the upper jawline of pygmy right whales curves medially and narrows, while that of Antarctic minke whales curves laterally (Jefferson *et al.*, 2015). The position of the dorsal fin also distinguishes the two species. In pygmy right whales, the dorsal fin is located two-thirds of the way back from the tip of the snout, whereas in Antarctic minke whales, it is positioned three-quarters of the way back (Matsuoka *et al.*, 1996, 2005; Kemper *et al.*, 1997; Kato and Fujise, 2000; Gill *et al.*, 2008). Another distinguishing characteristic is body length. Pygmy right whales reach a maximum length of 6.5 m (Kemper and Leppard, 1999; Gill *et al.*, 2008; Jefferson *et al.*, 2015), while Antarctic minke whales have a mean body length of 8.5–9.0 m (Jefferson *et al.*, 2015). However, identifying species based on body size alone may lead to confusion, particularly with smaller Antarctic minke whales. Therefore, it is recommended that arched jawline and other external morphological features be used to identify pygmy right whales, rather than body size alone.

The body colors of the two pygmy light whales observed in this study were consistent with those reported in previous studies (Ross *et al.*, 1975; Matsuoka *et al.*, 1996, 2005; Gill *et al.*, 2008; Jefferson *et al.*, 2015). However, there were some inconsistencies among previous studies regarding chevrons. Matsuoka *et al.* (1996), one of the authors of this study, reported double chevrons in his sightings of this species, as observed in this study. He described the first chevron as sweeping dorsally from the anterior surface of the flipper, with the second chevron positioned posterior to the first. However, other authors (Gill *et al.*, 2008; Jefferson *et al.*, 2015) contended that most whales have only a single chevron, located on the anterior part of the dorsum, with only a few whales showing a posterior chevron. The two whales sighted in this study both had double chevrons. These two chevrons differed in the amount of surface area they occupied (Fig. 5). The anterior chevrons swept up from the flipper insertions to the area behind the blowhole and were visible from both the lateral and dorsal views. The posterior chevrons, however, extended only about two-thirds of the way along the lateral body surface, making them impossible to observe from the dorsal view. The two chevrons also differed in brightness, with the anterior chevrons being brighter than the posterior chevrons depending on the viewing angle, the posterior chevrons may not be visible at all.

External measurements of pygmy right whales have been reported for stranded and captured individuals (reviewed in Ross *et al.*, 1975; Munday *et al.*, 1985). A total of 10 individuals have been recorded, with body length distributions as follows: 2.0 m range-1 individual, 3.0 m range-4 individuals, 5.0 m range-1 individual, 6.0 m range-4 individuals, with no reports in the 4.0 m range. Table 3 presents the external measurements reported in this study and previous studies. We compared the relative ratios of body parts in whales with similar body lengths (5.5 m) to the 5.6-m whale in this study. The length from the tip of the snout to the center of the eye (*TCE*) was 18.9% of body length in this study and 21.0% in the previous study (Ivashin *et al.*, 1972; reviewed in Ross *et al.*, 1975). The length from the tip of the snout to the blowhole (*TCB*) was 11.0% in this study and 14.4% in the previous study. The length from the tip of the snout to the anterior insertion of the flipper (*TAF*), which indicates flipper position, was 32.7% for the 5.6 m whale in this study and 33.1% for the 5.5 m whale in the previous study. The length to anterior insertion of dorsal fin (*TAD*) was 64.6% and 66.7%, respectively. The *TSF* in this study was 29.2% of body length, compared to 31.4% in the previous study. As a result, a comparison of proportions from two external measurement methods on two individuals of similar body length showed no significant differences between the two methods, suggesting that

Table 3. External measurements of the pygmy right whales recorded in this study and reported in previous studies (Modified from Ross *et al.*, 1975; Munday *et al.*, 1982). Measurements, except for body length, show the relative proportions of each body part to total body length.

Source	Measurement points (%)						
	BL (m)	*TCE*	*TCB*	*TAF*	*TAD*	*TSF*	*DF*
Present paper	5.6	18.9	11.0	32.7	64.6	29.2	8.4
Hale (1931)	2.8	—	—	—	—	19.7	—
Hale (1931)	3.3	21.5	—	—	66.9	—	—
Davies and Guiler (1957)	6.4	—	—	—	—	28.3	—
Guiler (1961)	6.4	15.1	11.9	—	—	—	—
Hale (1964)	3.1	22.5	—	35.1	73.1	20.0	—
Ivashin *et al.* (1972)	5.5	21.0	14.4	33.1	66.7	31.4	—
Ivashin *et al.* (1972)	6.2	21.4	13.9	31.9	67.0	—	—
Ross *et al.* (1975)	3.0	23.0	14.5	34.1	67.0	—	—
Ross *et al.* (1975)	3.4	—	—	—	—	—	—
Munday *et al.* (1982)	6.5	19.8	14.0	29.3	71.5	31.0	7.4

photogrammetry is as effective as manual measurement. In this study, we successfully obtained external measurement data for this species using photogrammetry, a non-lethal survey method employing a small UAV. This marks the first photogrammetric measurement of this species and the first attempt on a live whale sighted at sea. For future surveys of rare species such as this, photogrammetry using small UAVs will enable multiple external measurements to be obtained non-lethally, contributing to the accumulation of scarce biological data on this species.

Aerial observations using a small UAV have provided insights into the respiratory rhythms of this species. According to Ivashin *et al.* (1972), pygmy right whales typically spend 4–5 s at the surface for respiration (surface time). The interval between consecutive breaths has been reported to average 49 s, or even longer at 60 seconds (Ross *et al.*, 1975). Dive times of 3–4 min have also been documented by several authors (Ivashin *et al.*, 1972; Ross *et al.*, 1975; Matsuoka *et al.*, 1996, 2005; Jefferson *et al.*, 2015). In contrast, the whale (#002) observed in this study spent 3–4 s at the surface, a duration slightly shorter than previously reported. The Interval between consecutive breaths were also short, averaging 36 seconds. The duration of an observed dive (dive time) was 3 minutes and 5 seconds, consistent with the results of the previous study. The variation in these times compared to previous studies may be due to differences in the swimming conditions of the whales at the time of observation. The respiratory rhythm of Antarctic minke whales observed during this cruise ranged from 2 to 5 s for surface time, with intervals between consecutive breaths varying from 11 to 50 s, depending on swimming conditions. When swimming speed increased due to vessel approach, surface time ranged from 2 to 3 s, and intervals between consecutive breaths shortened to 11–22 seconds. Conversely, under stable and normal swimming conditions, the respiratory rhythm ranged from 3 to 5 seconds for surface time and 40–50 s for breath intervals. Previous studies (Ross *et al.*, 1975; Matsuoka *et al.,* 2005) have observed respiratory rhythms in pygmy right whales when their swimming speed was between 3 and 4 knots. This species is known to reach speeds of 6–8 knots or more when swimming fast (Jefferson *et al.*, 2015), suggesting that earlier observations were made under relatively calm conditions. In this study, respiratory rhythm was recorded when the whale's swimming speed increased due to vessel proximity and later returned to normal. Therefore, the respiratory rhythm reported here may reflect a fast-swimming condition for this species.

Sightings and strandings of pygmy right whales reported in previous studies have been concentrated between 30°S and 55°S (Kemper *et al.*, 2013; Jefferson *et al.*, 2015), and the sightings of the two whales in this study also fall within this range. This suggests that the primary distribution of the spe-

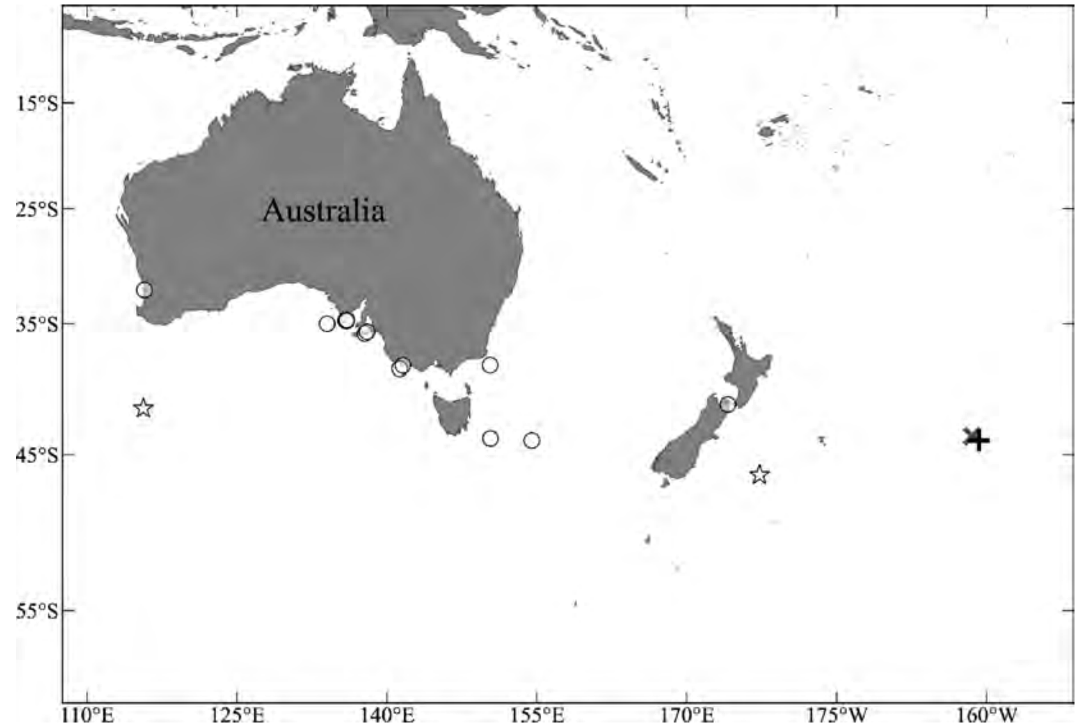

Fig. 6. Sighting locations of the pygmy right whales recorded in this study an reported in previous studies (Modified from Matsuoka *et al.*, 1996, 2005; Gill *et al.*, 2008; Kemper *et al.*, 2013). Black and gray crosses: sightings in this study. Stars: sightings reported by Matsuoka *et al.* (1996, 2005). Open circles: other sightings in previous studies. The sightings in this study represent the second and third records in the Southwestern Pacific and the most pelagic to date.

cies remains consistent. Previously reported sightings of this species have occurred in coastal areas of Australia, New Zealand, and South Africa (reviewed in Ross *et al.*, 1975; Gill *et al.*, 2008; reviewed in Kemper *et al.*, 2013). However, the two whales in this study were sighted in pelagic waters approximately 1,120 n.miles from Christchurch, New Zealand (Fig. 6). These sightings represent the second and third records of this species in the Southwestern Pacific and the most pelagic to date (Matsuoka *et al.*, 2005).

The Japanese government has conducted sighting surveys in the southern hemisphere for about 30 years, from 1987/1988 to the present. During this period, a total of 62,291.9 nautical miles were surveyed between 30°S and 55°S. In addition to pygmy right whales, other baleen whale species recorded include blue whales (*B. musculus*), fin whales (*B. physalus*), humpback whales (*Megaptera novaeangliae*), and Antarctic minke whales (*B. bonaerensis*). The number of sightings and the Density Index (DI) (schools of primary sightings/100 n.miles searched) of each whale species in this area during the study period are shown in Table 4. The fin whale had the highest number of sightings (92), followed by Antarctic minke whales (71), humpback whales (48), and blue whales (17). Only four sightings of pygmy right whales have been recorded, including two in this study and two reported by Matsuoka *et al.* (1996, 2005). Assuming that the detectability is similar between these species, the DI of pygmy right whales was 0.006, which is 25 times lower than that of fin whales (0.148), the most abundant species (Table 4). It was also about one-fifth of the DI of blue whales (0.027), a species with relatively few sightings. The relatively low number of sightings in this area, despite it being within the species' main distribution range, may be due to low abundance or the possibility that high-density areas have not yet been discovered. However, due to the lack of information on this species, no abundance estimates have been conducted (Jefferson *et al.*, 2015).

This species, with such a low DI, was sighted during this cruise in two groups of one individual each on the same day, in close proximity to each other (Fig. 2). A key environmental factor in the area

Table 4. Summary of sighting surveys conducted by the Government of Japan over 30 years (1987/1988–present) between 30°S and 55°S. The Density Index indicates the number of primary schools sighted/100 n.miles searched.

Survey period	Survey area	Searching Effort in n. miles	Species	Number of sightings	Density Index
1987/88–2022/23	30°S–55°S	62,291.9	Blue whale	17	0.027
			Fin whale	92	0.148
			Humpback whale	48	0.077
			Antarctic minke whale	71	0.114
			Pygmy right whale	4	0.006

where these sightings occurred is the Subtropical Convergence Zone (Deacon, 1937; Longhurst, 2006; Garcia-Rojas *et al.*, 2018). The Subtropical Convergence Zone, marking the northern boundary of the Southern Ocean, is where subantarctic and subtropical waters—with significant differences in nutrient concentrations—meet, creating a highly productive marine ecosystem (Deacon, 1937; Longhurst, 2006; Garcia-Rojas *et al.*, 2018). SSTs in this convergence zone are typically 9–13°C during the austral summer (Deacon, 1937; Kawamura, 1974). Copepod patches, which serve as prey for many baleen whales, often occur where SSTs range from 13 to 14°C (Kawamura, 1974). Copepods are a primary dietary component of pygmy right whales, along with sei whales (*B. borealis*) and southern right whales (*E. australis*) (Ivashin *et al.*, 1972; Kawamura, 1974; Sekiguchi *et al.*, 1992; Kato *et al.*, 1996; Kemper, 2002). Historically, the whaling grounds of sei whales have been closely associated with the Subtropical Convergence Zone due to the abundance of copepods (Kawamura, 1974). The two pygmy right whale sightings recorded by Matsuoka *et al.* (1996, 2005) also occurred within the Subtropical Convergence Zone. Matsuoka *et al.* (2005) reported that copepod patches were observed near the whales at the time of the sighting. While direct feeding behavior was not observed, numerous defecations were recorded. Based on this evidence, Matsuoka *et al.* (2005) suggested that pygmy right whales may concentrate in the Subtropical Convergence Zone to feed during the austral summer.

The SSTs recorded at the sighting locations in this study were 16.4°C and 17.7°C, respectively, which are higher than the mean SSTs in the Subtropical Convergence Zone during the austral summer. Additionally, we did not observe patches of copepods, the primary prey species of pygmy right whales, near the sighting locations, nor did we observe direct feeding or defecation behaviors, as reported in previous studies (Matsuoka *et al.*, 2005). Based on these SSTs and the absence of feeding-related observations, these sightings were likely outside the Subtropical Convergence Zone. However, a large number of seabirds were observed flying around the first sighting location (#001, Fig. 3). Additionally, some copepod patches have historically formed outside the northern boundary of the Subtropical Convergence Zone (Kawamura, 1974), and that area coincides with the sighting locations of this study. This suggests that prey species may be present in this area, albeit on a smaller scale.

Although we were unable to observe behaviors directly related to the life history of this species (e.g., feeding, reproduction) in this area, the fact that two sightings of this elusive species occurred on the same day in the same area by two vessels suggests that this region may play a role in the species' life history. Given the environmental and biological factors reported in previous studies (Deacon, 1937; Kawamura, 1974; Longhurst, 2006; Kemper, 2002; Matsuoka *et al.*, 2005; Gill *et al.*, 2008; Garcia-Rojas *et al.*, 2018), this area may be related to the feeding grounds of this species.

We report two new sightings of this poorly understood species, representing the most pelagic records to date and the first photogrammetric measurements of this species at sea using a small UAV. Further regular sighting surveys in this area, combined with experiments using various non-lethal methods, will contribute to the accumulation of knowledge on the life history and biology of this species.

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HIDING IN PLAIN SIGHT: MOLECULAR CHARACTERIZATION OF WHALE CYAMIDS FROM BOWHEAD WHALES (*BALAENA MYSTICETUS*)

Amy B. BAIRD[1*#], Mary GEORGES[1], Michelle LOKKESMOE[1],
Olga SHPAK[2], Gay SHEFFIELD[3], J. C. GEORGE[4†], Brian PERSON[4],
Todd L. SFORMO[4], Leandra DE SOUSA[4], Andrew L. VON DUYKE[4],
Kayla SCHEIMREIF[4], Frances J. OLEMAUN[4], Rita FRANTZ[4] and
Raphaela STIMMELMAYR[4#]

[1] Department of Natural Sciences, University of Houston–Downtown, Houston, TX, USA
[2] Independent Scientist, Kharkiv, Ukraine
[3] Alaska Sea Grant–Marine Advisory Program, University of Alaska, Fairbanks, Nome, AK, USA
[4] North Slope Borough Department of Wildlife Management, Utqiaġvik, AK, USA
[†] Deceased.
[#] These authors contributed equally to the research.
[*] Corresponding author: bairda@uhd.edu

Abstract

Bowhead whales (*Balaena mysticetus*) were previously thought to carry only one species of cyamid (whale louse), *Cyamus ceti*, which co-occurs on eastern and western gray whale (*Eschrichtius robustus*) stocks. We analyzed partial mtDNA COI gene sequences from archived cyamid samples to determine species present and the phylogenetic placement of bowhead whale cyamids. We explicitly tested Callahan's hypothesis (2008) that *C. ceti* on gray and bowhead whales represent distinct evolutionary lineages and may necessitate separate species level status. Findings from this study indicate that *C. ceti* on bowhead whales differs from *C. ceti* on gray whales, implying that bowhead and gray whale cyamids likely represent different evolutionary lineages. The *C. ceti* bowhead clade is shared between Bering-Chukchi-Beaufort Seas and Okhotsk Sea bowhead whales, suggesting that these cyamids likely shared a common ancestor relatively recently in their evolutionary history. We also document the limited presence of *C. scammoni* on bowheads, perhaps indicating horizontal transmission from interactions with gray whales.

Key words: Alaska, *Cyamus ceti*, *Eschrichtius robustus*, mitochondrial DNA, Okhotsk Sea, whale lice.

Introduction

The bowhead whale (*Balaena mysticetus*) is a species of baleen whales (Mysticeti) in the family Balaenidae. It is divided into four recognized populations, or stocks, ranging across the Arctic: 1) the Bering-Chukchi-Beaufort Seas (BCB) stock; 2) the East Canada–West Greenland stock (ECWG); 3) the Okhotsk Sea (OKS) stock; and 4) the East Greenland–Svalbard–Barents Sea stock (EGSB). These stocks are based on migration patterns, geographic distribution, movement data from satellite-linked instrumentation efforts, and population genetic analyses (Baird and Bickham, 2021). Commercial whaling severely reduced worldwide bowhead whale numbers from historical levels, and the BCB

Fig. 1. Dorsal view of a whale louse ("*Cyamus ceti*") specimen collected from a bowhead whale (*Balaena mysticetus*) near Utqiaġvik, Alaska. Scale equals 2.5 mm.

bowhead whale stock was listed under the Endangered Species Act in 1973 (United States) and listed as depleted under the Marine Mammal Protection Act. Since the moratorium on commercial whaling, BCB bowhead whales have strikingly recovered, with the most recent abundance estimate indicating a population size of 12,505 with 95% confidence interval of 7,994–19,560 and CV of 0.228 (Givens *et al.*, 2021).

The BCB stock winters in the Bering Sea, summers in the eastern Beaufort Sea (and in Russian waters of the Chukchi Sea), and migrates between these areas *via* the Bering Strait region during fall and spring. Their migration patterns take them near coastal villages in northern Alaska and eastern Russia (Chukotka), where Indigenous peoples have relied on the harvest of bowhead whales for subsistence purposes for thousands of years. Such harvests continue under management of the International Whaling Commission (IWC) and in US waters by the US National Oceanic and Atmospheric Administration (NOAA) and by the Alaskan Eskimo Whaling Commission (AEWC). The AEWC represents 11 Alaskan bowhead whaling communities and works extensively with the North Slope Borough Department of Wildlife Management (NSB-DWM) biologists and veterinarians who have been granted access to harvested bowhead whales for long term population, ecological, and health-related studies including their parasites (Von Duyke *et al.*, 2016; George *et al.*, 2020; Stimmelmayr *et al.*, 2021).

Whale lice (cyamids) are amphipod ectoparasites exclusive to cetaceans which feed on shed skin layers (Berzin and Vlasova, 1982; Rowntree, 1996; Schell *et al.*, 2000). Without a free-living aquatic stage, they undergo direct development on whale hosts. The colonization of a new individual host whale (intra- and interspecies) likely occurs through physical whale-to-whale contact (i.e., mating, nursing, and other social interactions; Leung, 1976, Samaras and Durham, 1985; Iwasa-Arai *et al.*, 2017). Cyamids survive for several days when removed from their whale host (Hurley and Mohr, 1957; Leung, 1976); thus, horizontal transmission of dislodged cyamids may rarely occur during co-occupation of the same aquatic habitat and possibly by fomite transmission (e.g., logs, sea ice, boulders).

Bowhead whales carry one species of whale louse, *Cyamus ceti* (Fig. 1; Heckmann *et al.*, 1987). The most recent phylogenetic analysis based on morphological data suggests Cyamidae to be a monophyletic lineage with eight genera and 28 clades (Iwasa-Arai and Serejo, 2018). *Cyamus ceti* belongs to Clade 19 identified by Iwasa-Arai and Serejo (2018), comprised of *C. ceti*, *C. eschrichtii*, *C. mesorubraedon*, *C. erraticus*, *C. boopis*, and *C. catodontis*. *Cyamus ceti* co-occurs on Eastern and Western gray whale (*Eschrichtius robustus*) stocks. It has also been reported from North Pacific right whales (*Eubalaena japonica*) in Japanese waters (Hurley and Moore, 1957; Leung, 1965, 1967, 1976;

Levin and Pfeiffer, 1999; Berzin and Vlasova, 1982). Gray whales of the Eastern North Pacific stock annually migrate to northern subarctic and arctic feeding grounds and thus overlap habitat with bowhead whales. Since recovery from commercial whaling, the Eastern North Pacific gray whale stock has experienced 2 unusual mortality events, one in 1999/2000 and the most recent in 2016–2023 (Stewart *et al.*, 2023). Both events led to increased strandings along the coast of Alaska including the North Slope. The NSB DWM is a longstanding member of the Alaska Marine Mammal Stranding Network and actively investigates beached cetacean carcasses.

The taxonomic history of bowhead cyamids is long and complicated. Cyamids on bowhead whales were first mentioned by naturalist Friderich Martens in 1675 (cited in Lütken, 1873), and specimens collected from Atlantic Ocean arctic waters during 1840–1889 were described by Linnaeus (1758) as *Oniscus ceti* (syn. *Cyamus ceti*), with the likely host being a bowhead whale. Later, Dall (1872) reported cyamids he referred to as *Cyamus mysticeti* from a bowhead in the Bering Strait. Lütken (1873) refers to the single species of cyamid present on bowheads as *Cyamus mysticeti*, though it is unclear why he did not use the name *C. ceti* of Linnaeus. Barnard (1932) rejected the name *C. ceti* in favor of *C. mysticeti*, as he considered the former a composite species. Stephensen (1942), however, accepted *C. ceti*, which was followed by most subsequent authors when referring to cyamids on bowhead whales. Margolis (1955) later considered *C. ceti* and *C. mysticeti* to be synonymous and *C. ceti* was given priority (Haney, 1999).

Hurley and Mohr (1957) were the first to report *C. ceti* from gray whales, taken from Barrow, Alaska. However, the identity of *C. ceti* on gray whales has been called into question by Rice and Wolman (1971), who pointed out that Margolis found minor differences between specimens from gray whales and bowheads. They emphasized that it would be highly unusual for cyamids to infest such distantly related hosts, as most cyamids are host-specific. Additionally, Haney (1999) performed the first modern cladistic revision of Cyamidae and reported subtle morphological differences (body size, number of mandibular incisors) between *C. ceti* specimens originating from gray whales versus BCB bowhead whales. More recently, Margolis *et al.* (2000) described a novel cyamid apparently restricted to gray whales, *C. eschrichtii*. The above observations result in some doubt about the true identity of cyamids on bowhead and gray whales.

Within cetacean biology at large, the study of cyamids has proven useful to address population histories of large whales, interspecies interactions, and function as visual health indicators for free-ranging large whales (Kaliszewska *et al.*, 2005; Iwasai-Arai *et al.*, 2017, 2021; Ten *et al.*, 2022). The key factors influencing cyamid load in baleen whales are not well understood, but the cyamid load on an individual whale likely depends on parasite pressure, animal health, and/or behavior, environmental characteristics, and is reflective of host ecology, behavior, and immunology (Dubodcq *et al.*, 2016; Hofmeester *et al.*, 2019). Cyamid presence and burden has been systematically addressed in landed BCB bowhead whales (Von Duyke *et al.*, 2016). On bowhead whales, whale lice, if present, are located within the gape of the mouth, eyelids, blowholes, genital slit, and peduncle, as well as any skin depressions, scars, cracks, or wounds. Cyamid prevalence (proportion of whales with cyamids) in examined BCB bowhead whales is around 20%, with an average burden (number of lice per whale) ranging between 1–5 per whale examined (Von Duyke *et al.*, 2016). Cyamid infestations (greater than 50 cyamids) are uncommon but have been observed in bowhead whales actively entangled in fishing gear (reducing swim speed) and bowhead whales with injuries or scar tissue that affect laminar water flow allowing cyamids to shelter in the resulting calmer leeward flow area (Von Duyke *et al.*, 2016; Rolland *et al.*, 2019). Cyamid burden has been visually assessed on free-ranging OKS bowhead whales, and based on photo image analysis appears to be greater than what is known for BCB bowhead whales (Shpak and Stimmelmayr, 2017). The OKS bowhead whales were extensively exploited during the commercial whaling period and the population has not fully recovered and remains small (Ivashchenko and Clapham, 2012). Though no formal stranding network is present, beach cast carcasses are assessed and samples collected opportunistically by local fishermen or bowhead whale

Fig. 2. Map of cyamid sample collection sites in this study. In Alaska, samples were collected from Pt. Hope, Utqiaġvik, and Kaktovik. In Russia, a sample was collected from Ul'banskiy Bay in the Sea of Okhotsk.

scientists. Bycatch and killer whale predation are the main causes of strandings (Shpak and Paramonov, 2018).

Given cyamids' obligate relationship with whales, the demographic history with their whale hosts is highly correlated (Berzin and Vlasova, 1982; Kaliszewska *et al.*, 2005; Callahan, 2008). The presence of *C. ceti* on gray whales and bowhead whales suggests that host switching (in the distant past) rather than association by descent have likely shaped the evolutionary and biogeographic history of *C. ceti* because bowheads and gray whales are distantly related. Based on morphological differences previously observed (Haney, 1999) and purported (though not published) molecular divergence between gray and bowhead cyamids, Callahan (2008) put forth the hypothesis that *C. ceti* on gray whales and bowhead whales likely represent distinct evolutionary lineages and may necessitate separate species level status.

Our objective was to generate DNA sequence data from bowhead cyamids to determine their species identification and to reconstruct the cyamid phylogeny to determine the placement of bowhead cyamids relative to previously sequenced species. We analyzed mitochondrial DNA (mtDNA) cytochrome oxidase I (COI) sequences from archived cyamid samples collected from bowhead whales. We explicitly tested Callahan's hypothesis (2008) that *C. ceti* on gray and bowhead whales represent distinct evolutionary lineages and likely necessitate separate cyamid species level status.

Materials and methods

Sample collection

Cyamid specimens were opportunistically collected from twenty-seven subsistence harvested BCB bowhead whales of mixed age and sex during routine post-mortem examination of landed whales (1987–2021) near Utqiaġvik, Kaktovik, and Point Hope in the North Slope Borough region of Alaska (Fig. 2). Briefly, the exposed skin of landed whales, in particular the oral commissures, eyelids, blowholes, genital slit, peduncle, and scars and wounds were examined for cyamid ectoparasites (Von Duyke *et al.*, 2016). Additional cyamids were collected during field stranding examinations from five stranded dead Eastern North Pacific Stock (ENPS) gray whales near Utqiaġvik (2012–2018) and from one dead OKS bowhead whale (2015) in Ul’banskiy Bay (Russia). Cyamids were either frozen (-20°C) or stored in 70% ethanol. Data on the sex, standard length, harvest date, and landed date for each harvested whale in US waters were obtained from the AEWC and/or NSB-DWM biologists. Sexual maturity of bowhead whales was based on previous work which found average length at sexual maturity in females is estimated to be 13.45 m (George *et al.*, 2024) and sexual maturity for males is estimated as a total body length equal to or greater than 13 m (O’Hara *et al.*, 2002). Sample collection from bowhead whales harvested for subsistence purposes was authorized under NMFS research permits to the NSB DWM (#814–1899–00, 01, 02, 03, 04; #17350; #17350–01; #21386). Sample collection from stranded whales on the North Slope Borough region occurred under separate authority by the NOAA Fisheries Alaska Marine Mammal Stranding Network. The NSB DWM is a member of the Alaska Marine Mammal Stranding Network and investigates beach cast marine mammals, including cetaceans. Sample collection from a whale in the Sea of Okhotsk, Russia, occurred under a Russian scientific research permit to A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow.

Molecular analytical methods

Whole genomic DNA was extracted from frozen or ethanol-preserved cyamids using a Qiagen DNEasy blood and tissue kit. DNA was subsequently quantified using a NanoDrop spectrophotometer. Partial mitochondrial DNA (mtDNA) cytochrome oxidase I (COI) was amplified using the methods described in Iwasa-Arai *et al.* (2017). Amplified fragments were purified using a modified ExoSAP protocol using 0.025 μL exonuclease I, 0.25 μL alkaline phosphatase, and 9.725 μL ultra pure water added to the PCR reaction. This mixture was then run on a thermal cycler at 37°C for 30 minutes, followed by 95°C for 5 minutes.

Sequencing and Phylogenetic Analysis

Purified PCR products were sequenced using standard Sanger sequencing protocols. Sequences were edited and aligned using Geneious version 9.1.8 (www.geneious.com). Additional cyamid sequences from GenBank were used to compare to newly sequenced bowhead and gray whale cyamids (Appendix 1). These sequences were originally generated by Kaliszewska *et al.* (2005) and Callahan (2008).

The program jModelTest v. 2.1.10 (Darriba *et al.*, 2012) was used to compute the most appropriate substitution model for the dataset. A Bayesian phylogenetic analysis was conducted using MrBayes v. 3.2.7 (Ronquist *et al.*, 2012). The Bayesian analysis was performed using 5 million generations with a sample frequency of 1,000 generations. A burn-in period of 25% was used. Trees were visualized using FigTree v. 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

We compared the resulting cyamid phylogeny to that of their hosts using the published baleen whale phylogeny of McGowen *et al.* (2019) which was based on genome sequences of whales.

Results

For bowhead whales with cyamids present, the total body length ranged between 6.6 and 16.9 (m) with a sex distribution of 18 females and ten males. Their age distribution was five mature and 23 immature bowhead whales. For gray whales with cyamids present, the total body length ranged between 7.3 and 11.7 (m) with a sex distribution of three females and two males. Their age distribution was one mature and four immature gray whales.

Fifty cyamid samples (15 from gray whales and 35 from bowheads) were processed and sequenced successfully for the phylogenetic analysis (GenBank accession numbers are provided in Appendix 1). In total, the analyzed nucleotide alignment consisted of 114 samples, including our newly sequenced

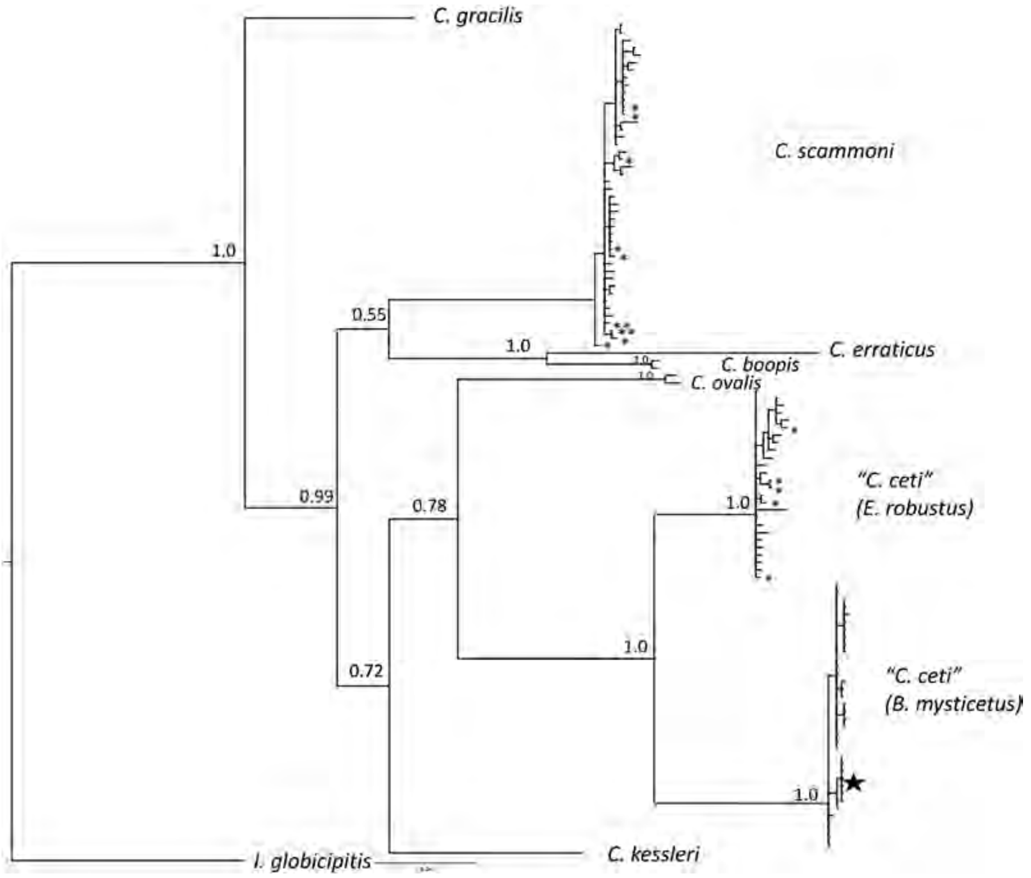

Fig. 3. Bayesian phylogenetic tree of cyamid whale lice based on partial COI sequences. Asterisks represent samples from newly sequenced gray whale cyamids sampled from gray whales in Alaska. Double asterisks in the *C. scammoni* clade represent cyamids sampled from bowhead whales in Alaska. All other whale lice from bowheads group in the "*C. ceti*" (*B. mysticetus*) clade. The star in the "*C. ceti*" (*B. mysticetus*) clade represents the placement of the cyamid sampled from an OKS bowhead. Numbers above nodes represent Bayesian posterior probabilities (only support values for major clades shown).

samples and those obtained from previously sequenced samples from GenBank. The nucleotide alignment was 741 base pairs in length. jModelTest selected the TPM3uf+I+G model of evolution as the best fit for the data, and this was implemented in the Bayesian Analysis as the GTR+I+G model.

Fig. 3 shows the cyamid sequence phylogeny. GenBank sequences from previous studies of *C. gracilis*, *C. erraticus*, *C. boopis*, *C. ovalis*, and *C. kessleri* were more distantly related than those found in our study. As expected, some of the newly sequenced cyamids from Alaskan gray whales were closely related to *C. ceti*, while the remaining Alaskan gray whale cyamids grouped with *C. scammoni*. Two bowhead cyamids also grouped with *C. scammoni* (one each from Utqiaġvik and Point Hope). The remaining bowhead cyamids formed a clade sister to *C. ceti* from gray whales but were highly divergent from it (approximately 10.7% sequence divergence between gray whale *C. ceti* and the bowhead clade; see Table 1). Cyamids from both the BCB and OKS bowhead stocks grouped within this bowhead-specific clade. Table 1 shows the average genetic distance (uncorrected p-distance) between cyamid clades for the mtDNA COI sequences. Numbers along the diagonal represent within-clade diversity where multiple individuals of each clade were sequenced.

Cyamus scammoni, a gray whale host-specific cyamid, was found on two mature bowhead whales, harvested and sampled at Point Hope (sample 87H2) and at Utqiaġvik (sample 89B3).

We also compared the topology of the cyamid phylogeny with the topology of the host phylogeny (Fig. 4). Of the host species, right whales (genus *Eubalaena*) and gray whales host multiple cyamid species. However, the cyamids present on each of those host species do not form monophyletic

Table 1. Percent genetic distance (uncorrected p-distance) within and among clades of cyamids. The column labeled “*C. ceti* (bowhead)” represents the clade of cyamids found exclusively on bowhead whales.

	“*C. ceti*” (gray)	“*C. ceti*” (bowhead)	*C. scammoni*	*C. kessleri*	*C. ovalis*	*C. boopis*	*C. erraticus*	*C. gracilis*
“*C. ceti*” (gray)	0.9							
“*C. ceti*” (bowhead)	10.7	0.5						
C. scammoni	15.3	15.4	0.8					
C. kessleri	16.4	17.7	13.7	NA				
C. ovalis	15.2	16.6	14.6	13.8	1.1			
C. boopis	17.8	17.4	14.7	14.9	15.5	0.5		
C. erraticus	18	19.6	17	17.4	17.4	12.8	NA	
C. gracilis	15.2	17.1	14.6	14.4	15	15.5	17.3	NA

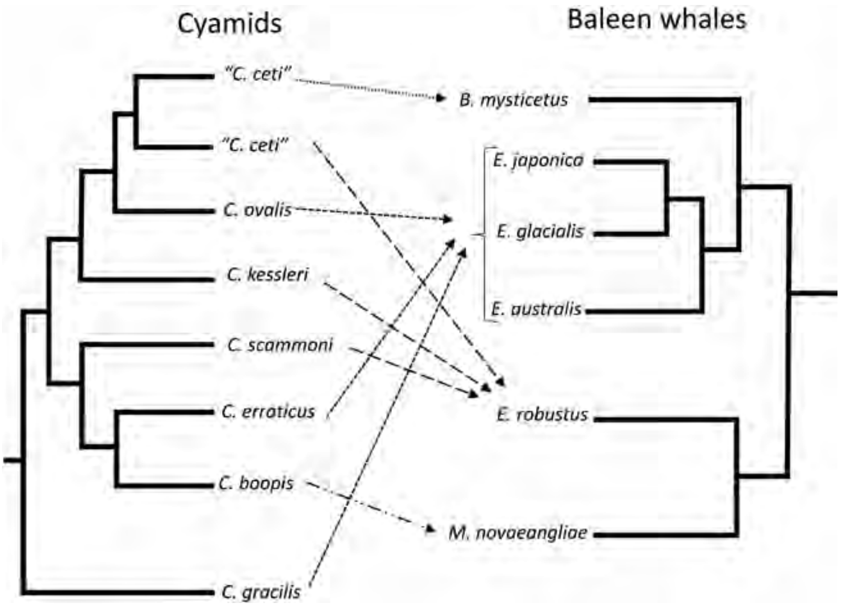

Fig. 4. Comparison of phylogenetic topologies for cyamids and their host species. Cyamid phylogeny simplified from Fig. 3. Baleen whale phylogeny derived from McGowen *et al.* (2019). Host whale species for cyamids are shown by arrows joining the two species. Note that hosts listed here are the typical host, and do not include sporadic records of cyamids on atypical hosts (such as the two *C. scammoni* we found on bowheads because that cyamid species is not normally found on bowheads).

groups. The host and parasite phylogenies do not appear to have co-evolved.

Discussion

Prior to our study, *C. ceti* was thought to be the cyamid species that occurred on both bowheads and gray whales (Callahan, 2008, Rowntree, 1983, Haney, 1999), although some morphological data has suggested that they may represent distinct species (Haney, 1999). The current study also documents *C. scammoni* on two BCB bowheads for the first time. We tested the hypothesis that “*C. ceti*” that occur on both gray and bowhead whales represent distinct evolutionary lineages. Our findings supported the idea that the “*C. ceti*” sequences from bowhead whales likely represent a distinct species as they are only distantly related to all currently known cyamid sequences.

The cyamid specimen from the OKS bowhead, which represents a bowhead stock distinct from the BCB stock where the rest of our samples were collected (Baird and Bickham, 2021), was nested within the clade of BCB bowhead "*C. ceti*" (Fig. 3). Currently, BCB and OKS bowheads are isolated from one another, with no known migration between these stocks (Baird and Bickham, 2021; Citta *et al.*, 2021; Heide-Jørgensen *et al.*, 2021). There is very little diversity within the bowhead "*C. ceti*" clade (0.5% average distance among samples; Table 1), which suggests these cyamids shared a common ancestor relatively recently in their evolutionary history. The level of divergence between cyamids from BCB and OKS aligns with the levels of stock divergence between BCB and OKS bowheads themselves (Meschersky *et al.*, 2014). Although we have not sequenced the same mtDNA COI gene in bowheads, other mtDNA genes show $<1\%$ sequence divergence among these two stocks of bowhead whales (Baird, unpubl. data). Therefore, "*C. ceti*" present on a common ancestor of these two modern day bowhead populations is plausible.

We refrain from officially classifying the taxonomy of the most common cyamid found on bowheads ("*C. ceti*") without additional data. The genetic distance of 10.7% between the bowhead "*C. ceti*" and gray whale "*C. ceti*" is slightly less than the divergence level seen among other cyamid species (Table 1). It is possible that these clades represent distinct species or subspecies. Additional work on mtDNA, nuclear DNA, and morphology is needed to test these hypotheses further. Therefore, we refer to the cyamids found on both gray and bowhead whales as "*C. ceti*." Additional molecular characterization of whale cyamids originating from the other bowhead whale stocks, namely the EGSB and EWGC would be informative to determine whether cyamid specimens from these bowhead whale stocks would be nested within the clade of BCB bowhead cyamids, as is the OKS cyamid.

Future studies should include a morphological analysis of cyamids from BCB and OKS bowhead whales to determine their level of morphological distinction from "*C. ceti*" found on gray whales. Margolis *et al.* (2000) noted in their description of *C. ceti* collected from BCB bowhead whales within Alaskan waters that the "material illustrated here may vary slightly from that taken from arctic bowhead whales figured by Lütken (1873 and others)". In their morphological analysis of Cyamidae, Margolis *et al.* (2000) grouped both gray and bowhead whale lice in *C. ceti*, while also describing a new species restricted to gray whales (*C. eschrichtii*). Margolis *et al.* (2000) considered *C. ceti* and *C. eschrichtii* different subgenera. To our knowledge, we had no *C. eschrichtii* samples. Because there is no type specimen of *C. ceti* (Linnaeus, 1758) with which to compare modern specimens from bowhead and gray whales, it complicates the taxonomic decision and necessitates further study, including the designation of a neotype for *C. ceti*.

Cyamus scammoni was also found on two BCB bowhead whales collected in the late 1980s. These samples were collected from different coastal communities in the North Slope Borough region of Alaska, namely Utqiaġvik and Point Hope. One of these cyamid samples is the sister taxon to a *C. scammoni* from an Alaskan gray whale (supported with a Bayesian posterior probability of 0.97), while the other sample is slightly more distantly related. Both instances might have been through horizontal transmissions from gray whales, which are known to seasonally co-occur with bowheads in the northern Bering, Chukchi, and Alaskan Beaufort Seas. Though novel, given the spatiotemporal overlap of both species within Arctic waters in present and historical time documented to extend deep into bowhead territory during the open water period (Marquette and Braham, 1982; Clarke *et al.*, 2016), it is somewhat expected that interspecies transmission can occur. Both bowhead whales, a male landed in Point Hope and a female landed in Utqiaġvik were mature, with total body length being 14.3 m and 16.94 m, respectively. We can only speculate on when the actual transmission event occurred, but during the late 1980s, the ENP gray whale stock was still increasing with the 1987–88 population size estimate being around 21,296 (CV=6.05%) whales (Buckland *et al.*, 1993). The two observed transmission events apparently did not lead to a successful subsequent cyamid colonization in BCB bowhead whales because they have not been observed on bowheads since the 1980s, as far as we know. It is not unprecedented to observe occasional instances of interspecies cyamid transmission among Mysticetes (Iwasa-Arai *et al.*, 2017).

The notable absence of *C. kessleri* in ENP gray whales in this study is likely reflective of sampling effort as all three types of cyamids have been previously documented in landed ENP gray whales from Utqiaġvik, Alaska (Leung, 1965). The three species of cyamids utilizing gray whales have definitive body locations (microhabitats) with both *C. scammoni* and *C. ceti* found clustered around barnacles on the gray whale (Leung, 1976; Rice and Wolman, 1971), while *C. kessleri* is not associated with barnacle clusters, but is found consistently in skin folds and around mammary and urogenital openings (Samaras and Durham, 1985). Of the three whale lice on gray whales, *C. kessleri* is the least abundant with *C. scammoni* being the most abundant, followed by *C. ceti*. Cyamid specimens in this study were opportunistically collected from different body regions from several stranded gray whales. Thus, we do not draw conclusions from the lack of cyamid species here as we did not collect and sequence every cyamid from the five gray whales included in this study.

The comparison of host and parasite phylogenies further emphasizes the hypothesis that horizontal transfer of cyamid parasites has occurred frequently throughout evolutionary time, not just recent observations. In many host/parasite interactions, cospeciation is common when parasites are isolated on their hosts and host switching does not readily occur. Examples of this can be seen in pocket gophers and their parasitic lice (Demastes *et al.*, 1993). From Fig. 4, it appears that several historical horizontal transfer events must have taken place, especially between gray and right whales (or their ancestors). Recent horizontal transfer events of cyamids between right and humpback whales (*Megaptera novaeangliae*) have been documented (Iwasa-Arai, 2017). Our data further confirm horizontal transfer events, this time between bowhead and gray whales with the observation of two *C. scammoni* on bowheads.

Our study emphasizes the importance of utilizing molecular data when making taxonomic changes and as a supplement to conducting morphological analyses in general. Many issues with relationships and taxonomy could be resolved quickly with molecular data taken from specimens examined morphologically. These issues will take further study to correlate the morphological description with our molecular data.

Lastly, this study further supports the use of parasites as an important biomarker for studying the biology of the hosts. Interspecies interactions between gray and bowhead whales have been revealed based on their sharing of *C. scammoni*. As global climate change causes additional species to inhabit northern waters, having a baseline understanding of bowhead parasites is critical to monitoring how host/parasite interactions may change over time. For example, if the “*C. ceti*” currently found only on bowheads spreads to other whale species in the future, this may indicate new whale species interactions, resource competition, etc. that may inform conservation or management actions.

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Appendix

Appendix 1. List of samples and GenBank sequences used in molecular analyses. Sample numbers are given for new gray and bowhead whale cyamids sequenced in this study.

Species	Sample number	GenBank accession number
Isocyamus globicipitis		FJ751181
C. scammoni		FJ751214
C. scammoni		FJ751213
C. scammoni		FJ751212
C. scammoni		FJ751211
C. scammoni		FJ751210
C. scammoni		FJ751209
C. scammoni		FJ751208
C. scammoni		FJ751207
C. scammoni		FJ751206
C. scammoni		F751205
C. scammoni		FJ751204
C. scammoni		FJ751203
C. scammoni		FJ751202
C. scammoni		FJ751201
C. scammoni		FJ751200
C. scammoni		FJ751199
C. scammoni		FJ751198
C. scammoni		FJ751197
C. scammoni		FJ751196
C. scammoni		FJ751195
C. scammoni		FJ751194
C. scammoni		FJ751193
C. scammoni		FJ751192
C. scammoni		FJ751191
C. scammoni		FJ751190
C. scammoni		FJ751189
C. scammoni		FJ751188
C. scammoni		FJ751187
C. scammoni		FJ751186
C. scammoni		FJ751185
C. scammoni		FJ751184
C. scammoni		FJ751183
C. scammoni		FJ751182
C. ovalis		DQ095032
C. ovalis		DQ095047
C. gracilis		DQ095104
C. erraticus		DQ095129
C. boopis		DQ095150
C. boopis		FJ751159
C. ceti		FJ751160
C. ceti		FJ751161
C. ceti		FJ751162
C. ceti		FJ751163

Appendix 1. Continued.

Species	Sample number	GenBank accession number
C. ceti		FJ751164
C. ceti		FJ751165
C. ceti		FJ751166
C. ceti		FJ751167
C. ceti		FJ751168
C. ceti		FJ751169
C. ceti		FJ751170
C. ceti		FJ751171
C. ceti		FJ751172
C. ceti		FJ751173
C. ceti		FJ751174
C. ceti		FJ751175
C. ceti		FJ751176
C. ceti		FJ751177
C. ceti		FJ751178
C. ceti		FJ751179
C. ceti		FJ751180
C. scammoni		FJ751214
C. kessleri		FJ751224
C. scammoni	2014GFD02_1	PV448945
C. scammoni	2014G1_2	PV448947
C. scammoni	12BGW2_1	PV448937
C. scammoni	12BGW1_2	PV448951
C. scammoni	2014GFD_1	PV448938
C. scammoni	87H2_2	PV448949
C. scammoni	89B3	PV448983
C. scammoni	12BGW1_1	PV448950
C. scammoni	2014GFD_2	PV448939
C. scammoni	2014G1_1	PV448946
C. ceti	2018BGW0914FD_B	PV448979
C. ceti	12BGW2_2	PV448980
C. ceti	2018BGWFD_A	PV448971
C. ceti	2018BGW0914FD_A	PV448973
C. ceti	2014GFD02_2	PV448944
C. ceti - bowhead clade	18B9_A	PV448975
C. ceti - bowhead clade	12B11_1	PV448940
C. ceti - bowhead clade	12B11_2	PV448941
C. ceti - bowhead clade	15B20	PV448955
C. ceti - bowhead clade	10B6_A	PV448982
C. ceti - bowhead clade	01B26	PV448954
C. ceti - bowhead clade	15RUS1	PV448981
C. ceti - bowhead clade	11B7_1	PV448942
C. ceti - bowhead clade	15B11_A	PV448960
C. ceti - bowhead clade	18B19_A	PV448961
C. ceti - bowhead clade	19B5	PV448963
C. ceti - bowhead clade	18B7_A	PV448974

Appendix 1. Continued.

Species	Sample number	GenBank accession number
C. ceti - bowhead clade	13B8_1	PV448934
C. ceti - bowhead clade	14B4_1	PV448935
C. ceti - bowhead clade	13B8_2	PV448936
C. ceti - bowhead clade	12B5_2	PV448943
C. ceti - bowhead clade	00B2	PV448948
C. ceti - bowhead clade	94B2	PV448978
C. ceti - bowhead clade	12B22_2	PV448952
C. ceti - bowhead clade	12B5_1	PV448953
C. ceti - bowhead clade	00KK3_A	PV448956
C. ceti - bowhead clade	10B1	PV448957
C. ceti - bowhead clade	16B8	PV448977
C. ceti - bowhead clade	16B8_B	PV448958
C. ceti - bowhead clade	15B12_A	PV448959
C. ceti - bowhead clade	19B2	PV448962
C. ceti - bowhead clade	19B10_A	PV448964
C. ceti - bowhead clade	19B10_B	PV448965
C. ceti - bowhead clade	19B4	PV448966
C. ceti - bowhead clade	21B2_A	PV448967
C. ceti - bowhead clade	21B2_B	PV448968
C. ceti - bowhead clade	21B4_A	PV448969
C. ceti - bowhead clade	21B4_B	PV448970
C. ceti - bowhead clade	05KK2_A	PV448972
C. ceti - bowhead clade	05KK2_B	PV448976

Review

Common minke whale, western North Pacific.

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Review

GENETICALLY IDENTIFIED J-STOCK COMMON MINKE WHALES: AN OVERVIEW OF THEIR BIOLOGICAL AND ECOLOGICAL FEATURES IN WATERS AROUND JAPAN

Mutsuo GOTO*, Tsutomu TAMURA,
Takeharu BANDO and Genta YASUNAGA

Institute of Cetacean Research, 4–5 Toyomi-cho, Chuo-ku, Tokyo 104–0055, Japan
**Corresponding author: goto@cetacean.jp*

Abstract

This paper presents and overview of the biological and ecological features of the J-stock common minke whale (*Balaenoptera acutorostrata scammoni*) in waters around Japan based on analyses of genetically identified individuals. Reviewed information included spatial/temporal distribution, morphology, morphometrics, reproductive characteristics, feeding ecology, environmental pollutants, and ecological markers. Except for feeding ecology and environmental pollutants, these features (e.g., spatial/temporal distribution, morphology such as flipper and fluke color pattern and ecological markers such as cookie cutter shark scars) confirm the biological and ecological uniqueness of the J-stock within the North Pacific common minke whale. Our analysis also confirms the existence of distinct genetically, biologically and ecologically independent stocks with characteristics so far not identified in any other baleen whales in the Western North Pacific, and corroborates the view that the minke whale J-stock should be managed independently.

Key words: North Pacific, common minke whale, stock assignment, morphology, feeding ecology, pollutants, ecological markers, reproductive parameters, J-stock.

Introduction

Biological stocks can be defined as a group of same-species organisms that are genetically self-sustaining and live isolated geographically or temporally during reproduction. The use of the term usually implies that a particular population is more or less isolated from other stocks of the same species. In the western North Pacific, at least two biological stocks of common minke whales (*Balaenoptera acutorostrata scammoni)* are known to exist: the Okhotsk Sea-West Pacific (O-stock) and the Sea of Japan-Yellow Sea-East China Sea (J-stock) (Omura and Sakiura, 1956; Ohsumi, 1977; 1983). The two stocks have been differentiated primarily through morphological and reproductive characteristics (Omura and Sakiura, 1956; Ohsumi, 1977; Kato, 1992; Kato *et al.*, 1992), as well as genetics (Wada and Numachi, 1991 for allozymes; Goto and Pastene, 1997 for mitochondrial DNA (mtDNA); and Kanda *et al.*, 2009a; Kanda *et al.*, 2009b for microsatellite DNA (msDNA)), with the differences reported suggesting their reproductive isolation. Kato (1992) estimated the breeding periods of both stocks from seasonal distribution of fetus body length. He proposed that the ‘autumn breeding stock’ distributes in the Yellow Sea, the East China Sea and the Sea of Japan and the ‘winter breeding stock’ distributes off the Pacific coast of northern Japan, with both stocks mixing in the southern Okhotsk Sea in early summer. Kato *et al.* (1992) examined the regional differences in minke whale flipper color patterns and found that they differed between the Sea of Japan and other areas (Okhotsk Sea and off the Pacific coast of northern Japan).

Following these studies, the International Whaling Commission (IWC) proposed and adopted some boundaries for these stocks between the Sea of Japan-Yellow Sea-East China Sea and the Okhotsk Sea-West Pacific (Donovan, 1991).

Various genetic studies have shown that both stocks mix with each other spatially and temporally in the southern part of the Okhotsk Sea (northern Hokkaido) (Wada, 1991; Pastene *et al.*, 1998) and on the Pacific side of Japan (Pastene *et al.*, 2016a). Since the publication of those studies, a substantial number of genetic samples of western North Pacific common minke whales became available, and modern and more powerful genetic markers have been applied in recent years to these samples. The application of such markers to both the previous samples as well as the new samples has enabled finer studies on stock structure of this species in this ocean basin (Pastene *et al.*, 2016a; b).

From 2009, msDNA has been used in genetic analyses of individual assignment to stocks (Kanda *et al.*, 2009a), for example, by using the program STRUCTURE (Pritchard *et al.*, 2000). This approach has allowed several biological and ecological aspects of J- and O-stock common minke whales to be studied separately.

The objective of this paper is to present an overview of the biological and ecological information (e.g., spatial/temporal distribution, morphology, morphometrics, reproductive characteristics, feeding ecology, environmental pollutants and ecological markers) so far accumulated for the J-stock common minke whales derived from analyses of genetically identified individuals with the aim of contributing to the better understanding and management of this stock.

Individual Assignment to Stocks Based on Microsatellite DNA Analyses

Microsatellite DNA

MsDNA became a popular genetic marker for many aspects of molecular ecology, in particular for intraspecific studies, because of its high mutation rate and polymorphisms compared to other markers (Estoup *et al.*, 2002). MsDNA consist of short tandem repeats of mono-, di-, tri-, or tetra-nucleotide repeats, e.g., (AT)n and (GATA)n, which are assumed to be randomly distributed throughout the genomes (Goldstein and Schlotterer, 1999). MsDNA show length variation that results from insertion and/or deletion of the repeat units, which is detected using PCR and separation of the products on capillary gel in the automated sequencer. Since allele sizes differ by as little as one base pair, it is required to have adequate and consistent standards to score the alleles.

Laboratory work of microsatellite DNA

Details of the laboratory procedures for msDNA analysis were described by Pastene and Goto (2016) and Taguchi *et al.* (2023). A summary is provided as follows.

MsDNA polymorphisms were analyzed using 16 loci: EV1, EV14, EV21, EV37, EV94, (Valsecchi and Amos, 1996), GT23, GT195, GT211, GT310, GT509, GT575 (Bérubé *et al.*, 2000), GAT A28, GATA98, GATA417, TAA31 (Palsbøll *et al.*, 1997), DlrFCB14 (Buchanan *et al.*, 1996). EV1, EV14, EV21 were developed from sperm whale, EV37, EV94, GT23, GT310, GT575, GATA28, GAT A98, GATA417, TAA31 from humpback whale, and DlrFCB14 from beluga whale. All GT, EV and DlrFCB primers are dinucleotide repeats, TAA31 trinucleotide repeats, and all GATA primers tetranucleotide repeats. Primer sequences and PCR profiles followed those of the original authors with slight modifications.

PCR amplifications were performed in 15 μL reaction mixtures containing 10–100 ng of DNA, 5 pmole of each primer, 0.625 units of Ex Taq DNA polymerase (Takara Shuzo), and 2 mM of each dNTP, and 10x reaction buffer containing 20 mM $MgCl_2$ (Takara Shuzo). PCR amplifications followed the manufacturer's instructions for the use of Ex Taq DNA polymerase (Takara Shuzo). Amplified products with internal size standard (GENESCAN400HD, Applied Biosystems Japan) were run on a 6% polyacrylamide denaturing gel (Long Ranger^{TM}) using a BaseStation TM100 DNA fragment analyzer (Bio-Rad) or were electrophoresed on an Applied Biosystems 3500 Genetic Analyzer. Allele sizes were determined using a 600 LIZ size standard and GeneMapper v. 5.0 (ABI).

Data analysis for assignment of individuals to stock

Pastene *et al.* (2016a) and Taguchi *et al.* (2017) described the analytical procedures for stock assignment based on msDNA, and a summary is provided below.

The Bayesian clustering approach was implemented with the microsatellite data in the program STRUCTURE version 2.0 (Pritchard *et al.*, 2000) to determine the most likely number of genetically distinct stocks present in the samples. The program is a model-based clustering method for inferring stock structure (K is the number of stocks in the model) using multilocus genotype data with and without information on sampling locations. STRUCTURE allowed for the analyses of the samples without choosing sample units that did not necessarily correspond to real biological stock boundaries. A conceptual diagram of individual assignment under STRUCTURE is shown in Fig. 1. In a case of allele frequency at single loci (bar plot in this figure) in each source population being available (Fig. 1(a)), it is highly possible that individual A originates from population 1 since it has two alleles that are major in population 1. In contrast, individual B is likely to come from population 2 since it has two alleles that are minor in population 1. Another case is individual assignment with no allele frequency in each source population (Fig. 1(b)). Here, genotypes at multiple loci in each individual allow the estimation of an allele frequency for source population and an assignment probability in each individual by repeating the following steps: (I) estimation of allele frequency from tentative clustering in Hardy-Weinberg equilibrium, and (II) individual assignment based on the tentative allele frequency according to the concept of Fig. 1(a).

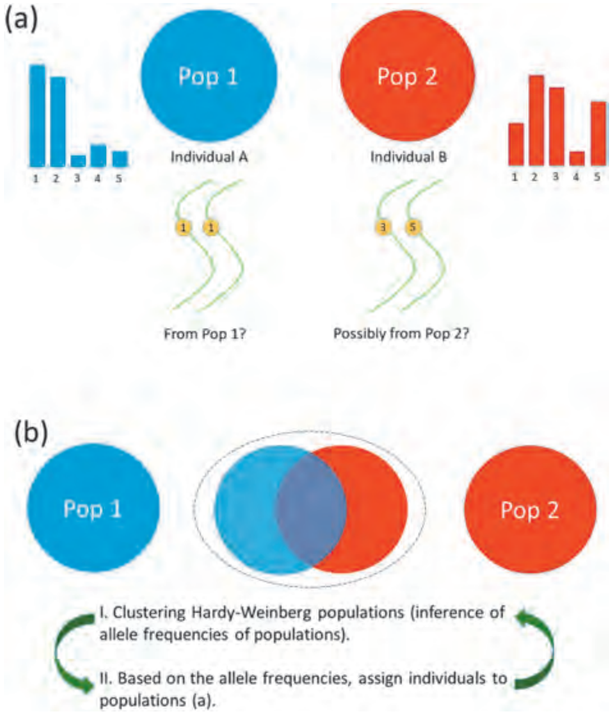

Fig. 1. Basic concept of individual assignment. Pop: population. (See "Individual assignment to stocks based on microsatellite DNA analyses" section for explanation).

Posterior probabilities for K were estimated from ten independent runs for each value of K from one to five with genetic information only. These data were calculated based on burn-in period of 10,000 iterations and runs of 100,000 iterations. Individual assignment was then conducted for the most plausible K using the estimated individual proportion of membership probability (90%). The ancestry model used for the simulation was the admixture model, which assumes individuals may have mixed ancestry. The allele frequency model used was the correlated allele frequencies model, which assumes that frequencies in the different stocks are likely to be similar due to migration or shared ancestry.

Unassigned whales are those with less than 90% membership probability in the STRUCTURE analyses. This could be due to lack of power, because when the number of loci used is increased, a larger number of individuals are assigned to either stock. Regarding the unassigned whales in the STRUCTURE analyses, a simple simulation exercise showed that the number of unassigned whales decreased with the increase in the number of microsatellite loci used, and that they were widely distributed geographically (Taguchi *et al.*, 2017). Therefore, it is confirmed that the number of loci used for assignment to the J- or O-stock is one of the factors leading to the unassigned individuals in the STRUCTURE analysis of common minke whale. This is also supported by an earlier study suggesting that, in practice, the accuracy of the assignments depends on the number of loci (Pritchard *et al.*, 2000).

Biological and ecological characterization of the J-stock

Several biological and ecological studies have been conducted on the J-stock common minke whale based on genetically assigned individuals to this stock as described in the above section. Table 1 shows a summary of studies examined in this overview by topic, data sources, number, sampling period and references. Unassigned individuals were excluded from the analyses of these topics, except for spatial/temporal distribution and ecological marker (cookie cutter shark scar) analyses. In this section, a brief summary of the results by study topic is provided.

As shown in Fig. 2(a), the IWC Scientific Committee (IWC SC) has defined sub-areas for the management of the common minke whales in the western North Pacific (IWC, 1994). Relevant sub-areas mentioned in this paper are sub-areas 7, 11, 2 and 6 (Fig. 2(b)). The western part of sub-area 7 (7W) corresponds to the coastal zone of Japan, while sub-areas 11, 2 and 6 correspond to northern Hokkai-

Table 1. Summary of different biological and ecological features studied on the J-stock common minke whales with sample information and key references.

Feature	Samples*	Year obtained	Source**	Reference
Distribution and movement				
Spatial distribution	$n=4{,}275$	1994 to 2014	JARPN/JARPNII; bycatch	Goto *et al.* (2017)
Temporal distribution	$n=2{,}522$	2001 to 2004	JARPNII; bycatch	Goto *et al.* (2017)
Distance from coastal line	$n=986$	1994 to 2007	JARPN/JARPNII; bycatch	Kanda *et al.* (2017)
Morphology and morphometry				
Flipper color pattern	$n=220$	2012 and 2013	JARPNII	Nakamura *et al.* (2016)
Fluke color pattern	$n=164$	2007	JARPNII	Nagatsuka (2008; 2010)
Morphometry	$n=500$	2000 to 2007	JARPN/JARPNII	Hakamada and Bando (2009)
Reproduction				
Conception date	$n=107$	1994 to 2007	JARPN/JARPNII	Bando *et al.* (2010a)
Feeding ecology				
Stomach contents	$n=742$	1996 to 2018	JARPN/JARPNII; NEWREP-NP	Goto *et al.* (2021)
Ecological markers				
Total Hg levels	$n=59$	2012 and 2013	JARPNII	Yasunaga and Fujise (2016)
Cookie cutter shark marks	$n=1{,}037$	2002 to 2007	JARPN/JARPNII	Bando *et al.* (2010b)

**n*: Number of animals used in the analyses.

**JARPN: Japanese Whale Research Program under Special Permit in the western North Pacific. JARPNII: JARPN Phase II; NEWREP-NP: New Scientific Whale Research Program in the western North Pacific.

do, the southern part of the Pacific side of Japan and the Sea of Japan side of Japan, respectively.

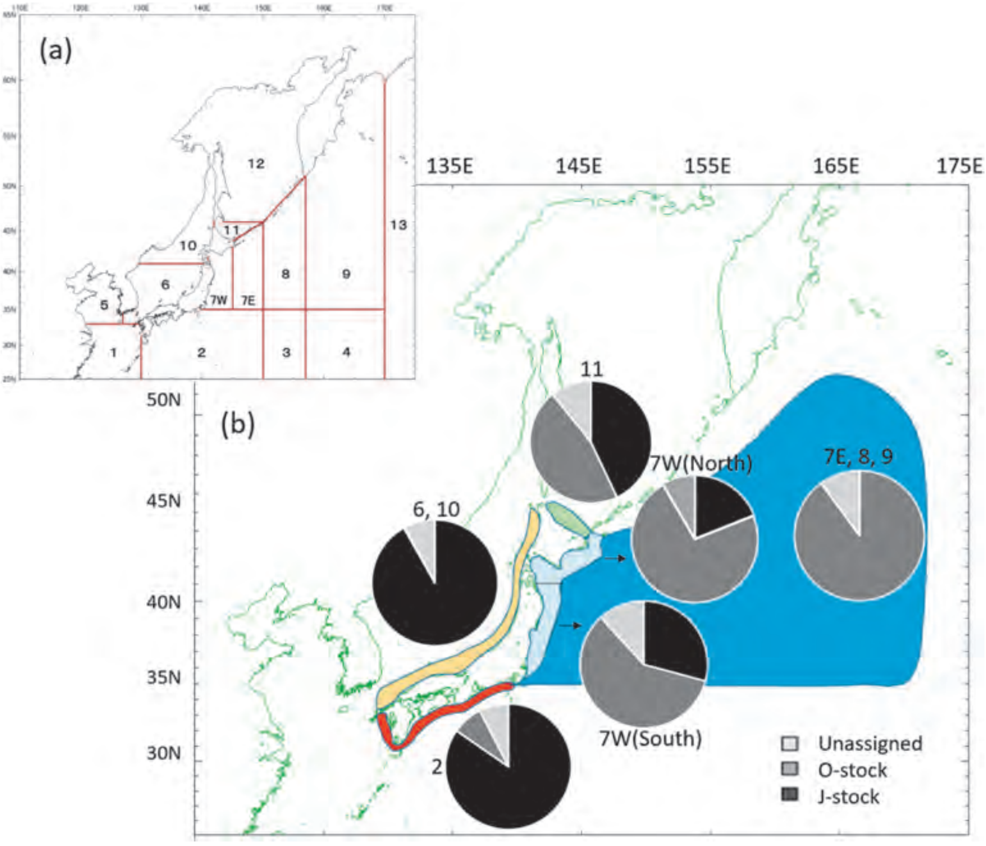

Fig. 2. (a) The 13 sub-areas defined for North Pacific common minke whale management trials (modified after IWC, 1994) and (b) spatial occurrence of O- and J-stock common minke whales in each sub-area around Japan based on genetic individual identification (modified after Goto *et al.*, 2017).

Distribution and movement

Spatial distribution of the J-stock along the coast of Japan

As shown in Fig. 2(b), almost all the individuals collected from the Sea of Japan side belong to the J-stock, whereas almost all of the individuals from the offshore North Pacific belong to the O-stock (Goto *et al.*, 2017). The southern part of the Pacific side of Japan was mainly occupied by the J-stock, while Northern Hokkaido and the northern part of the Pacific side of Japan are areas where both stocks overlap geographically (Goto *et al.*, 2017). Areas relevant for the J-stock are sub-areas 2, 6, 7W and 11.

Temporal distribution along the Pacific coast of Japan

Goto *et al.* (2017) showed the monthly occurrence of O- and J-stocks in sub-areas 2 and 7W (South) on the Pacific side of Japan (Fig. 3). In the southern part of the Pacific side of Japan (sub-area 2), J-stock was predominant throughout the year (around 80% in proportion). In the southern part of the Pacific side of Japan (sub-area 7W (South)), the proportion of the J-stock increased in autumn/winter and decreased in spring/summer. Conversely, the proportion of O-stock decreased in autumn/winter and increased in spring/summer. Goto *et al.* (2017) postulated that the fact that the J-stock is distributed in the southern part of the Pacific side of Japan throughout the year suggests that the Kuroshio Current—one of the strongest west boundary currents of the subtropical gyre—is serving as a dynamic stock boundary between O- and J-stocks.

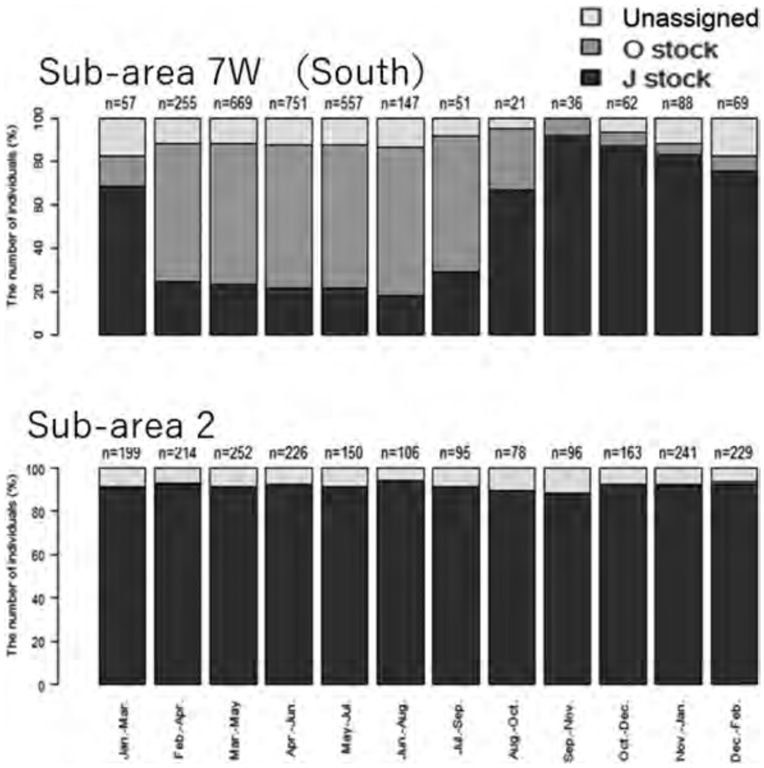

Fig. 3. Monthly occurrence of O- and J-stock common minke whales in sub-areas 7W (South) and 2 on the Pacific side of Japan. Each bar is expressed as a three-month moving average. Sample size (*n*) is shown on the top of each bar (modified after Goto *et al.*, 2017).

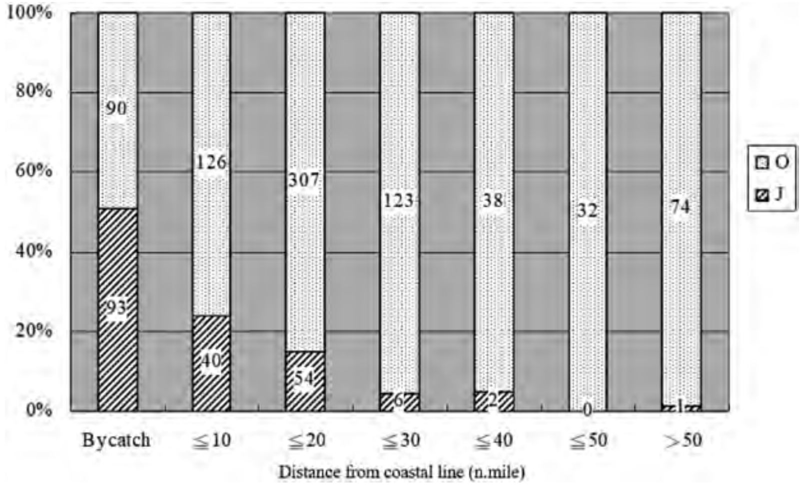

Fig. 4. Proportion of the common minke whales assigned to the J- and O-stocks collected from sub-area 7W by the distance from Japan's coastal line (after Kanda *et al.*, 2010). The numbers in the bars indicate sample size. Bycatches occur within 3 n.miles from the coastal line.

Distance from the coastal line

Kanda *et al.* (2010) estimated the proportion of the minke whales assigned to the J- and O-stocks collected from sub-area 7W by the distance from the Japanese coastal line (Fig. 4). J-stock whales have a more coastal distribution in comparison with the O-stock. The proportion of the J-stock whales decreased from coastal areas towards offshore areas. Such a clinal distribution supports the mixing of the two stocks in sub-area 7W. This means that the main migration routes of J-stock animals, especially juveniles which are predominant in the bycatch samples (Pastene *et al.*, 2016a), might be along the nearshore areas that follow the coastal line of Japan on the Pacific and Sea of Japan sides. The distribution of J-stock animals on the Pacific side of Japan decreased from coastal areas towards offshore areas (Fig. 4).

Migratory routes

Based on the studies by Hatanaka and Miyashita (1997) and Goto *et al.* (2010), it was assumed that the migratory routes of adult and juvenile J-stock animals to feeding areas were as shown in Fig. 5. Although the breeding area(s) of these animals had not been identified at this stage, migratory routes to breeding area(s) were assumed to be the reverse in the case of adults. Adult animals were assumed to migrate northward and southward for feeding and breeding, respectively, through the central corridor of the Sea of Japan. The northward migration limit was not clear at this stage because there were no genetic samples available from the central and northern parts of the Okhotsk Sea. In the case of juveniles, it was assumed that they were making short northward and southward migrations along the coastal area for feeding because bycatch juvenile animals were reported throughout the year on the Japanese coast (Pastene *et al.*, 2016a; Goto *et al.*, 2017).

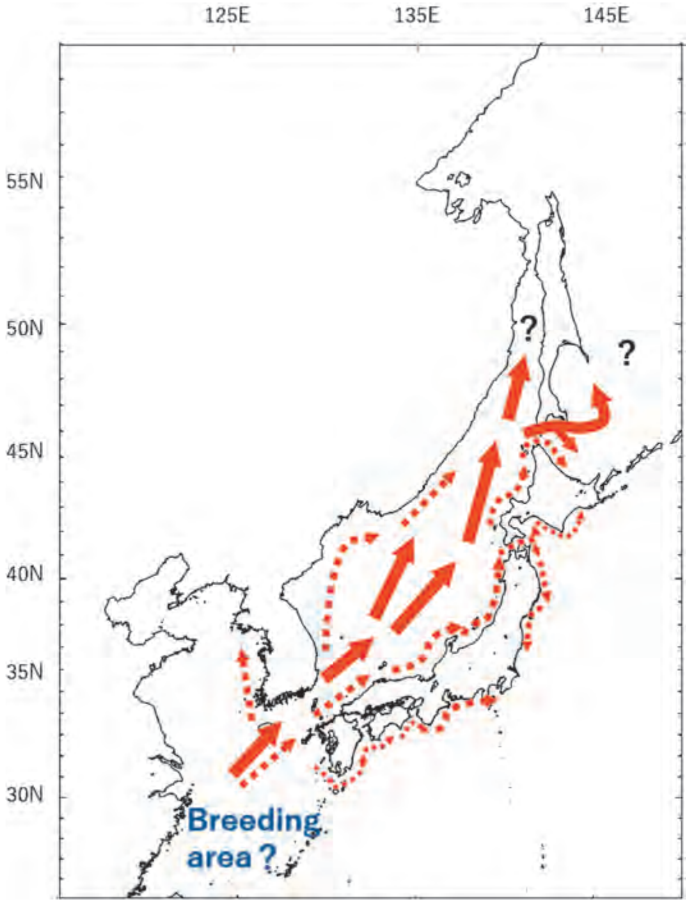

Fig. 5. Assumed feeding migration route of J-stock common minke whales (modified after Hatanaka and Miyashita, 1997 and Goto *et al.*, 2010). Solid red arrows: mature animals, dotted arrows: immature animals. The northward migration limit and the breeding areas of these animals has not been identified at this stage. Adult animals were assumed to migrate northward through the central corridor of the Sea of Japan, while juveniles were assumed to make short northward and southward migrations along the coastal area.

Morphology and morphometry

Morphology

Nakamura *et al.* (2016) studied the white patch on the flipper, which is characteristic of common

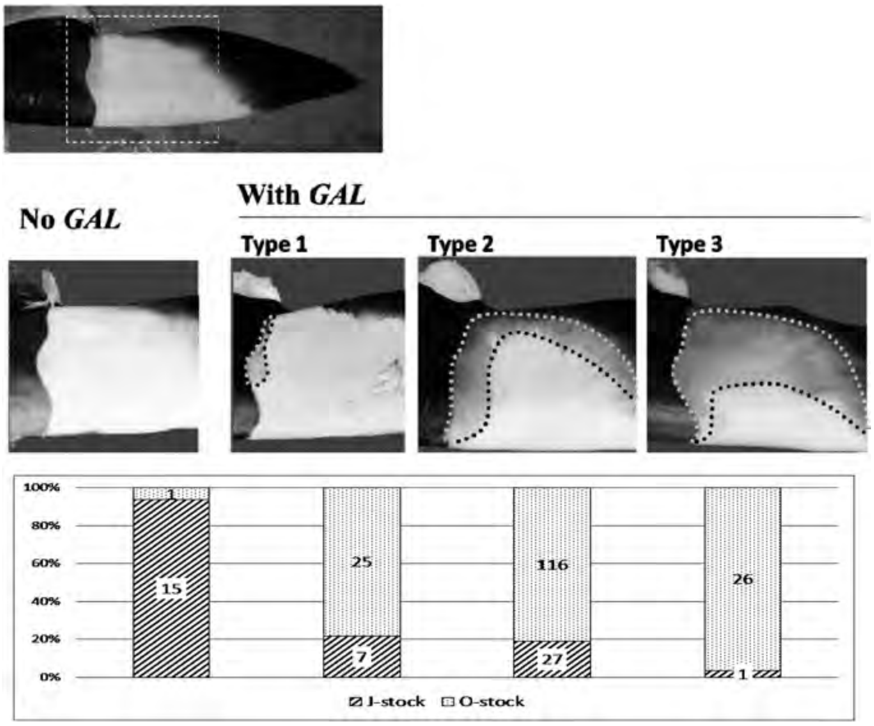

Fig. 6. Characteristics of the white patch along the ventral part of the flipper in common minke whales from the western North Pacific. The pictures show the basis for the classification based on the *GAL* types (*GAL*: surrounded by dotted line), and the bar plots show the proportion of each GAL types between J- and O-stocks (modified after Nakamura *et al.*, 2016). Bar figures indicate number of individuals.

minke whales, based on individuals assigned genetically to the J- and O-stocks. For the analyses on morphological differences the authors used whales sampled by the Japanese Whale Research Program under Special Permit in the western North Pacific Phase II (JARPNII) during 2012 and 2013. They focused on the morphological differences in the size and pattern of the white patch on the flipper of each whale. The length of the white patch along the anterior (ventral) margin of the flipper tended to be proportionally smaller in the J-stock. The pattern of the boundary area of the white patch named as the 'Grayish Accessary Layer (GAL)' was remarkably different between the two stocks (Fig. 6). Among animals with 'no GAL' type, 94% were J-stock. Conversely, 96% of the animals with GAL expanding over half of the flipper width were O-stock.

Fluke color pattern

Nagatsuka (2008) found that common minke whales had different black and white color patterns in the ventral fluke pigmentation and characterized their color patterns into three types, according to the proportion of white and black colors: white fluke, intermediate fluke and black fluke (Fig. 7). Statistically significant differences in the frequencies of these three types were observed between the individuals assigned genetically as J- and O-stocks sampled during the 2007 JARPNII survey in sub-area 7W. The white type was predominant in the J-stock whales while the intermediate and black types were predominant in the O-stock.

Morphometry

Hakamada and Fujise (2000) examined external measurement data of whales obtained during the 1994–1999 JARPN surveys (external measurements for V1–V9 in Fig. 8 and additional data for length of tip to posterior insertion and maximal width of flipper, and for width of fluke tip). They found statistically significant differences between the individuals identified genetically as J- and O-stocks. The

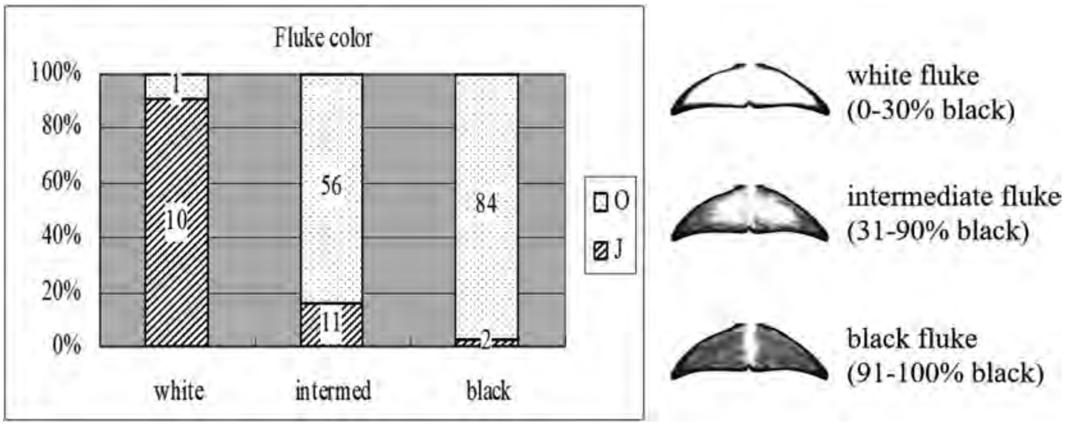

Fig. 7. Proportion of J- and O-stock-assigned common minke whales collected from sub-area 7W by the fluke ventral color pattern, and diagram of the three patterns (after Kanda *et al.*, 2010). The numbers in the bars indicate the sample size.

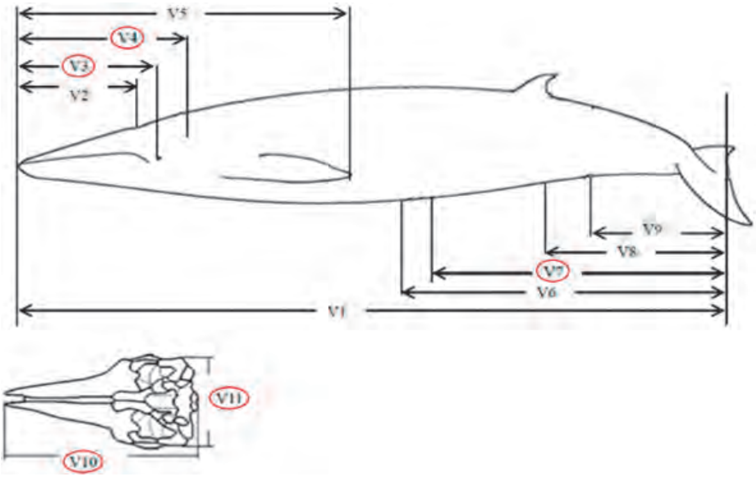

Fig. 8. External measurements of western North Pacific common minke whales examined for comparative stock analyses (after Hakamada and Bando, 2009). Measurements V3, V4, V7, V10 and V11, indicated with red ellipses, showed significant differences in morphometrics between J- and O-stocks.

average marginal mean of the length of the measurements V2–V4, width of flipper and width of fluke tip were longer for J-stock animals than for O-stock animals.

Hakamada and Bando (2009) examined morphometric data (Fig. 8) of common minke whales sampled by JARPNII and identified genetically as J- and O-stocks. Measurements V3, V4, V7, V10 and V11 showed statistically significant differences between J- and O-stocks. This result suggested that external measurements can be used as a non-genetic marker to differentiate J-stock from the O-stock. For example, the average marginal mean of the length of the measurements V2–V5 were longer for J-stock animals than for O-stock animals. Measurements of V6–V9 were shorter for J-stock animals than for O-stock animals, while measurements of V10–V11 were longer for J-stock animals than for O-stock animals. These results suggested that J-stock animals tend to have bigger heads and shorter tail bodies than O-stock animals.

Reproduction

Conception date

Kato (1992) estimated conception date from fetal body length. He found two peaks of conception in samples from southern Okhotsk Sea and the Sea of Japan, one in autumn and another in winter. This

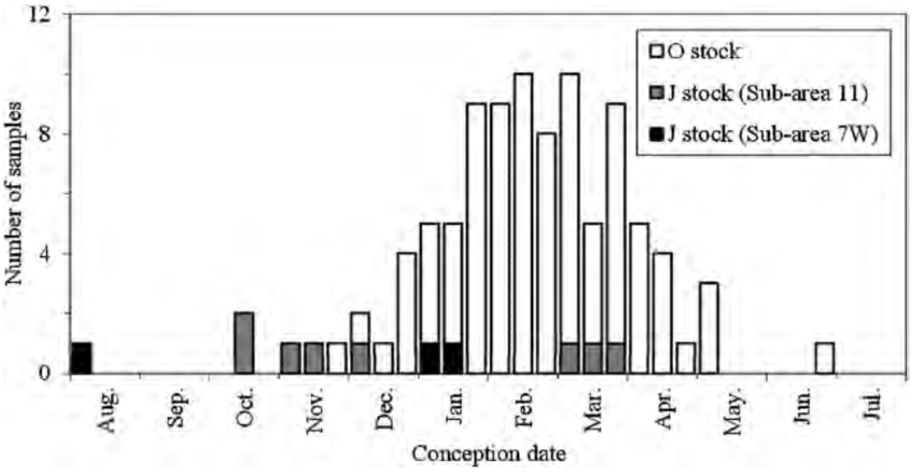

Fig. 9. Seasonal distribution of estimated conception dates of the J- and O-stock common minke whales in ten-day periods (after Bando *et al.*, 2010a).

was further endorsed by Best and Kato (1992). Subsequently, Bando *et al.* (2010a) examined conception dates of common minke whales sampled in sub-area 7W and sub-area 11 during the 1994–2007 JARPN/JARPN II surveys and identified genetically as either J- or O-stock individuals. Conception dates were estimated based on the formula of Kato and Miyashita (1991), which was developed for Antarctic minke whales and used for common minke whale in Kato (1992). In sub-area 7W the conception date of J-stock whales was in August ($n=1$) and January ($n=2$); in sub-area 11 it was between October and March ($n=8$) (Fig. 9). These results suggested that the conception period of the J-stock extends from autumn to winter, while the O-stock whales appear to have one peak in winter. However, the distributions of conception period for J- and O-stock overlapped with each other.

Feeding ecology

The feeding ecology of common minke whales around Japan has been examined by Kasamatsu and Tanaka (1992), Tamura and Fujise (2002) and Konishi *et al.* (2009). However, there have been few published papers specifically focused on the feeding habits of J-stock common minke whales. In order to simplify the comparison of feeding indices, Goto *et al.* (2021) divided prey species into the following based on the stomach contents of these whales: copepods, krill, Japanese sandlance *(Ammodytes personatus)*, Japanese anchovy *(Engraulis japonicus)*, Pacific saury *(Cololabis saira)*, walleye pollock *(Gadus chalcogrammus)*, Japanese common squid *(Todarodes pacificus)*, and others. The relative prey composition (%) in weight of each prey species in each month and sub-area was calculated. Results of the first analyses of genetically identified J-stock individuals showed that these whales fed on various prey species and that the main prey species changed both yearly and geographically (Fig. 10). These results suggested that the J-stock common minke whales are opportunistic feeders, changing their prey species in response to availability, having a feeding habit similar to the O-stock whales.

Environmental pollutant (total Hg) levels

Yasunaga and Fujise (2016) compared the accumulation patterns of total Hg concentrations in muscle and liver in genetically identified J- and O-stock common minke whales. Their analyses were based on J- and O-stock immature animals taken from sub-area 7W in the 2012 and 2013 JARPNII surveys (Fig. 11). Statistical analyses showed no significant differences in the level of pollutant concentration confounding factors such as age, sex, blubber thickness and year. This result suggests that there are few differences in trophic levels and food items between the J- and O-stocks of immature whales in sub-area 7W.

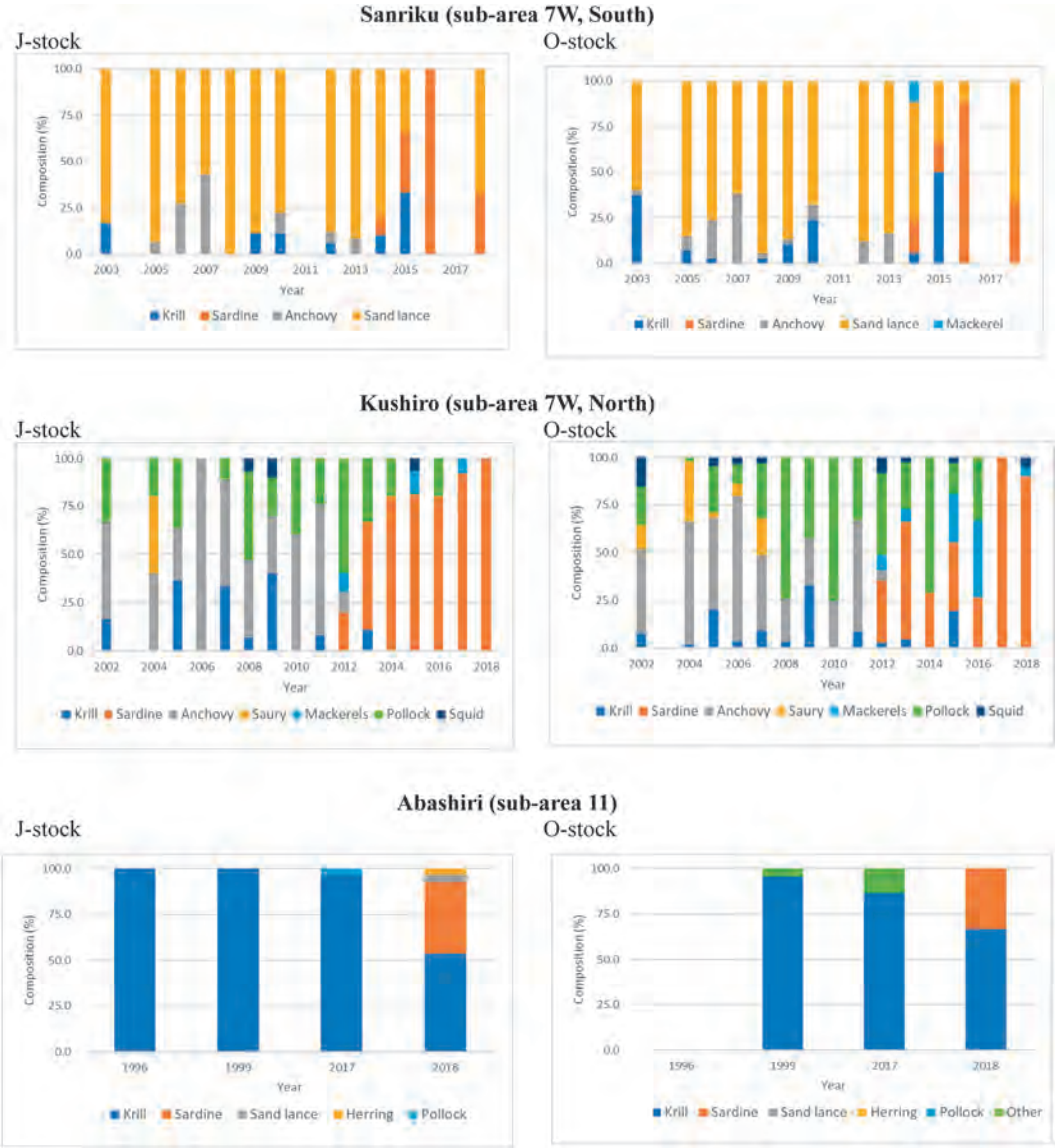

Fig. 10. Yearly and geographical change of main prey species of J- and O-stock common minke whales in Sanriku (southern part of sub-area 7W), Kushiro (northern part of sub-area 7W) and Abashiri (sub-area 11). (After Goto *et al.*, 2021; this study).

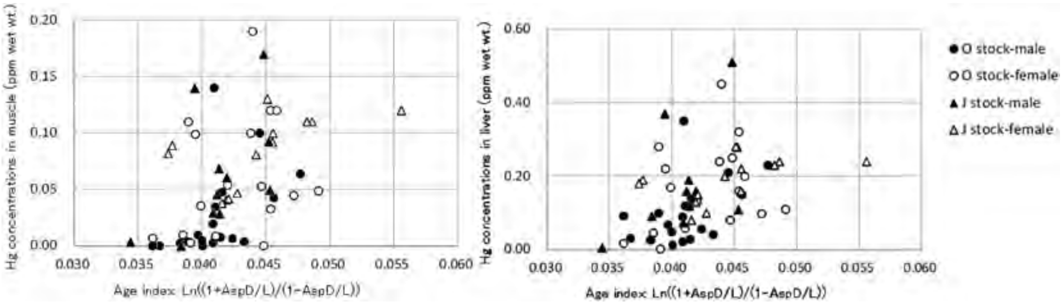

Fig. 11. Relationship between Hg concentrations (ppm wet wt.) and age in muscle (left) and in liver (right) in common minke whales from sub-area 7W (after Yasunaga and Fujise, 2016).

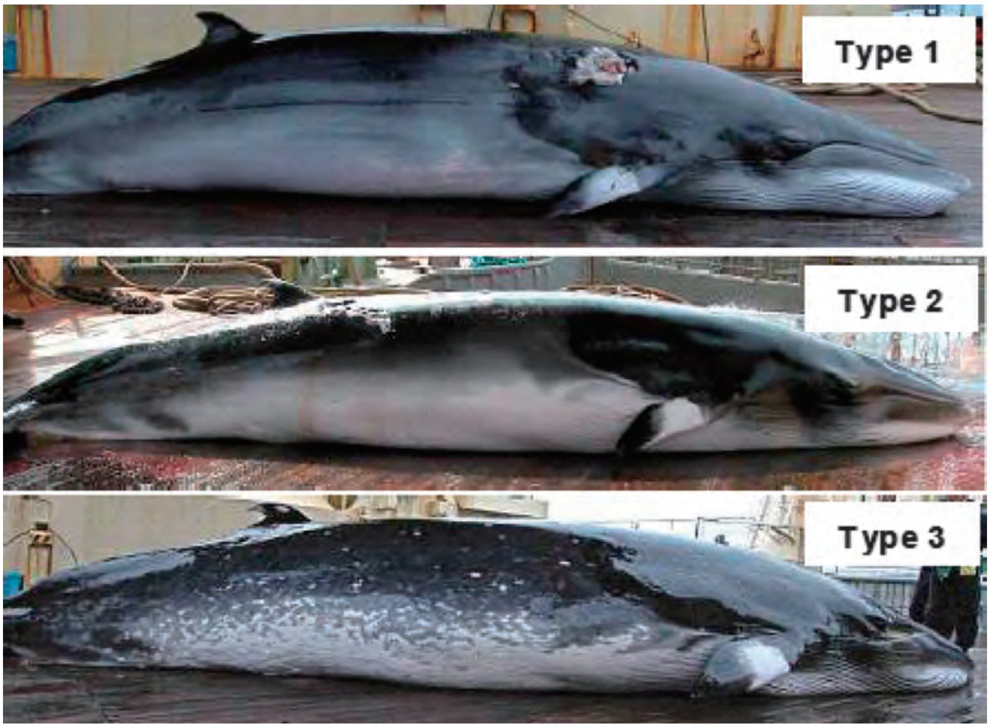

Fig. 12. Three types of cookie cutter shark-induced scar presence patterns in common minke whales. Type 1: no scars on the body (Sample No. 2006NP-M080: J-stock), Type 2: 1–20 scars on a single body side (2002NP-M061: J-stock), and Type 3: more than 20 scars on a single body side (2006NP-M067: O-stock) (after Bando *et al.*, 2010b).

Table 2. Types of cookie cutter shark-induced scars in common minke whales in the coastal areas of western North Pacific off sub-area 7W (North and South) and Pacific offshore area (sub-areas 8 and 9) (modified from Bando *et al.*, 2010b).

Sub-area	Type of scar		Microsatellite DNA		
			O	?	J
7W North	*Type 1*	None	0	2	17
	Type 2	1–20 scars	14	5	31
	Type 3	more than 20 scars	291	31	5
	Total		305	38	53
7W South	*Type 1*	None	0	3	19
	Type 2	1–20 scars	10	5	22
	Type 3	more than 20 scars	213	25	2
	Total		223	33	43
8	*Type 1*	None	0	0	0
	Type 2	1–20 scars	3	1	0
	Type 3	more than 20 scars	95	11	0
	Total		98	12	0
9	*Type 1*	None	0	0	0
	Type 2	1–20 scars	4	1	0
	Type 3	more than 20 scars	203	23	1
	Total		207	24	1

?: Unassigned.

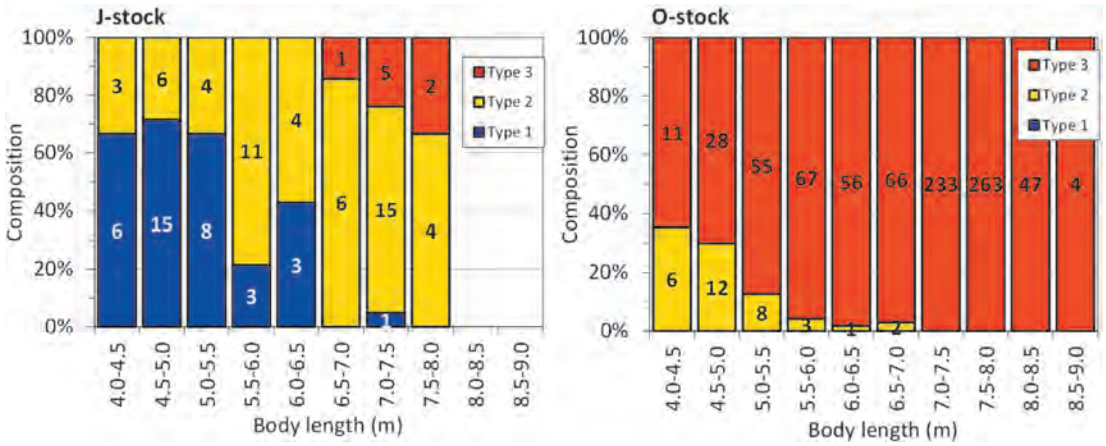

Fig. 13. Proportion of cookie cutter shark-induced scar types by body length class in J- and O-stock common minke whales. Bar numbers indicate sample size (after Bando *et al.*, 2010b).

Ecological markers

Cookie cutter shark scar

Bando *et al.* (2010b) investigated the presence of cookie cutter shark-induced scars in common minke whales identified genetically as J- and O-stock individuals. Whales examined were sampled in sub-areas 7W and 8 and 9 by JARPNII surveys during 2002–2007. Three types of common minke whales were identified from the density of scars found in the lateral side of the body: Type 1: no scars on the body, Type 2: 1–20 scars on a single side of the body, and Type 3: more than 20 scars on a single side of the body (Fig. 12). Prevalence of scars differed clearly between both stocks, and J-stock animals had fewer scars than the O-stock animals (Table 2 and Fig. 13). Although the scar prevalence increased with body length in both stocks, there are distinct differences consistent with their occurrence. J-stock whales with fewer scars were distributed in coastal areas while the O-stock whales with more scars were distributed in both coastal and offshore areas.

Conclusion

Table 3 shows a summary of the biological and ecological characteristics of genetically identified J-stock common minke whales. The individual identification from genetic marker analysis has been very useful in determining stock characterization and investigating differences in several features, such as distribution and movement, morphology and morphometry, reproduction, feeding ecology and environmental pollutants. Except for feeding ecology and environmental pollutant (total Hg) levels, these features indicate that J-stock individuals are biologically and ecologically differentiated from O-stock individuals. The existence of genetically, biologically and ecologically distinct and independent stocks mixing in a specific geographical area is unusual for baleen whales. The J-stock can be defined as a group of individuals sharing a common gene pool maintained by random mating and should therefore be managed independently. Some future works are being considered to improve the biological and ecological knowledge of the J-stock: i) investigation of the possibility whether some morphological and ecological features (e.g., white patch on the flippers and cookie cutter shark scars) can be used to identify J-stock individuals from the vessels in areas where biopsy samples for genetics cannot be collected (e.g. in the Russian territorial waters), ii) investigation of the northern limit of migration and distribution of J-stock animals by conducting sighting surveys and biopsy sampling in the relevant areas, iii) undertaking focused research to understand migratory corridors and breeding ground locations using the satellite tagging and to collect and analyze the genetic, biological and ecological information from these localities and iv) estimate other biological and ecological characteris-

Table 3. Summary of the biological and ecological features of the genetically identified individuals of J-stock common minke whales examined in this study.

Feature	Overview
Spatial distribution	Whales occupy the Sea of Japan side and the southern part of the Pacific side of Japan; they overlap geographically with O-stock in northern Hokkaido and the northern part of the Pacific side of Japan.
Temporal distribution	Whales are predominant throughout the year in the southern part of the Pacific side of Japan. Their proportion increases in autumn/winter and decreases in spring/summer in the northern part of the Pacific side of Japan.
Distance from the coastal line	Their proportion decreases from coastal towards offshore areas.
Flipper color pattern	Characterized for almost no GAL* in their flippers in comparison with the O-stock (Fig. 6).
Fluke color pattern	Characterized by a higher proportion of white color in the ventral side of flukes in comparison with the O-stock (Fig. 7).
Morphometry	Characterized by bigger heads and shorter tail bodies in comparison with the O-stock.
Conception date	Most likely extends from autumn to winter.
Feeding ecology	Feeding habits are similar to those of the O-stock.
Environmental pollutant (total Hg) levels	Levels are similar to those of the O-stock in the coastal waters of Japan. Levels suggest that the health risk is low.
Cookie cutter shark scar	Fewer scars in comparison with the O-stock (Fig. 13).

*: Grayish Accessory Layer.

tics such as abundance, growth and maturity. It is also important that efforts are made to investigate the occurrence, distribution and stock structure of common minke whales migrating around Chinese and Korean Peninsula waters, and the genetic, biological and ecological relationship with whales distributed in the sub-areas around Japan. Investigation of the stock structure in those waters is important as a number of annual bycatches have been reported from the Korean Peninsula through the collaboration with Korean scientists. All such projects would be aimed at further enhancing the assessment and the understanding and management of J-stock common minke whales.

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Others

A sperm whale school in the North Pacific.

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Historical Records

Initial Remarks

The paper below was a meeting document submitted to the International Cachalot Assessment Research Planning Workshop (CARP) sponsored by the IWC steering group, held at Woods Hole in 2005 (Smith, Reeves and Bannister, 2005)[1]*. However, unfortunately, all the documents that were submitted to the workshop were not to be objects of individual publication and thus became unavailable while they contained valuable and original information. Nevertheless, the Workshop report summarized the paper as follows:*

> *"Kato introduced CARP/LH/2, which examined the age- and body-length structure of a sperm whale school composed of 14 males that stranded on the Ohura coast, Kagoshima, Japan, on 22 January 2022. The authors succeeded in obtaining body lengths for all animals and ages for 12 of the 14. Although one exceptionally large male (15.5 m, 41 yr) was involved, the lengths (mean 12.81, range 12.1–13.7 m) and ages of the remaining animals were consistent with those for medium-sized bachelors as defined by Best (1979)*[2]*. Thus, these data were interpreted as supporting the existence and definition of a male social unit. The authors gave two alternate interpretations for the presence of the large male: either this animal was socially still immature, or large males do not always segregate permanently from other social units."*

For this opportunity, we, the Publication Committee for the Cetacean Population Studies (CPOPS), retrieve the paper as in the original form (with minor edits to improve clarity) from the point view of its biological importance for understanding the social structure of sperm whales.

[1] *Smith, T. D., Reeves, R. R. and Bannister, J. L. (eds.) 2005. Report of the International Cachalot Assessment Research Planning Workshop, Woods Hole, Massachusetts, 1–3 March 2005. US Department of Commerce, National Oceanic and Atmospheric Administration, National Marine Fisheries Service. 45 pp.*

[2] *Best, P. B. 1979. Social organization in sperm whales, Physeter macrocephalus. Pp. 227–289 in H. E. Winn and B. L. Olla (eds.). Behavior of marine mammals: current perspectives in research. Vol 3: Cetaceans. Plenum Press, New York. xix +438 pp. doi: 10.1007/978-1-4684-2985-5_7.*

CARP/LH/2 (Rev.)

AGE AND BODY LENGTH STRUCTURE OF A MALE SPERM WHALE SCHOOL STRANDED ON THE OHURA COAST, KAGOSHIMA, JAPAN IN JANUARY 2002

Hidehiro KATO[1], Toshiya KISHIRO[1], Takeharu BANDO[2], Kazuyo OHATA[3],
and Kanji TAMAI[4]

[1]National Research Institute of Far Seas Fisheries, 5–7-1 Orido, Shimizu-ku, Shizuoka 424–8633, Japan
*(contact e-mail: katohide@affrc.go.jp)**
[2]Institute of Cetacean Research, 4–5 Toyomi, Chuo-ku, Tokyo 104–0055, Japan
[3]Kasasa Ebisu Maritime Museum, 14847–1, Kataura, Kasasa-cho, Kawabe-gun, Kagoshima 897–1301, Japan;

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*Present contact: katohide@kaiyodai.ac.jp

Graduate School of Kuroshio Marine Science, Kochi University,
200 Monobe-otsu, Nankoku, Kochi 783–8502, Japan
[4]*Division of Veterinary Medicine, Faculty of Agriculture, Kagoshima University, Kagoshima 890–0065, Japan*

Abstract

A school of 14 male sperm whales, *Physeter macrocephalus*, stranded approximately at 31.22N–130.13E on Kominato-Kantaku beach, Ohura Town, Kagoshima, Japan, in the morning of 22 January 2002. The stranded school was mainly composed of typical medium-sized bachelors whose mean age was 21.36 yrs (SD: 2.993) and mean body length of 12.81 m (SD: 0.467); however, this school involved also one exceptionally larger male (41 yrs and 15.5 m). Interpretations of the presence of such a large male are made.

Key words: sperm whale, mass stranding, social units, medium and large bachelors, age and body length structure.

Introduction

On the morning of January 22, 2002, a mass stranding of sperm whales, *Physeter macrocephalus*, composed of 14 males took place on the west coast of Kagoshima Prefecture, southern Japan. The school stranded on Ohura Town's Kominato-Kantaku beach approximately at 31.22N–130.13E, Kagoshima, Japan (Fig. 1).

Through extensive efforts spent for management of the mass stranding, we were able to rescue one animal. While we further spent much effort, the other 13 animals were finally dead. Subsequently, 12 carcasses were sunk to the bottom of the sea except for one which was buried for future skeletal study and educational display. The chain of events was like an ordeal. We think this event is worth of being reported and expect it will be available somewhere.

As reported by Rice *et al.* (1986), also currently by Evans (2002) and Wright (2005), the mass stranding of sperm whales gives a rare opportunity to investigate school structure or social structure which is hard to clarify. By official request from the governor of the Kagoshima Prefecture, Kato engaged in the management process of the operation as technical and scientific advisor and had an opportunity to collect and investigate biological data from the stranded animals in cooperation with Kishiro, Bando and other volunteers from Kagoshima University. Here, we briefly report some biological aspects of the stranded sperm whale school.

Materials and Methods

Body length

Body length data used for the present study were measured in two opportunities. The primary measurement was made on the deck of the salvage boats, which had enough space to conduct body length measurements, during their operation to carry whale carcasses for sinking in the sea bottom. We measured the body length of the respective animals as being from the posterior tip of the upper jaw (head) to the notch of the tail flukes to the nearest 10 cm. With this method we finally got good body length measurements for 11 animals (OU1–OU6, OU8–OU12). Additionally, we also made body length measurements of the animals when they were moored at the pier; however, under such conditions the position of the carcasses did not necessarily provide a suitable orientation for body length measure-

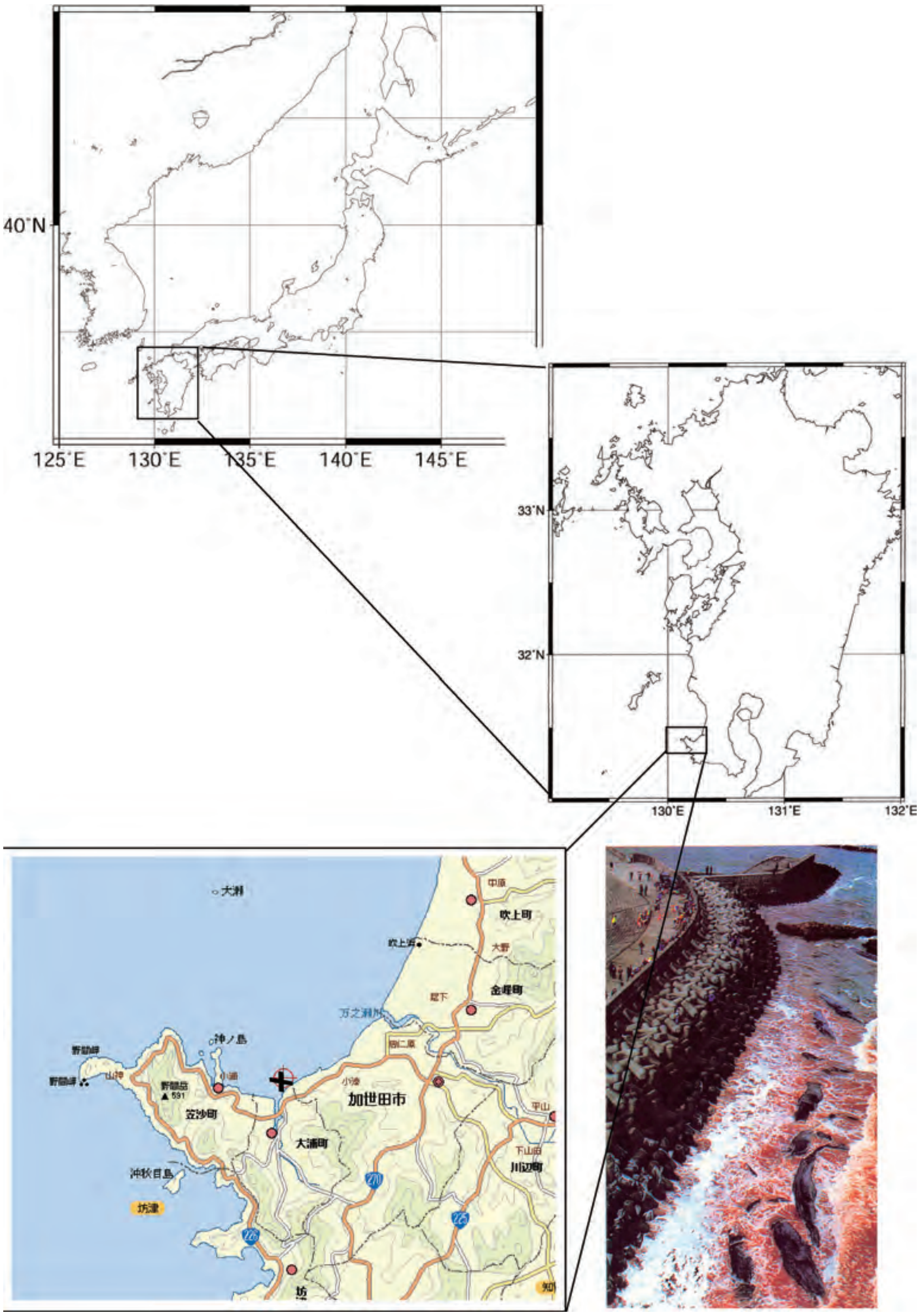

Fig. 1. Geographical location of the present sperm whale stranding that took place in January 22, 2002. A bold cross symbol in the bottom map represents the detailed location of the stranding, Kominato-Kantaku beach. Photograph by Mr. Yamano, Minami Nihon New Press.

ments. We used such measurement data for one animal (OU7) for which we had been unable to obtain an enough qualified measurement by the primary method, due to the crooked posture of its body axis.

Some other measurements for the stranded animals were also tried by other people working at the stranding location during the earlier stage of the event, although the sea and topographic conditions of the site were obviously not suitable, and the situation of the animals did not necessarily allow a suitable posture for the measurements. We have also referred to some of such measurements by Messrs. Naoto Higashi (Okinawa Churaumi Aquarium), Masayuki Nakamura (Marine World Uminonakamichi

Aquarium), Nobutaka Kubo (Iwo World Kagoshima Aquarium) and their colleagues, for the animal that was buried. Because there is a gap between their data set and our data set such that their measurements are significantly larger than our measurements for the 11 animals (overlapped discrepancy as being 2.5% or 33 cm in average), we corrected their direct measurements and used the estimated value of 13.0 m body length for the buried individual (OU13).

As to the body length of the rescued animal (OU14), no measurement had been made at the stranding site including any provisional one. However, we were able to obtain verbal evidence from the head of the workers engaging in the rescue process that the animal was rather small than the majority (Mr. C. Mori, personal communication) and also obtained both photographs and video images of this individual while stranded and swimming afterwards. Under such circumstances, we incorporate the body length estimate by one of the authors (Kato), who has extensive field experience for sperm whale sightings including works under the commercial whaling era. This estimation is 12.5 m based on photograph/video sequences and verbal evidence.

Age

At least one maxillary tooth was collected from the palate of each respective animal. After removing the adhering flesh by corrosion, the tooth was bisected longitudinally on the ISOMET saw, and one cut face was polished on a wet stone. The polished half was etched for 30 hours in a 10% formic acid solution (Clark *et al.*, 1968; Bow and Purdy, 1966). The growth layers in the dentine were counted using a stereoscopic microscope under reflecting light, and the respective age was determined by such counting growth layers in dentine under the assumption that each postnatal dentine layer represents one year. Kato and Kishiro independently aged on all the animals.

Others

We also collected morphological data, tissues for genetic analysis, and other biological samples; however, these were not used for the present study.

Results and Discussion

The sex of all of the stranded school components including one rescued individual was determined by observation of their external sexual organ. It was confirmed that all of them were males; thus, the stranded school was composed of 14 males. Although their total body size range was rather spread out between 12.1 and 15.5 m, their size range is close between each other, ranging from 12.1 m to 13.7 m, with a mean of 12.81 m (SD 0.467) if we exclude one large animal (Fig. 2). It was significantly bigger than the other animals; it had a body length that was up to 15.5 m. However, as confirmed by many people, the large individual stranded at the same time as the other animals. Thus, undoubtedly this large male was one of the components of the stranded school.

Figure 3 plots the relationship between body length and age for the 12 males for which their ages were determined and also indicates the ideal growth curve of body length and age for males assumed by Kato (1995). The plot almost agrees with the line of the ideal growth curve, and then we understand our age information is mostly acceptable. Looking at the age distribution (Fig. 4), the youngest male was 17 yrs and the oldest one 41 yrs, but again if we exclude the oldest animal of 41 yrs, the animal ages are rather close each other between 17 and 28 yrs with a mean of 21.36 yrs (SD, 2.993).

From the above, the present materials can be summarized as: the stranded male school was composed of 14 males, and the biological features of the majority (13 out of 14 individuals) shared similar characteristics in terms of animal age and body length, however, the school also involved one very larger and elder male than the others.

Several scientists pioneered investigations on the social structure of male sperm whales, such as

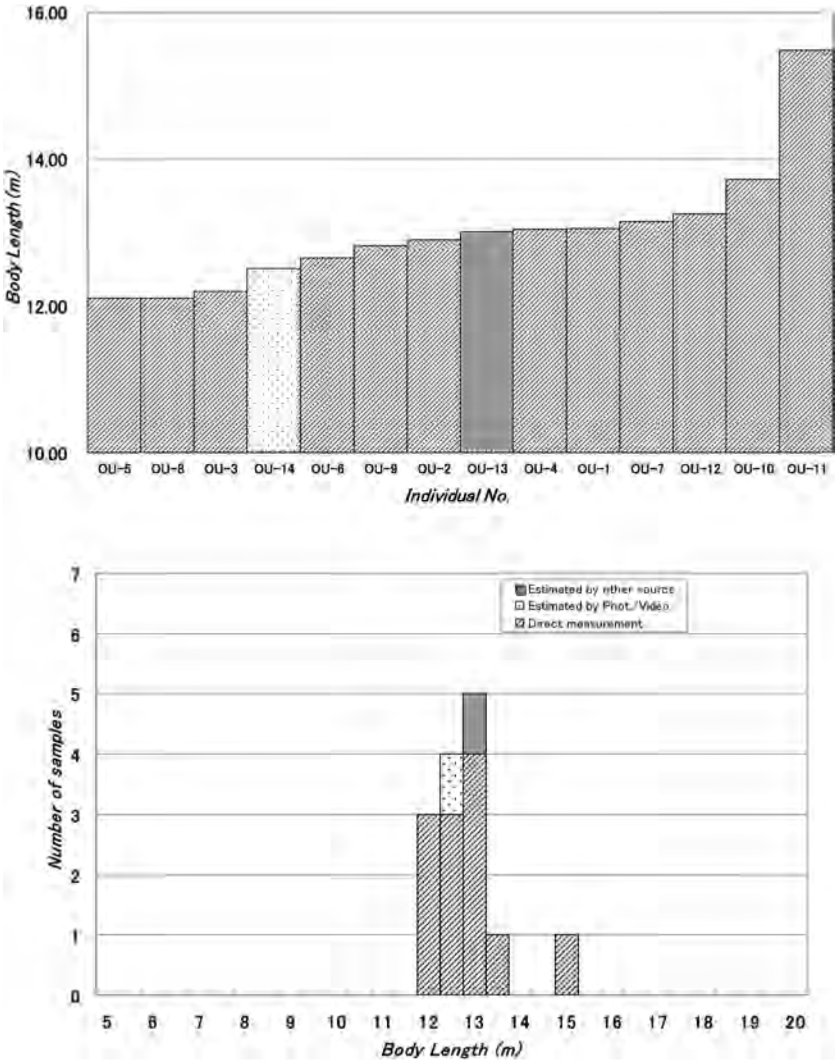

Fig. 2. Body length composition of the stranded sperm whale school by the order of their size from smaller to larger (Upper), and frequency distribution of the body length by every 50 cm (Bottom). Hutched bar represents direct measurement, dark colored and light-colored bars represent estimate by other source and photograph/video estimate (see text).

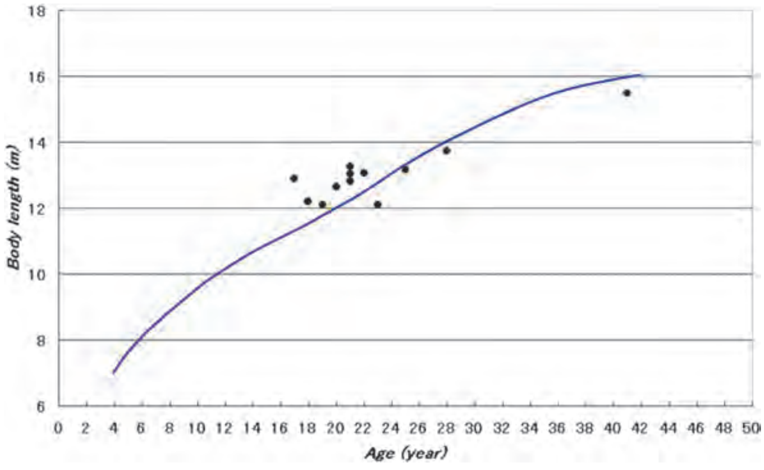

Fig. 3. Plot of the relationship between body length and age of the stranded sperm whale school, in conjunction with the ideal growth curve assumed by Kato (1995).

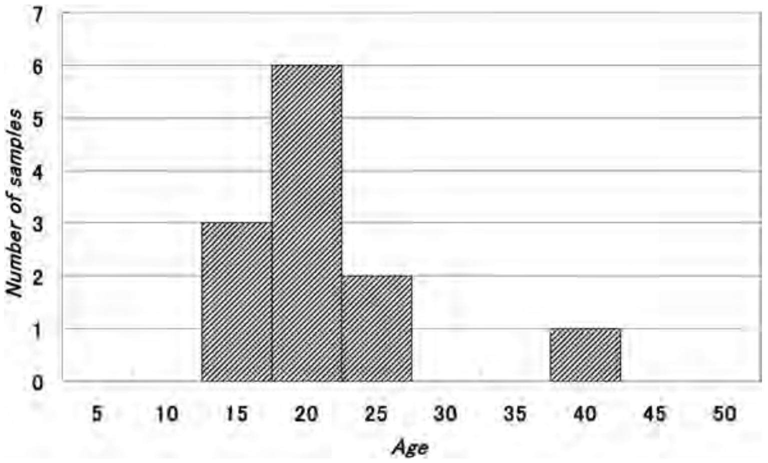

Fig. 4. Age composition of the stranded sperm whale school, based on counting growth layers in maxillary teeth.

Table 1. Comparison of age and body length of the present materials with values by social unit based on Tables II and IV in Best (1979). Body length values are converted to metric units.

	Best (1979), Tables II and IV, values converted to meters	Present study excluding an exceptional large male
Body length		
Small bachelors	10.95 m (SD, 0.415) Range: 9.4–11.9 m (31–39 ft)	12.81 m (SD. 0.467) Range: 12.1–13.7 m
Medium-sized bachelors	12.80 m (SD, 0.516) Range: 12.2–13.7 m (40–45 ft)	
Large bachelors	14.45 m (SD, 0.456) Range: 14 m–46 ft)	
Age		
Small bachelors	16.28 yrs (SD,16.248) Range: 10–25 yrs	21.36 yrs (SD, 2.993) Range: 17–28 yrs
Medium-sized bachelors	21.59 yrs (SD, 3.737) Range: 15–29 yrs	
Large bachelors	26.42 yrs (SD, 6.651) Range: 21–42 yrs	

Best (1969, 1979, 1979), Ohsumi (1966), Gaskin (1970) and others. Among them, Best (1979) clarified the nature of the social units and classified them into Small bachelors, Medium-sized bachelors and Large bachelors. In Table 1 we compared age and length of the present materials with the values given by Best (1979).

Our present samples mostly correspond to the range of the medium size bachelors. However, the reason why the exceptional large male was involved in such medium size bachelor group is still uncertain. One interpretation is that the large male concerned here had not yet been independent, still remaining in the medium bachelor school due to some biological or physiological reasons.

Unfortunately, because testicle samples were not collected due to the highly difficult situation the sexual or social status of the large male is not known. Best (1979) and Kato (1984) reported that parallel scars on the head region represent intra-sexual fighting among the large males to have mating and that the magnitude of the scaring can be used as an indication of attainment of the social maturity. Scaring on head region of the present large male was rather scarce and no parallel scar was recognized, this may indicate the present large male had fewer experiences of the intra-sexual fighting and may suggest the large male is socially immature.

An alternative interpretation is that the present large male had already attained the social maturation but opportunistically joined the medium size bachelor school due to some behavioral or social reason. Otherwise, involvement of a large male with the medium size bachelor group is not a surprising one and may happen especially in the non-feeding season at which usually the large males segregate to higher latitudes.

Acknowledgements

We are largely indebted to the many persons who engaged in extensive and hard work to manage the mass standing, especially Messrs. Teruyuki Maeno (Mayor of Ohura Town), Kazumi Maeda (Director of the Fisheries Division, Kagoshima Prefecture) and Chiaki Mori (President of Mori-gumi Co. Ltd.). Also, Mses. Yuko Nishikido, Kyoko Hamamoto and Chie Tokuzane (Division of Veterinary Medicine, Faculty of Agriculture, Kagoshima University) assisted with data and sample collection from the stranded animals. Messrs. Naoto Higashi (Okinawa Churaumi Aquarium), Masayuki Nakamura (Marine World Uminonakamichi Aquarium) and Nobutaka Kubo (Iwo-world Kagoshima Aquarium) kindly provided us with their measurements of the stranded animals, which were very useful as comparison materials. Finally, we also appreciate the encouragement by many peoples who joined the stranding site in the earlier stage, especially Drs. Tadasu Yamada (National Science Museum) and Akihiko Shinomiya (Faculty of Fisheries, Kagoshima University), and Messrs. Kotaro Ogino and Shigehisa Shima (Iwo-world Kagoshima Aquarium).

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Guide for Authors

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