# APPENDIX D

## CETACEAN MONITORING IN THE MARIANA ISLANDS RANGE COMPLEX, 2014

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**14. ABSTRACT**

The Pacific Islands Fisheries Science Center's (PIFSC) Cetacean Research Program (CRP) has been conducting visual surveys for cetaceans in the waters surrounding Guam and the Commonwealth of the Northern Mariana Islands (CNMI) and collecting long-term passive acoustic monitoring data at two sites in CNMI as part of an ongoing effort to develop a record of cetacean occurrence in the region. Visual surveys, conducted aboard small boats (7.6 – 12.2 m), have been ongoing since 2010 off the southern Mariana Islands of Guam, Rota, Saipan, Tinian, and Aguijan. These surveys include the collection of photographs for individual identification, tissue samples for genetic analysis of population structure, and the deployment of satellite tags for assessment of individual movements through the broader region. These surveys have been carried out in partnership with the Commander, U.S. Pacific Fleet Environmental Readiness Division. PIFSC has also maintained long-term acoustic monitoring sites in CNMI since 2010. The various datasets from these efforts are collectively being used to evaluate the seasonal occurrence and distribution, stock structure, and movements of cetaceans within the study area. This report includes a summary of the most recent survey (summer 2014), updates on the status of existing photo-identification catalogs and the creation of new photo-identification catalogs, and summaries of genetic analyses of bottlenose dolphin and short-finned pilot whale samples collected in the region, preliminary interpretation of satellite telemetry datasets, and the year-round occurrence of cetacean sounds recorded. The Appendices contain the more detailed reports on the mitochondrial and nuclear DNA analyses of bottlenose dolphins and short-finned pilot whales sampled in the Mariana Islands.

The PIFSC CRP conducted small boat visual surveys within the waters surrounding Guam, Saipan, Tinian, Aguijan, and Rota between 15 May and 20 June 2014 and surveyed 2,958 km of trackline. The survey team encountered 37 groups of cetaceans that were identified to species. In order of encounter frequency from highest to lowest, those species included spinner dolphin, pantropical spotted dolphin, short-finned pilot whale, bottlenose dolphin, false killer whale, Blainville's beaked whale, and Cuvier's beaked whale. Additional encounters included 2 groups of unidentified Mesoplodont whales, a group of unidentified beaked whales, and an unidentified small whale. The overall encounter rate was 1.39 encounters/100km of survey effort. Over 22,000 photos were taken during the 37 encounters and 36 biopsy samples were collected from false killer whales, pilot whales, and bottlenose dolphins. Thirty-one green sea turtles and 34 sea turtles of unknown species were observed during the surveys. A total of 13 Wildlife Computers satellite tags were deployed on 3 cetacean species (short-finned pilot whale, false killer whale, and bottlenose dolphin). To date, individual photo-identification catalogs have been created for 6 species (short-finned pilot whales, bottlenose dolphins, spinner dolphins, false killer whales, pygmy killer whales, and rough-toothed dolphins). Genetic analyses confirmed hybridization between Fraser's and bottlenose dolphins now evident in bottlenose dolphins sampled in the Marianas. The data suggest that the Fraser's dolphin ancestry in the Mariana Islands bottlenose dolphin population is the result of a single hybridization event in the past. The samples of Mariana Islands bottlenose dolphins exhibited low genetic diversity compared to other bottlenose dolphin populations, suggesting that they represent a small, genetically isolated population. Complete mitochondrial genomes from 99 short-finned pilot whales were sequenced to infer evolutionary relationships and patterns in the Pacific. Results indicate that there are three major groups in the pilot whale phylogeny, corresponding to the two known morphotypes (called Naisa and Shiho based on original descriptions in Japan), and a third, widely distributed group that spans the range of the other two groups in the Pacific. These results suggest evolutionary divergence of multiple types of pilot whales.

PIFSC maintains long-term passive acoustic datasets collected by High-frequency Acoustic Recording Packages (HARPs) at 2 sites in the Marianas; one west of Saipan since 2010 and another east of Tinian since 2011.
Analyses reported here were conducted on passive acoustic data collected from 21 July 2013 to 13 June 2014 at the Tinian site. Several odontocete species were detected within the 2013-14 Tinian HARP dataset including sperm whales, Kogia spp, Blainville's beaked whales, unidentified beaked whale classified as BWC, killer whales, short-finned pilot whales, false killer whales, and Risso's dolphins

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# Cetacean Monitoring in the Mariana Islands Range Complex, 2014

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## Mission

The Pacific Islands Fisheries Science Center's (PIFSC) Cetacean Research Program (CRP) has been conducting visual surveys for cetaceans in the waters surrounding Guam and the Commonwealth of the Northern Mariana Islands (CNMI) and collecting long-term passive acoustic monitoring data at two sites in CNMI as part of an ongoing effort to develop a record of cetacean occurrence in the region. Visual surveys, conducted aboard small boats (7.6 – 12.2 m), have been ongoing since 2010 off the southern Mariana Islands of Guam, Rota, Saipan, Tinian, and Aguijan (Figure 1). These surveys include the collection of photographs for individual identification, tissue samples for genetic analysis of population structure, and the deployment of satellite tags for assessment of individual movements through the broader region. These surveys have been carried out in partnership with the Commander, U.S. Pacific Fleet Environmental Readiness Division. PIFSC has also maintained long-term acoustic monitoring sites in CNMI since 2010. The various datasets from these efforts are collectively being used to evaluate the seasonal occurrence and distribution, stock structure, and movements of cetaceans within the study area. This report includes a summary of the most recent survey, updates on the status of existing photo-identification catalogs and the creation of new photo-identification catalogs, and summaries of genetic analyses of bottlenose dolphin (*Tursiops truncatus*) and short-finned pilot whale (*Globicephala macrorhynchus*) samples collected in the region, preliminary interpretation of satellite telemetry datasets, and the year-round occurrence of cetacean sounds recorded. The Appendices contain the more detailed reports on the mitochondrial and nuclear DNA analyses of bottlenose dolphins and short-finned pilot whales sampled in the Mariana Islands.

## Methods

### *Visual Surveys*

Visual surveys were conducted in spring and summer 2014. Summary results from the spring survey are included in Hill et al. (2014) and will not be detailed further here. Summer surveys were conducted aboard chartered vessels between 15 May and 20 June 2014 (Table 1). Off of Guam surveys were conducted aboard two different vessels, the *Lucky Strike* and *Mieko*. Surveys off of Saipan, Tinian, and Aguijan were conducted aboard two different vessels, the *Sea Hunter* and *Regulator*. Surveys were conducted off of Rota aboard a single vessel, *Asakaze*.

### *Field Methods*

Visual survey effort was designed to cover representative habitat within the study area and did not conform to systematic (e.g. line-transect) design. Vessel tracks were spread out from day to day to ensure broad survey coverage over a wide range of depths and were also dictated by weather and sea conditions. The survey vessels traveled at a speed of 15-26 km/h, depending on the size of the vessel and sea conditions. Five vessels were chartered for these surveys ranging from 5.8 to 12.2 m length*. Lucky Strike, Mieko, and Sea Hunter* had flying bridges. The vessels were operated by locally experienced captains, with knowledge of cetacean sighting locations. Captains allowed the research team to operate the vessel when approaching cetaceans for photo-identification, biopsy, and satellite tagging. Between four and six observers scanned for marine mammals with unaided eye or occasional use of 7x and 10x binoculars, collectively searching 360-degrees around the vessel.

All cetacean groups encountered were approached for species confirmation, group size estimates, and photo-identification. During encounters with certain species, biopsy sampling and satellite tagging operations were conducted. Photo-identification and biopsy protocols were identical to those described by Hill et al. 2014.

Satellite tagging was conducted using a Dan Inject air rifle and deployment arrows designed by Wildlife Computers. Two types of tags were deployed. One type was a location-only Wildlife Computers SPOT5 tag. The other tag type was the Wildlife Computers SPLASH10, which provided location as well as depth, temperature, and light level. Both tag types were deployed in the LIMPET configuration. The tags were attached to the dorsal fin with two sterilized, titanium darts with backward facing petals. Two dart lengths were used depending on the species (4.5 cm for small to medium odontocetes or 6.5 cm for large odontocetes). The programming of the tag configurations varied depending on the species and followed the specifications used by Cascadia Research Collective (CRC) based on the average number of respirations per hour, speed of surfacing, and the likelihood that a tag would remain attached for longer than a month, which were determined in previous tagging studies by CRC (Baird et al. 2013). SPLASH10 location-dive tags were programmed to collect time-series dive data every 1.25 minutes for false killer whales and 2.5 minutes for short-finned pilot whales. Dive statistics (number of dives, dive depths, and dive durations) were also collected for dives equal to 30m depth or greater and durations of 2 minutes or greater. To conserve battery life, the tag sensors were duty cycled to collect dive data for the first 2 days of deployment then alternately 3 days off and 1 day on for false killer whales, and 1 day off and 1 day on for pilot whales.

The occurrences and locations of turtles were recorded but neither photos nor biological samples were collected.

***Passive Acoustic Data Collection***

PIFSC maintains long-term passive acoustic datasets collected at 2 sites in the Marianas; 1 west of Saipan since 2010 and another east of Tinian since 2011. High-frequency Acoustic Recording Packages (HARPs; Wiggins & Hildebrand 2007) were used to record underwater sounds from 10 Hz to 100 kHz with 16-bit quantization. The HARP sensor and mooring package are described in Wiggins and Hildebrand (2007). For the Marianas deployments, the HARP was configured as a mooring, anchored on the seafloor with the hydrophone suspended 30 m above.

Analyses reported here were conducted on passive acoustic data collected from 21 July 2013 to 13 June 2014 at the Tinian site (15° 2.40’ N, 145° 45.38’ E, 695 m depth). Data were collected with a duty-cycle, such that data were collected for 5 minutes and then the recorder was off for 2 minutes. This duty-cycle was chosen to allow for year-round recording at 200 kHz sample rate, and was facilitated through use of high energy-density lithium batteries housed within two pressure cases.

***Data Processing and Analyses***

*Visual Surveys and Encounters*

The methods and bathymetry data used in the processing and analysis of the visual survey and encounter data are identical to those described in Hill et al. 2014.

*Satellite Telemetry*

The methods used to process and analyze the satellite tag location data are identical to those described in Hill et al. 2014. The SPLASH10 tag dive data were extracted as .csv files using Wildlife Computer's DAP Processor 3.0 and were analyzed for median and maximum dive depths and durations in Microsoft Excel.

*Photo-Identification*

Photo analysis was continued to add to existing individual photo-identification catalogs for short-finned pilot whales, bottlenose dolphins, and spinner dolphins (*Stenella longirostris*) (Hill et al. 2014) and to create new catalogs for false killer whales (*Pseudorca crassidens*), rough-toothed dolphins (*Steno bredanensis*), and pygmy killer whales (*Feresa attenuata*). The details of how the photos were processed and analyzed are described in detail in Hill et al. (2014). Photos used in the creation of and comparison to current catalogs include those taken of all species by PIFSC in 2010-2014, photos taken of spinner dolphins, bottlenose dolphins, and short-finned pilot whales by HDR in 2011-2012 (HDR 2011, 2012)[1], and photos taken of bottlenose dolphins, short-finned pilot whales, and false killer whales by a Navy contractor in 2007 during the MISTCS (Mariana Islands Sea Turtle and Cetacean Survey) (U.S. Navy 2007, Fulling et al. 2011)[2] .

*Tissue Sample Analysis*

Two genetics projects were conducted in 2014 on existing biopsy samples collected from Marianas animals. Previously, Martien et al. (2014) conducted mitochondrial DNA analyses and found that 5 of the 15 bottlenose dolphins sampled in the Marianas shared a haplotype with Fraser's dolphins (*Lagenodelphis hosei*) leading to the conclusion that introgressive hybridization may have occurred within this bottlenose dolphin population. Here, we further investigated the extent and origin of hybrid ancestry in Mariana Islands bottlenose dolphins by analyzing mitochondrial DNA sequence data and nuclear microsatellite genotype data. Bottlenose dolphin biopsy samples collected in the Marianas were compared to biopsy and stranding samples from Hawaiʻi and other North Pacific areas, as well as to Fraser's dolphin samples from the Philippines and elsewhere in the Pacific and Indian Oceans. Analysis methods are detailed in the report by Martien et al. (Appendix I).

Martien et al. (2014) also detailed analyses of Marianas short-finned pilot whale samples and revealed that significant differences were found in mitochondrial DNA haplotype

[1] HDR conducted small boat surveys in the waters surrounding Guam and Saipan during 17 February – 3 March, 2011 and 15-29 March, 2012. All photos were contributed by the Navy to PIFSC for photo-identification analysis.
[2] A Navy contractor conducted shipboard surveys within the CNMI EEZ during 1 January – 14 April, 2007. All photos were contributed by the Navy to PIFSC for photo-identification analysis.

frequencies between short-finned pilot whales samples near Guam and those sampled in CNMI. Here, more detailed analyses of the entire mitogenome are evaluated to determine the relationship between short-finned pilot whales in the Marianas and two sub-types identified near Japan, as well as those elsewhere in the Pacific. Short-finned pilot whale samples collected in the Marianas were reanalyzed along within samples of short-finned pilot whales from throughout the Pacific. Analysis methods are detailed in Appendix II authored by Morin et al.

*Passive Acoustics*

The 2013-2014 Tinian datasets was analyzed for hourly occurrence of all cetacean sounds. The original HARP data were decimated into 2 lower frequency datasets to allow more efficient viewing at the appropriate frequency and time resolution for a subset of sound types. A low-frequency (LF) dataset was created by decimating the HARP data to 2 kHz sample rate, and a mid-frequency (MF) dataset was created by decimating the full-bandwidth data to 10 kHz sample rate.

Either manual or automated scanning of the datasets was carried out depending on the species of interest. Table 2 lists the species, call types, and primary literature source of each of the sound types searched for as part of this analysis. Low-frequency data were manually scanned for the occurrence of blue (*Balaenoptera musculus*), fin (*B. physalus*), sei (*B. borealis*), and Bryde's (*B. edeni*) whales, as well as other low-frequency sounds likely to be produced by baleen whales, but whose source is not currently known. The MF datasets were manually scanned for minke (*B. acutorostrata*) and humpback (*Megaptera novaeangliae*) whales. All baleen whale detections were noted in hourly bins; that is, if at least one call was detected in an hour, the analyst did not search for further calls from the same species in the same hour, as encounters may consist of individual calls or long calling bouts by a single individual. Use of hourly bins reduces bias associated with oversampling an individual caller. The full-bandwidth dataset was used for detection of all odontocete species. Sperm whales (*Physeter macrocephalus*) were manually detected within the full-bandwidth data, but with the analysis viewing window extending only up to 40 kHz. Delphinid species were manually marked within the full 100 kHz viewing area and beaked whales were automatically detected and manually classified following the methods of Baumann-Pickering et al. (2013) and as described in Oleson et al. (2015). All odontocete detections were noted as the start and end of the calling bout and presented as cumulative detection time, such that it is possible that overall detection of individual species is much less than one hour.

Each data set was visually and aurally analyzed using the program Triton, a Matlab-based software package for acoustic data display and analysis (Wiggins 2003). A long-term spectral average (LTSA) was computed for each data set by averaging power spectral density (Welch 1967) in 5-s time bins and 1-Hz frequency bins for LF data, 10-Hz bins for MF data, and 100-Hz bins for full-bandwidth data. The analyst visually inspected the LTSA spectrogram display to search for potential calls of each species, and calls were verified by visual examination of spectrograms and, in some cases, audio playback. For those species marked manually, the presence of calls and other sounds was logged on a per hour basis. Calls were assigned to species based on resemblance to known calls published in the literature.

## Results

*Visual Surveys and Encounters*

The PIFSC CRP conducted small boat visual surveys within the waters surrounding Guam, Saipan, Tinian, Aguijan, and Rota between 15 May and 20 June 2014 and surveyed 2,958 km of trackline (Table 1, Figures 2-4). Less than half (43%, 1268 km) of the on-effort trackline was surveyed in Beaufort sea state conditions of 0-3, while a nearly equal amount was surveyed in Beaufort sea state conditions of 4 (42%, 1253 km)(Figure 5). Most (96%, 2839 km) of the on-effort trackline was surveyed in swell heights of 0-4 ft (Figure 6). Approximately 1/5 (21%, 40 hours) of the total time on-effort was surveyed inside of the 100 m depth contour (Figure 4). Effort was distributed fairly evenly over 101 – 1100 m depth bins and was reduced gradually over depths of 1200 – 2800 m (Figure 7).

The survey team encountered 37 groups of cetaceans that were identified to species (Tables 3-4, Figures 2-4). In order of encounter frequency from highest to lowest, those species included spinner dolphin, pantropical spotted dolphin (*Stenella attenuata*), short-finned pilot whale, bottlenose dolphin, false killer whale, Blainville's beaked whale (*Mesoplodon densirostris*), and Cuvier's beaked whale (*Ziphius cavirostris*) (Table 4). Additional encounters included 2 groups of unidentified Mesoplodont whales, a group of unidentified beaked whales, and an unidentified small whale (Tables 3-4, Figures 2-4). The overall encounter rate was 1.39 encounters/100km of survey effort (Table 4). Over 22,000 photos were taken during the 37 encounters and 36 biopsy samples were collected from false killer whales, pilot whales, and bottlenose dolphins (Table 3).

Thirty-one green sea turtles (*Chelonia mydas*) and 34 sea turtles of unknown species were observed during the surveys (Table 5, Figure 8).

*Satellite Telemetry*

A total of 13 Wildlife Computers satellite tags were deployed on 3 cetacean species (short-finned pilot whale, false killer whale, and bottlenose dolphin) (Table 6). Eight satellite tags were deployed on short-finned pilot whales during 4 encounters; 2 off Guam and 2 off Rota. Two of the individuals tagged off Guam on 25 May (tag IDs 128910 and 128914) had been previously photographed together off Guam in July 2013. The other two individuals tagged off Guam on 19 May (tag IDs 128889 and 128920) were photographed for the first time and were subsequently resighted off of Rota a month later on 17 June. On 16 June three satellite tags were deployed on short-finned pilot whales off Rota. Two of the individuals (tag IDs 128899 and 137726) were photographed for the first time and were resighted during 2 additional encounters off Rota on 17 and 18 June. The third individual tagged on 16 June (tag ID 137727) had been previously photographed off Rota in September 2011 and off Guam in June 2013. On 17 June the last satellite tag for these surveys was deployed on a short-finned pilot whale (tag ID 137728) off Rota. This individual was photographed for the first time off Guam on 19 May and was accompanied by the previously tagged individuals (tag IDs 128889 and 128920). The median distance of the Douglas Argos filtered tag locations from shore for all 8 individuals was

17.1 km and the median depth was 1188 m (Table 6, Figure 9). Tag 128889 was a SPLASH10 location-dive tag. It provided 443.9 hrs of dive and surfacing data and 1321 distinct dives with median and maximum depths of 167.5 m and 1167.5 m, and median and maximum dive durations of 9.93 min and 27.27 min (Table 7, Figure 10).

Four satellite tags were deployed on false killer whales during 2 separate encounters; the first off Guam on 21 May (tag IDs 128887 and 128902) and the other off Tinian on 12 June (tag IDs 128888 and 128901). None of the four individuals had been previously photographed. The median distance of the Douglas Argos filtered tag locations from shore for the 4 individuals was 48.0 km and the median depth was 3180 m (Table 6, Figure 11). Two of the satellite tags that were deployed on false killer whales were SPLASH10 location-dive tags (tag IDs 128887 and 128888). They provided 868.1 hrs of dive and surfacing data (658.9 hr for tag 128887 and 209.2 hrs for tag 128888) (Table 7). Tag 128887 recorded 167 dives with median and maximum dive depths of 240.5 m and 1359.5 m, and median and maximum dive durations of 5.37 min and 17.57 min (Table 7, Figure 12). Tag 128888 registered 332 dives with a median depth of 95.5 m and maximum dive depth of 847.5 m. Median and maximum dive durations were 4.20 min and 13.13 min (Table 7, Figure 13).

A single satellite tag was deployed on a bottlenose dolphin during an encounter off Saipan/Tinian on 12 June (tag ID 128912). The dorsal fin of the individual was not well marked; therefore its sighting history is unknown. The median distance of the Douglas Argos filtered tag locations from shore was 4.6 km and the median depth was 503 m (Table 6, Figure 14).

*Photo-Identification*

To date, individual photo-identification catalogs have been created for 6 species (short-finned pilot whales, bottlenose dolphins, spinner dolphins, false killer whales, pygmy killer whales, and rough-toothed dolphins). Tables 8-13 list, by species, details of the photo data from each encounter used in the analyses and creation of the individual photo-identification catalogs. Hill et al. (2014) provided a summary of the data through 2013 for short-finned pilot whales and spinner dolphins and through April 2014 for bottlenose dolphins.

During the May-June 2014 PIFSC surveys, 5 encounters with short-finned pilot whales provided resights of individuals within the catalog, as well as the addition of 32 new individuals to the catalog bringing the total to 178 individuals (Table 8). In addition, 4 short-finned pilot whale encounters during the 2007 Navy-contracted MISTCS (Mariana Islands Sea Turtle and Cetacean Survey) were analyzed. Four individuals from an encounter in March 2007 off the northeast side of Guam were matched to the existing catalog. These individuals were photographed together off the west side of Tinian in September 2011 and off the west side of Guam in March 2012. Although there were other distinctive short-finned pilot whale individuals photographed during the MISTCS encounters, no other matches or additions to the catalog were made because the photographic quality did not meet the threshold for new additions.

There were 4 bottlenose dolphin encounters during the May - June 2014 PIFSC surveys. Thirteen individuals were matched to the existing catalog and 5 individuals were added to the catalog bringing the total to 52 individuals (Table 9). Two encounters during the 2007 MISTCS surveys were analyzed; both were outside of the EEZ boundary. No matches or additions were made to the catalog from those encounters.

During the 2014 April and May-June PIFSC surveys there were 27 encounters with spinner dolphins (Table 10). The initial processing of photos and within-encounter matching has been completed for 8 encounters from the 2014 May-June surveys. Individuals noted within encounters have not yet been compared to the catalog, such that no new matches or additions to the catalog have been made. There are currently 307 individuals in the catalog. Spinner dolphins were photographed during a single sighting during the 2007 MISTCS surveys. There was 1 distinctive individual that did not match to the existing photo-identification catalog and the quality rating of the photograph did not meet the threshold for entry into the catalog.

New individual photo-identification catalogs were created for 3 species (false killer whales, pygmy killer whales, and rough-toothed dolphins). Five false killer whale encounters during the June - July 2013 and May - June 2014 PIFSC surveys, and 7 encounters during the January - April 2007 MISTCS surveys were analyzed (Table 11). The resulting catalog contains 40 individuals. Nine of those individuals were photographed twice. Two individuals were photographed off Guam on 22 June 2013 and again off Guam on 21 May 2014. Two individuals were photographed off Rota on 6 July 2013 and then off Tinian on 12 June 2014. Five individuals were photographed off Rota on 7 July 2013 and then off Guam on 21 May 2014. A single individual, photographed within the offshore waters of the southern part of the EEZ during a February 2007 MISTCS survey, was added to the catalog but was not photographed during any subsequent surveys (Table 11). There were 6 additional distinctive individuals from MISTCS encounters on 16 February and 17 March 2007, but the quality ratings of the photographs did not meet the threshold for entry into the catalog.

The individual photo-identification catalog of pygmy killer whales resulted from 2 encounters off the west side of Guam by PIFSC (Table 12). The first encounter occurred in June 2013 just north of Orote Pt. Eight individuals were present during the encounter and 6 of those individuals had sufficiently distinctive marks to be entered into the catalog. The second encounter occurred in April 2014 northwest of Cocos Island. The same 8 individuals were present, as well as a calf. One of indistinct individuals from 2013 had a changed fin that made it distinctive enough for the catalog but the quality ratings of the photographs did not meet the threshold for entry into the catalog. Pygmy killer whales were not photographed during the 2007 MISTCS surveys.

The rough-toothed dolphin photo-identification catalog includes 6 individuals that were originally photographed by PIFSC off Aguijan on 15 July 2013 (Table 13). Four of the 6 individuals were subsequently photographed off Saipan on 20 July 2013. The same 4 individuals were photographed off Aguijan on 16 April 2014. Rough-toothed dolphins were not photographed during the 2007 MISTCS surveys.

*Tissue Sample Analysis*

Appendix I describes the detailed results of genetic analyses to examine introgression of Fraser's dolphin DNA into bottlenose dolphins in the Marianas. Previous analyses (Martien et al. 2014) revealed that 5 of 15 individual bottlenose dolphins sampled from the Mariana Islands had a Fraser's dolphin haplotype. The analyses described in Appendix I are based on a dramatically expanded set of samples, including greater geographic coverage of bottlenose dolphins and the addition of Fraser's dolphin samples, and include nuclear microsatellite loci in addition to mitochondrial sequence data. Assessment of nuclear loci confirmed hybridization between Fraser's and bottlenose dolphins now evident in bottlenose dolphins sampled in the Marianas. On average, approximately 14% of the Marianas bottlenose dolphin nuclear DNA ancestry was derived from Fraser's dolphins. This was in contrast to findings that the Fraser's dolphin samples and bottlenose dolphin samples from other locations received, on average, over 99% of their nuclear DNA ancestry from Fraser's dolphins and bottlenose dolphins respectively. The data suggest that the Fraser's dolphin ancestry in the Mariana Islands bottlenose dolphin population is the result of a single hybridization event in the past, though the possibility of ongoing hybridization cannot be rejected. In addition, the bottlenose dolphin samples from the Mariana Islands exhibited low genetic diversity compared to other bottlenose dolphin populations.

Appendix II describes the detailed results of analysis of short-finned pilot whale mitogenome structure across the central and western Pacific. Previous studies have identified two genetically distinct groups of short-finned pilot whales in the Pacific, which correlate with two morphologically distinct forms identified off of Japan (Oremus et al. 2009, Van Cise et al. submitted). Van Cise et al. (submitted) have shown that the two groups have non-overlapping ranges, with the Shiho-like group restricted to northern Japan and the eastern Pacific and the more broadly distributed Naisa-like group occurring in Hawai'i, and the western and southern Pacific Ocean, and Indian and Atlantic Oceans. A hypothesized third group (hereafter 'stock 3') appears to be restricted to the western and southern Pacific Ocean. The three groups are sufficiently distinct that it has been suggested that they represent separate subspecies (Kasuya et al. 1998, Oremus et al. 2009). However, previous genetic studies have been limited to only sequence from the control region of the mitochondrial genome and have therefore lacked the necessary resolution to evaluate the taxonomic status of the groups. The study described in Appendix II used full mitochondrial genome sequences from 100 samples taken from throughout the Pacific Ocean to examine the evolutionary relationships between the Naisa, Shiho, and stock 3 groups of SFPWs. This expanded data set revealed the three groups fall into three strongly supported clades on a phylogenetic tree, which is consistent with possible subspecific status. However, additional data from the Indian and Atlantic Oceans and data from nuclear markers will be necessary to date the divergence of the clades and provide a definitive answer regarding their taxonomic status. The samples from the Mariana Islands included sequences associated with both the Naisa-like group and stock 3, indicating that it is an area of unusually high diversity and overlap between divergent types.

*Passive Acoustics*

Four species of mysticetes were recorded within the 2013-14 Tinian dataset: blue, fin, sei, and humpback whales (Figure 15). No known Bryde's whale sounds were detected, though 2 unidentified whale sounds were commonly heard, and these may have been produced by Bryde's whales based on their similarity to Bryde's whale sounds recorded in other regions. Fin whale 20 Hz downsweeps were the most commonly detected baleen whale call identified to species; heard on 20 days from January to April 2014, with a peak in occurrence in mid- to late-March. Humpback song was detected on 15 days from January to March 2014 with periods of occasional singing lasting 2-4 days, followed by several days to weeks with no humpback song detected. Central Pacific blue whale calls were detected on 4 days in May and June 2014 and downswept D calls were heard on 2 consecutive days in December 2013. Sei whale call detections were rare, heard on only 3 days over the monitoring year in February and March 2014. Minke calls were not detected within the dataset.

Two unidentified whale sounds were detected within the Tinian dataset. The more commonly detected call was a slight downsweep from an average start frequency of 42 Hz and end frequency of 32 Hz over an average duration of 2.5 s (Figure 16). These calls occurred throughout the year, but with a marked peak in detection from September through November. These calls were only sporadically detected from January through May (Figure 17). The second unidentified call type was a pulsed call that often occurred in a series of 2-3 pulses. These calls had an average start frequency of 116 Hz and end frequency of 102 Hz with 0.7 s duration. Pulsed calls were heard sporadically from the start of the deployment in July 2014 to March 2014, but with 2 periods of intense calling in November and December (Figure 17).

Several odontocete species were detected within the 2013-14 Tinian HARP dataset including sperm whales, *Kogia* spp, Blainville's beaked whales, unidentified beaked whale classified as BWC (see Baumann-Pickering et al. 2013), killer whales (*Orcinus orca*), short-finned pilot whales, false killer whales, and Risso's dolphins (*Grampus griseus*). A variety of additional delphinid sounds were detected that could not be identified to species. Sperm whales, *Kogia* spp, and both species of beaked whales were detected year-round (Figure 18) with no distinct seasonal cycle. Sperm whales were the most commonly detected within this group, with detections of Blainville's beaked whales occurring regularly, but with short overall encounter durations. Detections of BWC were relatively rare. Short-finned pilot whales and false killer whales were heard year-round, but where heard for only a few hours each week on average (Figure 19). Risso's dolphins were heard on only a few occasions, primarily in December and January, but also during January and February. Killer whales were heard on 3 days in October and November 2013 and April 2014, with very short encounter durations, suggesting they are uncommon in the region and not highly vocal when they occur. Unidentified dolphins were commonly detected year-round, with only one week during the monitoring effort with no detections (Figure 19). This group may comprise several species of small and medium odontocete, as well as undescribed whistles produced by pilot whales, false killer whales, killer whales, or Risso's dolphins that did not occur with distinctive echolocation clicks. Unidentified odontocetes are the only group that was detected with a distinct diel pattern, occurring primarily at night (Figure 20). Individual species differences among this collective group are likely, but cannot be separated until additional species-specific reference signals are available for species classification.

## Discussion

The May – June 2014 visual surveys and assessment of 2013-14 year-round passive acoustic data collected near Tinian represent a continuation of the collaborative effort between the PIFSC's CRP and the U.S. Navy towards a better understanding of the occurrence and distribution of cetaceans in waters off of Guam and the southernmost islands of CNMI (Saipan, Tinian, Aguijan, and Rota) (Hill et al. 2014, Oleson et al. 2015).

The NMFS (PIFSC) is responsible for the assessment of marine mammal stocks in the Exclusive Economic Zone (EEZ) waters of Guam and CNMI. The U.S. Navy is mandated by permits and Biological Opinions issued under the Marine Mammal Protection Act (MMPA) and the Endangered Species Act (ESA) to monitor cetacean presence within the Mariana Island Range Complex (MIRC). Although addressed in greater detail by Hill et al. (2014), additional preliminary results for questions presented within the U.S. Navy's monitoring plan are discussed below.

1. What species of beaked whales and other odontocetes occur around Guam and Saipan?

During the 2014 May-June PIFSC visual surveys 7 cetacean species were encountered in the waters surrounding Guam, Saipan, Tinian, Aguijan, and Rota. Five of these species (bottlenose dolphin, spinner dolphin, pantropical spotted dolphin, short-finned pilot whale, and false killer whale) had been encountered in previous years during other PIFSC surveys (see Hill et al. 2014). Although beaked whales had been encountered during previous PIFSC surveys, they had not been identified to species. The 2014 May-June encounters were the first confirmed sightings of Cuvier's and Blainville's beaked whales. The Cuvier's beaked whale encounter occurred 19 km off the west side of Saipan in 1700m-deep water (Table 4, Figure 3). The Blainville's beaked whale encounter occurred 11 km west-southwest of Rota in 1200m-deep water (Table 4, Figure 4).

Analysis of the passive acoustic dataset collected near Tinian in 2013-14 reveals the occurrence of 11 species, including 6 not previously seen during prior PIFSC surveys in the region. Blue, fin, humpback, and sei whales, and two types of unidentified whale calls were detected, though fin and humpback whales were the most common within this group. The unidentified whale calls were similar in structure to calls previously reported from Bryde's whales in other parts of the Pacific (Oleson et al. 2003), though there are currently no visually-verified reference signals from the Marianas or elsewhere in the western Pacific to determine species-ID of these signals. None of these species have been observed during PIFSC visual surveys, though all except sei whales were present within passive acoustic datasets collected near Tinian and Saipan from 2010 through mid-2013 (Oleson et al. 2015). Fin whales were significantly more common in the 2013-14 dataset than in previous years at either monitoring location, though detection of blue whales remained rare. Minke whales were detected in prior years at this site (Oleson et al. 2015), though were not common. Although there were several detections of minke and sei whales during the MISTCS survey (Norris et al. 2012), most of the MISTCS minke whale detections were offshore and none occurred near the Tinian HARP and the reported sei whale signals were not detected in our dataset. Sperm whales, *Kogia* spp, Blainville's beaked whales, unidentified beaked whale BWC, killer whales, false killer whales, short-finned pilot whales, and Risso's dolphins were also detected within the passive acoustic dataset. All of these species except killer whales and BWC have been seen during prior PIFSC surveys in the region. The occurrence of beaked whales has been evaluated in earlier Tinian and Saipan datasets (Oleson et al. 2015), with the only notable difference being the absence of Cuvier's beaked whale within the 2013-14 Tinian dataset.

2. Are there locations of greater relative cetacean abundance around Guam and Saipan?

Patterns of habitat use (depth and distance from shore) evident from the 2014 May-June visual surveys were similar to those described by Hill et al. 2014. Spinner dolphins remained the most frequently encountered species and were seen at Marpi Reef and at all islands except for Tinian (Figures 2-4). Most of the encounters were within 1 km of shore and in water depths less than 300 m (Tables 3-4).

Pantropical spotted dolphins remained the second most frequently encountered species (Table 4) as was reported by Hill et al. 2014. Except for a single encounter off Guam, all encounters occurred around Rota during the 2014 May-June visual surveys (Figures 2, 4). All of the encounters occurred within 8 km from shore and were in locations where the water depth was 500 – 1600 m (Table 4). Hill et al. 2014 reported a median distance from shore of 6.4 km and a median depth of 784 m.

Short-finned pilot whales were encountered off Guam and Rota during the 2014 May-June visual surveys with an encounter rate of 0.17 encounters/100 km surveyed (Table 4, Figures 2, 4). Hill et al. 2014 reported a rate of 0.09 encounters/100 km surveyed. The increase observed during the 2014 May-June visual surveys is related to the repeated encounters with the same group (or part of the same group) over a 3-day period off Rota. The encounter locations and filtered satellite tag locations demonstrate the continued use of areas close to shore by short-finned pilot whales as was reported by Hill et al. 2014 (Figures 2, 4, 6). None of the satellite-tagged short-finned pilot whales traveled long distances offshore as the individual with tag 128885 had done in 2013 (Hill et al. 2014). Median distances from shore for encounter locations and filtered satellite tag locations were 3.8 km and 17.1 km respectively (Table 4). The median depth of encounter locations was 794 m and that of satellite tag locations was 1188 m (Table 4) compared to 720 m and 1086 m reported by Hill et al. 2014. Preliminary dive data from a single SPLASH10 tag revealed that short-finned pilot whales in the Marianas will dive to a maximum depth of 1168 m and for maximum periods of 24.4 min (Table 7, Figure 10). In addition, the tag recorded deep dives (> 800 m) during the day and night. Baird et al. 2003 reported that short-finned pilot whales in Hawaiʻi dove to maximum depths of 800 m for maximum periods of 27 min during the nighttime. The photo-identification data continue to show that individual short-finned pilot whales associate with the southern islands of the Mariana Archipelago and do so over many years.

False killer whales were encountered off Guam and Tinian and continued to exhibit a broad range of habitat use based on encounter locations and filtered satellite tag locations from the 2014 May-June visual surveys (Tables 4, 6, Figures 2, 3, 7, 11). Most of the filtered satellite tag locations were to the west of the islands with some as far out as the West Mariana Ridge (Figure 11). Individuals with tag IDs 128888 and 128902 traveled up the island chain as far north as Pagan (Figure 11). Distances from shore ranged 5.9 km – 8.4 km for encounter locations and 0.3 km – 216 km for filtered satellite tag locations (Tables 4, 6). Depths of encounter locations were 673 m – 1003 m and those of filtered satellite tag locations were 52 m – 4959 m (Tables 4, 6). Preliminary dive data from 2 SPLASH10 tags revealed that false killer whales in the Marianas will dive to depths of 1360 m and for periods as long as 17.6 min (Table 7, Figures 12, 13). Baird et al. 2013 recorded a maximum dive depth of 1272 m with a 14.7 min duration for a false killer whale tagged off the island of Oʻahu in Hawaiʻi and recorded deep dives during the day and night. The photo-identification data suggest that some individuals repeatedly associate with the southernmost islands of the Marianas but that there is likely a larger population that travels throughout the EEZ waters and beyond.

Bottlenose dolphins were encountered at locations with higher median values for both distance from shore (6.0 km) and water depth (800 m) during the 2014 May-June visual surveys than previously observed (Table 4). Hill et al. 2014 reported that the median distance from shore for bottlenose dolphin locations was 0.9 km and the median water depth was 88 m. The filtered satellite tag locations from the single bottlenose dolphin tagged on 12 June 2014 reveal the individual's use of a wide range of depths (12 m – 1407 m) over the 3.7 days of the satellite tag's deployment (Table 6, Figure 14). The photo identification data demonstrate that most of the cataloged individuals move between all of the southernmost islands of the Marianas and associate with the islands over periods of years. Analyses of the mitochondrial and nuclear DNA suggest that the Mariana Islands bottlenose dolphin population is a small, genetically isolated population with a history of hybridization with Fraser's dolphins (Appendix I, Martien et al. 2014).

The Blainville's beaked whale encounter off Rota was closer to shore (10.9 km) than the two unidentified Mesoplodont whale encounters off Guam (at Tracey Seamount) and Saipan (30.6 km and 20.3 km respectively) during the 2014 May-June visual surveys (Table 4, Figures 2-4). The depth of the Blainville's beaked whale encounter location of 1200 m fell within the range of the unidentified Mesoplodont encounter location depths of 1074 m and 1614 m off Guam and Saipan respectively (Table 4).

3. What is the baseline abundance and population structure of odontocetes which may be exposed to sonar and/or explosives in the nearshore areas of Guam, Saipan, Tinian, and Rota?

As previously addressed by Hill et al. 2014, baseline abundance and population structure is not straightforward and requires further research to determine which cetaceans may be exposed to sonar and explosives.

Based on filtered satellite tag locations from pilot whales and false killer whales, as well as the observed habitat use of pilot whales, false killer whales, pantropical spotted dolphins and beaked whales during the 2014 May-June surveys it is possible that these species could be exposed to underwater detonations at the Piti Floating Mine Neutralization Area and the Agat Bay UNDET Area sites off Guam (Tables 4, 6, Figures 7, 21).

4. What is the seasonal occurrence of baleen whales around Guam, Saipan, Tinian, and Rota?

Baleen whales were not observed during May-June 2014 visual surveys, nor have they been observed on any previous PIFSC visual survey. The passive acoustic data collected in 2013-14 from near Tinian reveal that blue, fin, sei, and humpback whales were in the region during this period. In contrast to analyses of passive acoustic data collected near Saipan and Tinian from 2010 through mid-2013 (Oleson et al. 2015), fin whales were detected more frequently at Tinian in 2013-14 than in prior years. Two sounds that were likely produced by Bryde's whales, but whose species-identity cannot be confirmed at this time, occurred year-round and were more prevalent in 2013-14 than in previous years. All baleen whale calls were detected in the winter and spring, with very few acoustic detections outside of that period, with the exception of the unidentified tonal and pulsed calls.

*Ongoing and Future Work*

The analysis of photos and the creation of new photo-identification catalogs will be on-going. Work has begun on the creation of a catalog for melon-headed whales.

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## Tables

Table 1.- Summary of cetacean visual surveys in the waters surrounding Guam, Rota, Saipan, Tinian, and Aguijan (May-June 2014).

| Date (2014) | Location | Vessel | Survey Description | Time On Effort (h:mm) | On Effort Distance (km) |
|---|---|---|---|---|---|
| 15-May | Guam | *Lucky Strike* | Hagåtña north to Rota Bank | 8:47 | 121.4 |
| 16-May | Guam | *Lucky Strike* | Hagåtña west to Tracey Seamount | 6:36 | 97.8 |
| 17-May | Guam | *Mieko* | Agat north - offshore loop down to Facpi Pt. | 5:12 | 92.3 |
| 19-May | Guam | *Mieko* | Agat - SW zig zag | 6:48 | 118.1 |
| 21-May | Guam | *Mieko* | Hagåtña - northwest | 5:55 | 55.1 |
| 22-May | Guam | *Mieko* | Agat - SW loop to then north to Piti | 5:29 | 92.2 |
| 23-May | Guam | *Mieko* | Cabras - NW loop nearshore-offshore | 5:39 | 93.5 |
| 24-May | Guam | *Mieko* | Agat - SW spiral | 5:39 | 120.9 |
| 25-May | Guam | *Mieko* | Agat - Agat Bay west loop | 4:33 | 25.7 |
| 26-May | Guam | *Mieko* | Agat- SW loop | 3:53 | 72.0 |
| 27-May | Guam | *Mieko* | Hagåtña - NW zig zag | 5:58 | 117.0 |
| 30-May | CNMI-Saipan | *Sea Hunter* | Saipan - west circuit | 5:31 | 83.5 |
| 31-May | CNMI-Saipan/Tinian | *Sea Hunter* | Saipan-Tinian west loop offshore to inshore | 6:19 | 104.6 |
| 1-Jun | CNMI-Saipan | *Sea Hunter* | Saipan-NW loop | 6:57 | 98.3 |
| 2-Jun | CNMI-Saipan/Tinian | *Sea Hunter* | Tinian circumnavigation | 5:35 | 91.5 |
| 4-Jun | CNMI-Saipan | *Sea Hunter* | Saipan-NW loop | 5:52 | 75.3 |
| 5-Jun | CNMI-Saipan/Tinian | *Sea Hunter* | Saipan-Tinian west offshore loop | 6:35 | 104.3 |
| 6-Jun | CNMI-Saipan/Marpi Reef | *Regulator* | Saipan-west to Marpi Reef then Saipan-east offshore | 6:18 | 115.3 |
| 7-Jun | CNMI-Saipan/Tinian/Aguijan | *Regulator* | Tinian east to Aguijan and south to "Marie's Reef" return on west side | 7:55 | 147.2 |
| 8-Jun | CNMI-Saipan/Tinian/Esmeralda Bank | *Regulator* | Saipan-Tinian west out to Esmeralda Bank and Coke Reef | 6:33 | 133.7 |
| 10-Jun | CNMI-Saipan | *Regulator* | Saipan west offshore triangle | 5:16 | 97.4 |
| 11-Jun | CNMI-Saipan | *Regulator* | Saipan nearshore circumnavigation | 5:50 | 84.3 |
| 12-Jun | CNMI-Saipan/Tinian | *Regulator* | Saipan-Tinian west offshore | 7:35 | 99.9 |
| 13-Jun | CNMI-Saipan | *Regulator* | Saipan west spiral | 5:41 | 115.1 |

| Date (2014) | Location | Vessel | Survey Description | Time On Effort (h:mm) | On Effort Distance (km) |
|---|---|---|---|---|---|
| 14-Jun | CNMI-Saipan/Tinian/Aguijan | *Regulator* | Saipan-Tinian west and partial Aguijan circumnavigation | 6:04 | 118.1 |
| 16-Jun | CNMI-Rota | *Asakaze* | Rota NW loop offshore | 7:46 | 88.8 |
| 17-Jun | CNMI-Rota | *Asakaze* | Rota SSE loop | 6:30 | 89.7 |
| 18-Jun | CNMI-Rota | *Asakaze* | Rota circumnavigation offshore | 8:20 | 127.3 |
| 19-Jun | CNMI-Rota | *Asakaze* | Rota circumnavigation at 2-4km distance | 3:33 | 70.0 |
| 20-Jun | CNMI-Rota | *Asakaze* | Rota circumnavigation along shore then loop of north side | 7:40 | 107.5 |
| | | | **Total** | **186:35** | **2957.7** |

Table 2. Species and associated call types searched for as part of the analysis of the 2013-14 Tinian HARP dataset. Publications generally refer to the earliest description of a given call type. In most cases there are no published reference signals recorded in the Marianas Archipelago or western Pacific, so other Pacific call types are referenced.

| **Species** | **Signal type** | **Reference** |
|---|---|---|
| **Mysticetes** | | |
| Blue whale | central Pacific song | McDonald et al 2006 |
| | D call | Thompson et al 1996 |
| Fin whale | 20Hz downsweep | Thompson et al 1992 |
| | 40Hz downsweep | |
| Sei whale | Low-frequency downsweep | Rankin & Barlow 2007 |
| Bryde's whale | All Pacific types | Oleson et al 2003 |
| Humpback whale | general song structure | Payne & McVay 1971 |
| Minke whale | Boing | Rankin & Barlow 2005 |
| Unidentified whale | Call-tonal, Call-pulsed | |
| | | |
| **Odontocetes** | | |
| Sperm whales | clicks, creaks, codas, slow clicks | Madsen et al 2002, Watkins & Schevill 1977 |
| Kogia spp. | clicks | based on very high frequency (extending above 1000kHz), see Madsen et al 2005 |
| Blainville's beaked whale | clicks | Johnson et al 2006 |
| Cuvier's beaked whale | clicks | Zimmer et al 2005 |
| Unidentified beaked whale- "BWC" | clicks | Baumann-Pickering et al 2013 |
| Unidentified beaked whale- other | Upswept unclassified click types | see Baumann-Pickering et al 2013 |

| | | |
|---|---|---|
| Short-finned pilot whale | clicks, whistles | Baumann-Pickering et al *in review*, Oswald et al 2003 |
| False killer whale | clicks, whistles | Baumann-Pickering et al *in review*, Oswald et al 2003 |
| Risso's dolphin | clicks | based on similarity in structure to Soldevilla et al 2008 |
| Killer whale | clicks, pulsed calls, whistles | based on similarity to Au et al 2004, Thomsen et al 2002 |
| Unidentified dolphin | Clicks<20kHz, Clicks >20kHz, Whistles<10khz, Whistles >10khz | |

Table 3.-- Details of encounters with cetacean groups during small vessel visual surveys off Guam, Saipan, Tinian, Aguijan, and Rota (15 May - 20 June 2014) including within-day resights. The number of calves includes the best estimate of the young of the year and neonates combined.

| Date (2014) | Sight | Common Name | Time (GMT +10) | Location | Latitude | Longitude | Total Best | Calves Best | Behaviors | Bft. | Swell Height (ft) | Depth Bin (m) | Shore Distance (km) | No. Biopsy Samples | No. Tags | No. Photos |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 15-May | 1 | Spinner dolphin | 5:51 | Guam | 13.4864 | 144.7446 | 65 | 1 | slow travel, mill, boat approach, bow ride, synch dive/surface, head slap | 1 | 2 to 4 | 0-100 | 0.59 | 0 | 0 | 530 |
| 15-May | 2 | Unid. small whale | 7:38 | Guam | 13.6346 | 144.8002 | 1 | 0 | log, dive | 1 | 2 to 4 | 501-600 | 4.12 | 0 | 0 | 0 |
| 16-May | 3 | Unid. Mesoplodont | 9:01 | Guam | 13.6252 | 144.4015 | 1 | 0 | dive | 4 | 2 to 4 | 1001-1100 | 30.59 | 0 | 0 | 0 |
| 19-May | 4 | Short-finned pilot whale | 12:49 | Guam | 13.4360 | 144.6175 | 23 | 0 | slow travel, spy hop, boat approach, bow ride, tail slap | 3 | 0 to 2 | 301-400 | 0.64 | 2 | 2 | 719 |
| 21-May | 5a | False killer whale | 7:41 | Guam | 13.5533 | 144.7059 | 13 | 0 | mod travel | 4 | 2 to 4 | 1001-1100 | 8.36 | 9 | 2 | 1227 |
| 21-May | 5b | Bottlenose dolphin | 9:57 | Guam | 13.6326 | 144.7348 | 4 | 0 | boat approach, bow ride, porpoise, wave ride | 5 | 2 to 4 | 801-900 | 11.06 | 0 | 0 | 83 |
| 22-May | 6 | Spinner dolphin | 9:48 | Guam | 13.4697 | 144.6937 | 15 | 0 | mill, synch dive/surface, rest | 4 | 2 to 4 | 0-100 | 0.42 | 0 | 0 | 293 |
| 23-May | 7 | Spinner dolphin | 7:45 | Guam | 13.4862 | 144.7585 | 16 | 0 | slow travel, boat approach, bow ride, synch dive/surface | 4 | 2 to 4 | 0-100 | 0.73 | 0 | 0 | 475 |

| Date (2014) | Sight | Common Name | Time (GMT +10) | Location | Latitude | Longitude | Total Best | Calves Best | Behaviors | Bft. | Swell Height (ft) | Depth Bin (m) | Shore Distance (km) | No. Biopsy Samples | No. Tags | No. Photos |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 23-May | 8 | Spinner dolphin | 8:21 | Guam | 13.5110 | 144.7885 | 31 | 0 | slow travel, synch dive/surface, leap, boat approach, bow ride | 4 | 2 to 4 | 0-100 | 0.54 | 0 | 0 | 530 |
| 23-May | 9 | Pantropical spotted dolphin | 10:12 | Guam | 13.5842 | 144.7462 | 105 | 4 | leap, mod trav, porpoise, boat approach, bow ride, tail slap | 5 | 2 to 4 | 801-900 | 7.73 | 0 | 0 | 871 |
| 25-May | 10 | Short-finned pilot whale | 6:29 | Guam | 13.3788 | 144.6274 | 19 | 0 | slow travel, log, boat approach, spy hop, low swim | 2 | 0 to 2 | 501-600 | 2.46 | 5 | 2 | 1047 |
| 26-May | 11 | Spinner dolphin | 10:32 | Guam | 13.3665 | 144.6406 | 5 | 0 | synch dive/surface, social, boat approach, bow ride, spy hop | 4 | 2 to 4 | 101-200 | 0.92 | 0 | 0 | 122 |
| 30-May | 12 | Spinner dolphin | 6:52 | CNMI-Saipan | 15.2638 | 145.7760 | 47 | 2 | slow travel, boat approach, bow ride, spin, leap | 4 | 2 to 4 | 0-100 | 0.74 | 0 | 0 | 389 |
| 1-Jun | 13 | Unid. Mesoplodont | 8:58 | CNMI-Saipan | 15.3528 | 145.5871 | 1 | 0 | slow travel | 4 | 2 to 4 | 1601-1700 | 20.28 | 0 | 0 | 21 |
| 4-Jun | 14 | Cuvier's beaked whale | 8:45 | CNMI-Saipan | 15.3098 | 145.5683 | 4 | 0 | slow travel | 4 | 2 to 4 | 1701-1800 | 18.82 | 0 | 0 | 230 |

| Date (2014) | Sight | Common Name | Time (GMT +10) | Location | Latitude | Longitude | Total Best | Calves Best | Behaviors | Bft. | Swell Height (ft) | Depth Bin (m) | Shore Distance (km) | No. Biopsy Samples | No. Tags | No. Photos |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5-Jun | 15 | Spinner dolphin | 6:03 | CNMI-Saipan | 15.2283 | 145.6909 | 29 | 1 | slow travel, mill, synch dive/surface, boat approach, bow ride | 1 | 0 to 2 | 0-100 | 2.93 | 0 | 0 | 695 |
| 6-Jun | 16 | Spinner dolphin | 7:35 | CNMI-Marpi Reef | 15.4251 | 145.8682 | 98 | 3 | slow travel, synch dive/surface, boat approach, spin, leap, head slap, bow ride, social, porpoise | 3 | 2 to 4 | 0-100 | 16.14 | 0 | 0 | 1168 |
| 7-Jun | 17 | Spinner dolphin | 6:14 | CNMI-Saipan | 15.2307 | 145.6832 | 28 | 1 | leap, mill, boat approach, bow ride, synch dive/surface, social | 0 | 0 to 2 | 101-200 | 3.8 | 0 | 0 | 640 |
| 7-Jun | 18 | Spinner dolphin | 8:58 | CNMI-Aguijan | 14.8563 | 145.5815 | 135 | 1 | boat approach, bow ride, leap, spin, mill, synch dive/surface, social, head slap, porpoise | 2 | 2 to 4 | 201-300 | 0.37 | 0 | 0 | 935 |
| 8-Jun | 19 | Spinner dolphin | 12:06 | CNMI-Saipan | 15.2231 | 145.6990 | 21 | 1 | mill, synch dive/surface, leap, boat approach, bow ride, head slap, social | 4 | 0 to 2 | 0-100 | 1.93 | 0 | 0 | 776 |

| Date (2014) | Sight | Common Name | Time (GMT +10) | Location | Latitude | Longitude | Total Best | Calves Best | Behaviors | Bft. | Swell Height (ft) | Depth Bin (m) | Shore Distance (km) | No. Biopsy Samples | No. Tags | No. Photos |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 11-Jun | 20 | Spinner dolphin | 6:41 | CNMI-Saipan | 15.2578 | 145.7480 | 19 | 0 | slow travel, boat approach, bow ride, leap, spin, porpoise, tail slap, synch dive/surface | 2 | 0 to 2 | 0-100 | 1.77 | 0 | 0 | 778 |
| 11-Jun | 21 | Spinner dolphin | 8:06 | CNMI-Saipan | 15.2746 | 145.8312 | 50 | 0 | mill, surf waves, boat approach, bow ride, leap, porpoise | 5 | 2 to 4 | 0-100 | 0.19 | 0 | 0 | 688 |
| 11-Jun | 22 | Spinner dolphin | 9:14 | CNMI-Saipan | 15.2381 | 145.8107 | 19 | 0 | boat approach, bow ride, slow travel, synch dive/surface | 3 | 2 to 4 | 0-100 | 0.26 | 0 | 0 | 190 |
| 12-Jun | 23a | False killer whale | 8:13 | CNMI-Tinian | 14.9908 | 145.5301 | 2 | 0 | mod travel, boat approach, bow ride | 5 | 2 to 4 | 601-700 | 5.89 | 1 | 1 | 220 |
| 12-Jun | 23b | Bottlenose dolphin | 8:14 | CNMI-Tinian | 14.9908 | 145.5301 | 1 | 0 | boat approach | 5 | 2 to 4 | 601-700 | 5.89 | 0 | 0 | 0 |
| 12-Jun | 23b-resight | Bottlenose dolphin | 10:14 | CNMI-Tinian | 15.0361 | 145.5312 | 1 | 0 | boat approach, bow ride, evasive | 5 | 2 to 4 | 701-800 | 5.83 | 1 | 0 | 46 |
| 12-Jun | 23a-resight | False killer whale | 10:18 | CNMI-Tinian | 15.0344 | 145.5081 | 9 | 0 | mod travel, boat approach, bow ride | 5 | 2 to 4 | 801-900 | 8.19 | 6 | 1 | 735 |
| 12-Jun | 23c | Bottlenose dolphin | 12:28 | CNMI-Tinian | 15.1237 | 145.5593 | 16 | 0 | mod travel, boat approach, bow ride | 5 | 2 to 4 | 901-1000 | 8.2 | 0 | 1 | 524 |

| Date (2014) | Sight | Common Name | Time (GMT +10) | Location | Latitude | Longitude | Total Best | Calves Best | Behaviors | Bft. | Swell Height (ft) | Depth Bin (m) | Shore Distance (km) | No. Biopsy Samples | No. Tags | No. Photos |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 14-Jun | 24 | Spinner dolphin | 9:18 | CNMI-Aguijan | 14.8625 | 145.5797 | 67 | 0 | bow ride, mill, synch dive/surface, leap, spin | 4 | 2 to 4 | 0-100 | 0.13 | 0 | 0 | 571 |
| 16-Jun | 25 | Pantropical spotted dolphin | 8:01 | CNMI-Rota | 14.2445 | 145.2745 | 36 | 0 | boat approach, bow ride, mill | 2 | 2 to 4 | 901-1000 | 5.2 | 0 | 0 | 739 |
| 16-Jun | 26 | Short-finned pilot whale | 9:17 | CNMI-Rota | 14.2159 | 145.3139 | 48 | 1 | slow travel | 1 | 2 to 4 | 701-800 | 3.8 | 9 | 3 | 2102 |
| 16-Jun | 27 | Spinner dolphin | 14:03 | CNMI-Rota | 14.1649 | 145.1487 | 5 | 0 | slow travel | 1 | 2 to 4 | 0-100 | 0.77 | 0 | 0 | 99 |
| 17-Jun | 28 | Pantropical spotted dolphin | 6:32 | CNMI-Rota | 14.1750 | 145.0994 | 19 | 0 | mill, slow travel | 2 | 2 to 4 | 901-1000 | 5.5 | 0 | 0 | 214 |
| 17-Jun | 29 | Short-finned pilot whale | 9:00 | CNMI-Rota | 14.0544 | 145.2383 | 36 | 0 | mod travel, slow travel | 0 | 2 to 4 | 1401-1500 | 7.29 | 2 | 1 | 1558 |
| 17-Jun | 30 | Pantropical spotted dolphin | 10:20 | CNMI-Rota | 14.1018 | 145.2719 | 16 | 0 | boat approach, bow ride, porpoise | 0 | 2 to 4 | 1501-1600 | 5.48 | 0 | 0 | 100 |
| 18-Jun | 31 | Spinner dolphin | 6:19 | CNMI-Rota | 14.1391 | 145.1311 | 5 | 1 | slow travel, boat approach, bow ride, synch dive/surface | 0 | 0 to 2 | 0-100 | 0.28 | 0 | 0 | 149 |
| 18-Jun | 32 | Pantropical spotted dolphin | 7:24 | CNMI-Rota | 14.2640 | 145.2206 | 40 | 1 | mill, feed, boat approach, bow ride, leap, porpoise | 1 | 2 to 4 | 801-900 | 7.38 | 0 | 0 | 470 |
| 18-Jun | 33 | Unid. Ziphiid whale | 8:54 | CNMI-Rota | 14.2227 | 145.3457 | 2 | 0 | slow travel | 2 | 2 to 4 | 901-1000 | 7.02 | 0 | 0 | 0 |
| 18-Jun | 34 | Blainville's beaked whale | 12:25 | CNMI-Rota | 14.0692 | 145.0340 | 1 | 0 | slow roll, evasive | 3 | 2 to 4 | 1101-1200 | 10.9 | 0 | 0 | 107 |

| Date (2014) | Sight | Common Name | Time (GMT +10) | Location | Latitude | Longitude | Total Best | Calves Best | Behaviors | Bft. | Swell Height (ft) | Depth Bin (m) | Shore Distance (km) | No. Biopsy Samples | No. Tags | No. Photos |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 18-Jun | 35 | Short-finned pilot whale | 13:22 | CNMI-Rota | 14.1674 | 145.0890 | 15 | 0 | slow travel, dive | 2 | 2 to 4 | 901-1000 | 5.7 | 0 | 0 | 162 |
| 20-Jun | 36a | Bottlenose dolphin | 7:05 | CNMI-Rota | 14.1922 | 145.2926 | 2 | 0 | boat approach, bow ride, mill, leap | 1 | 2 to 4 | 201-300 | 0.37 | 1 | 0 | 77 |
| 20-Jun | 36b | Spinner dolphin | 7:08 | CNMI-Rota | 14.1905 | 145.2947 | | 0 | spin, mill, boat approach, bow ride | 1 | 2 to 4 | 101-200 | 0.49 | 0 | 0 | 0 |
| 20-Jun | 36b-resight | Spinner dolphin | 8:30 | CNMI-Rota | 14.1621 | 145.2853 | 64 | 0 | spin, mill, boat approach, bow ride, synch dive/surface, social | 1 | 2 to 4 | 101-200 | 0.16 | 0 | 0 | 721 |
| 20-Jun | 37 | Pantropical spotted dolphin | 12:41 | CNMI-Rota | 14.1937 | 145.1388 | 145 | 0 | boat approach, bow ride, leap, porpoise, social, slow travel | 1 | 2 to 4 | 501-600 | 3.62 | 0 | 0 | 1212 |
| | | | | | | | | | | | | | **Total:** | **36** | **13** | **22213** |

Table 4.—Summary of cetacean encounters during the 2014 May-June visual surveys including encounter rates, distances from shore, and water depth. The total distance surveyed was 2,958 km. The number of encounters and the encounter rate calculation excludes within-day resights. Summaries of shore distance and depth for those species denoted with * include 1 within-day resight encounter location.

| Species | No. Encounters | Encounters/ 100km effort | Shore Distance (km) - median (min-max) | Water Depth (m) - median (min-max) |
|---|---|---|---|---|
| Spinner dolphin* | 18 | 0.61 | 0.6 (0.1-16.1) | 56 (2-260) |
| Pantropical spotted dolphin | 6 | 0.20 | 5.5 (3.6-7.7) | 907 (528-1543) |
| Short-finned pilot whale | 5 | 0.17 | 3.8 (0.6-7.3) | 794 (341-1443) |
| Bottlenose dolphin* | 4 | 0.14 | 6.0 (0.4-11.1) | 800 (243-934) |
| False killer whale* | 2 | 0.07 | 8.2 (5.9-8.4) | 872 (673-1003) |
| Unid. Mesoplodont | 2 | 0.07 | 25.4 (20.3-30.6) | 1344 (1074-1614) |
| Blainville's beaked whale | 1 | 0.03 | 10.9 | 1200 |
| Cuvier's beaked whale | 1 | 0.03 | 18.8 | 1706 |
| Unid. small whale | 1 | 0.03 | 4.1 | 568 |
| Unid. Ziphiid whale | 1 | 0.03 | 7.0 | 972 |
| **Total:** | **41** | **1.39** | | |

Table 5.-- Turtle sightings during cetacean visual surveys in the waters off Guam, Saipan, Tinian, Aguijan, and Rota (May - June 2014).

| Date (2014) | Time | Island | Latitude | Longitude | Description |
|---|---|---|---|---|---|
| 15-May | 6:17 | Guam | 13.4851 | 144.7500 | Green Turtle-large (>2.5 ft) |
| 15-May | 6:20 | Guam | 13.4850 | 144.7513 | Turtle-med (1.5-2.5 ft) |
| 19-May | 7:01 | Guam | 13.3663 | 144.6464 | Turtle-small (<1.5 ft) |
| 22-May | 9:52 | Guam | 13.4724 | 144.6927 | Turtle-med (1.5-2.5 ft) |
| 22-May | 10:24 | Guam | 13.4709 | 144.6934 | Green Turtle-med (1.5-2.5 ft) |
| 22-May | 10:26 | Guam | 13.4727 | 144.6916 | Turtle-large (>2.5 ft) |
| 23-May | 6:51 | Guam | 13.4571 | 144.6573 | Green Turtle-med (1.5-2.5 ft) |
| 23-May | 7:35 | Guam | 13.4833 | 144.7309 | Turtle-med (1.5-2.5 ft) |
| 23-May | 8:50 | Guam | 13.5228 | 144.7992 | Green Turtle-large (>2.5 ft) |
| 23-May | 8:59 | Guam | 13.5430 | 144.8039 | Turtle-large (>2.5 ft) |
| 23-May | 9:01 | Guam | 13.5503 | 144.8068 | Turtle-large (>2.5 ft) |
| 23-May | 9:03 | Guam | 13.5555 | 144.8086 | Turtle-med (1.5-2.5 ft) x 2 |
| 24-May | 8:47 | Guam | 13.4069 | 144.6560 | Turtle-med (1.5-2.5 ft) |
| 24-May | 9:52 | Guam | 13.2693 | 144.6584 | Green Turtle-med (1.5-2.5 ft) |
| 26-May | 8:36 | Guam | 13.3992 | 144.6571 | Turtle-small (<1.5 ft) |
| 26-May | 8:44 | Guam | 13.4125 | 144.6458 | Green Turtle-med (1.5-2.5 ft) |
| 27-May | 11:01 | Guam | 13.5127 | 144.7918 | Turtle-med (1.5-2.5 ft) |
| 30-May | 11:44 | Saipan | 15.2274 | 145.7207 | Green Turtle-med (1.5-2.5 ft) |
| 31-May | 10:09 | Tinian | 14.9302 | 145.6282 | Green Turtle-med (1.5-2.5 ft) |
| 31-May | 11:11 | Saipan | 15.0467 | 145.5926 | Green Turtle-med (1.5-2.5 ft) x2 |
| 31-May | 12:29 | Saipan | 15.2085 | 145.6947 | Green Turtle-large (>2.5 ft) |
| 31-May | 12:31 | Saipan | 15.2128 | 145.6958 | Turtle-med (1.5-2.5 ft) |
| 31-May | 12:34 | Saipan | 15.2195 | 145.6979 | Green Turtle-med (1.5-2.5 ft) |
| 31-May | 12:43 | Saipan | 15.2278 | 145.7156 | Turtle-med (1.5-2.5 ft) |
| 1-Jun | 13:05 | Saipan | 15.2256 | 145.6906 | Turtle-med (1.5-2.5 ft) |
| 2-Jun | 6:11 | Saipan | 15.2084 | 145.6950 | Green Turtle-large (>2.5 ft) |
| 2-Jun | 11:46 | Saipan | 15.2277 | 145.7170 | Green Turtle-med (1.5-2.5 ft) |
| 4-Jun | 12:02 | Saipan | 15.2283 | 145.7100 | Green Turtle-med (1.5-2.5 ft) |
| 5-Jun | 12:35 | Saipan | 15.2272 | 145.7033 | Turtle-small (<1.5 ft) x2 |
| 5-Jun | 12:40 | Saipan | 15.2279 | 145.7157 | Turtle-small (<1.5 ft) |
| 5-Jun | 12:42 | Saipan | 15.2270 | 145.7198 | Turtle-med (1.5-2.5 ft) |
| 5-Jun | 12:43 | Saipan | 15.2259 | 145.7211 | Turtle-med (1.5-2.5 ft) |
| 6-Jun | 6:10 | Saipan | 15.2288 | 145.6952 | Green Turtle-small (<1.5 ft) x2 |
| 6-Jun | 6:10 | Saipan | 15.2288 | 145.6942 | Green Turtle-small (<1.5 ft) |
| 6-Jun | 6:11 | Saipan | 15.2287 | 145.6907 | Green Turtle-small (<1.5 ft) |
| 6-Jun | 6:12 | Saipan | 15.2292 | 145.6878 | Turtle-med (1.5-2.5 ft) |
| 6-Jun | 12:05 | Saipan | 15.1661 | 145.6800 | Green Turtle-large (>2.5 ft) |

| Date (2014) | Time | Island | Latitude | Longitude | Description |
|---|---|---|---|---|---|
| 6-Jun | 12:25 | Saipan | 15.2207 | 145.7006 | Green Turtle-large (>2.5 ft) |
| 6-Jun | 12:27 | Saipan | 15.2251 | 145.7029 | Turtle-med (1.5-2.5 ft) |
| 6-Jun | 12:32 | Saipan | 15.2256 | 145.7208 | Turtle-med (1.5-2.5 ft) |
| 7-Jun | 14:09 | Saipan | 15.2259 | 145.7200 | Turtle-med (1.5-2.5 ft) |
| 8-Jun | 6:15 | Saipan | 15.2284 | 145.6973 | Turtle-small (<1.5 ft) |
| 8-Jun | 6:16 | Saipan | 15.2286 | 145.6942 | Turtle-small (<1.5 ft) |
| 8-Jun | 6:16 | Saipan | 15.2286 | 145.6917 | Turtle-small (<1.5 ft) |
| 10-Jun | 11:41 | Saipan | 15.2267 | 145.7164 | Turtle-small (<1.5 ft) |
| 10-Jun | 11:42 | Saipan | 15.2253 | 145.7199 | Turtle-large (>2.5 ft) |
| 11-Jun | 9:07 | Saipan | 15.2531 | 145.8141 | Green Turtle-large (>2.5 ft) |
| 11-Jun | 10:24 | Saipan | 15.1585 | 145.7942 | Turtle-large (>2.5 ft) |
| 11-Jun | 10:27 | Saipan | 15.1489 | 145.7936 | Turtle-large (>2.5 ft) |
| 11-Jun | 10:46 | Saipan | 15.1377 | 145.7449 | Green Turtle-large (>2.5 ft) |
| 11-Jun | 10:53 | Saipan | 15.1224 | 145.7575 | Green Turtle-large (>2.5 ft) |
| 11-Jun | 11:54 | Saipan | 15.2008 | 145.6952 | Green Turtle-med (1.5-2.5 ft) |
| 11-Jun | 12:01 | Saipan | 15.2195 | 145.6971 | Turtle-med (1.5-2.5 ft) x2 |
| 11-Jun | 12:07 | Saipan | 15.2276 | 145.7152 | Green Turtle-small (<1.5 ft) |
| 11-Jun | 12:08 | Saipan | 15.2273 | 145.7162 | Green Turtle-small (<1.5 ft)x2 |
| 12-Jun | 13:50 | Saipan | 15.2253 | 145.7210 | Green Turtle-med (1.5-2.5 ft) |
| 12-Jun | 13:50 | Saipan | 15.2243 | 145.7220 | Green Turtle-med (1.5-2.5 ft) |
| 13-Jun | 12:02 | Saipan | 15.2256 | 145.7195 | Green Turtle-med (1.5-2.5 ft) |
| 13-Jun | 12:02 | Saipan | 15.2249 | 145.7208 | Turtle-med (1.5-2.5 ft) |
| 14-Jun | 9:54 | Aguijan | 14.8615 | 145.5852 | Green Turtle-large (>2.5 ft) |
| 14-Jun | 12:06 | Saipan | 15.2027 | 145.6916 | Turtle-large (>2.5 ft) |
| 14-Jun | 12:08 | Saipan | 15.2082 | 145.6952 | Turtle-med (1.5-2.5 ft) |
| 14-Jun | 12:18 | Saipan | 15.2270 | 145.7159 | Green Turtle-small (<1.5 ft) |
| 20-Jun | 6:32 | Rota | 14.1891 | 145.2040 | Green Turtle-med (1.5-2.5 ft) |
| 20-Jun | 8:59 | Rota | 14.1729 | 145.2868 | Turtle-med (1.5-2.5 ft) |

Table 6.-- Summary of satellite tags deployed during cetacean visual surveys in the waters off Guam, Saipan, Tinian, Aguijan, and Rota (May - June 2014) including depths and distances from shore of the Douglas Argos filtered locations.

| Species and Tag IDs | Tag Type | Deployment Location | Deployment Date-Time (GMT +10) | Duration (Days) | Shore Distance (km) - median (min-max) | Water Depth (m) - median (min-max) |
|---|---|---|---|---|---|---|
| Short-finned pilot whale | | | | | 17.1 (0.03-110.1) | 1188 (15-4615) |
| 128889 | SPLASH10 | Guam | 05/19/2014 13:26 | 34.7 | 17.3 (1.4-91) | 887 (24-4176) |
| 128920 | SPOT5 | Guam | 05/19/2014 13:54 | 39.7 | 20.7 (0.5-96.1) | 912 (26-4249) |
| 128914 | SPOT5 | Guam | 05/25/2014 8:10 | 35.3 | 11.1 (0.03-109.8) | 1085 (17-4191) |
| 128910 | SPOT5 | Guam | 05/25/2014 9:50 | 62.4 | 13.5 (0.1-110.1) | 1300 (15-4277) |
| 128899 | SPOT5 | CNMI-Rota | 06/16/2014 9:36 | 83.5 | 19.1 (1.3-88.1) | 1386 (17-4615) |
| 137726 | SPOT5 | CNMI-Rota | 06/16/2014 11:27 | 50.9 | 18.1 (0.3-88.4) | 1386 (52-4571) |
| 137727 | SPOT5 | CNMI-Rota | 06/16/2014 13:12 | 94.6 | 17.5 (0.4-85.3) | 1212 (29-4498) |
| 137728 | SPOT5 | CNMI-Rota | 06/17/2014 10:07 | 10.5 | 11.2 (0.6-39.9) | 1104 (36-2317) |
| False killer whale | | | | | 48 (0.3-216.4) | 3180 (52-4959) |
| 128887 | SPLASH10 | Guam | 05/21/2014 7:50 | 31.4 | 16.9 (0.8-154.7) | 3286 (482-4792) |
| 128902 | SPOT5 | Guam | 05/21/2014 8:44 | 39.0 | 95.7 (1.5-203.1) | 3437 (351-4416) |
| 128888 | SPLASH10 | CNMI-Tinian | 06/12/2014 8:29 | 22.3 | 35.9 (0.6-108.3) | 2756 (53-4308) |
| 128901 | SPOT5 | CNMI-Tinian | 06/12/2014 11:05 | 30.7 | 53.9 (0.3-216.4) | 3000 (52-4959) |
| Bottlenose dolphin | | | | | 4.6 (0.2-13.9) | 503 (12-1407) |
| 128912 | SPOT5 | CNMI-Saipan/ Tinian | 06/12/2014 12:44 | 3.7 | 4.6 (0.2-13.9) | 503 (12-1407) |

Table 7.-- Summary of dive data (depths and durations) from SPLASH10 satellite tags deployed on 2 false killer whales and a short-finned pilot whale during cetacean visual surveys in the waters off Guam, Saipan, Tinian, Aguijan, and Rota (May - June 2014).

| Species and Tag IDs | Total Dive/Surface Data (hrs) | No. of Dives ≥ 30m | Median Dive Depth (m) | Maximum Dive Depth (m) | Median Dive Duration (min) | Maximum Dive Duration (min) |
|---|---|---|---|---|---|---|
| Short-finned pilot whale | | | | | | |
| 128889 | 443.9 | 1321 | 167.5 | 1167.5 | 9.9 | 24.4 |
| False killer whale | 868.1 | 499 | | | | |
| 128887 | 658.9 | 167 | 240.5 | 1359.5 | 5.4 | 17.6 |
| 128888 | 209.2 | 332 | 95.5 | 847.5 | 4.2 | 13.1 |

Table 8.-- Details of short-finned pilot whale encounters analyzed for individual photo-identification including the number of cataloged individuals identified during each encounter (including new individuals) and the number of new individuals added to the catalog after each encounter. The total number of cataloged individuals identified represents all encounters with cataloged individuals including resights. The total number of new cataloged individuals represents the current catalog size.

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 2/11/2007 | 41 | MISTCS | West Mariana Ridge | 17.1000 | 142.8500 | 23 | 0 | 0 |
| 3/16/2007 | 111a | MISTCS | High Seas- south of CNMI EEZ | 10.1833 | 144.1167 | 108 | 0 | 0 |
| 3/20/2007 | 127 | MISTCS | Guam | 13.6167 | 145.0667 | 23 | 4 | 0 |
| 3/28/2007 | 133 | MISTCS | Mariana Trough-central | 17.7833 | 143.7167 | 42 | 0 | 0 |
| 2/22/2011 | 5a | HDR | Guam | 13.5785 | 144.7613 | 649 | 13 | 13 |
| 8/27/2011 | 2 | PIFSC | Guam | 13.5791 | 144.7501 | 389 | 10 | 10 |
| 9/8/2011 | 2 | PIFSC | Saipan | 15.3039 | 145.7113 | 445 | 19 | 10 |
| 9/15/2011 | 1 | PIFSC | Rota | 14.1136 | 145.1259 | 996 | 32 | 32 |
| 9/29/2011 | 3 | PIFSC | Tinian | 15.0219 | 145.5413 | 792 | 30 | 30 |

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 3/21/2012 | 6 | HDR | Guam | 13.3889 | 144.5954 | 583 | 20 | 0 |
| 5/26/2012 | 3 | PIFSC | Guam | 13.7076 | 144.8246 | 676 | 19 | 0 |
| 6/8/2012 | 14a | PIFSC | Aguijan | 14.7827 | 145.4912 | 533 | 20 | 20 |
| 6/8/2012 | 14c | PIFSC | Aguijan | 14.7960 | 145.5292 | 200 | 5 | 5 |
| 6/10/2012 | 17 | PIFSC | Esmeralda Bank | 14.9935 | 145.2356 | 373 | 9 | 9 |
| 6/30/2013 | 6b | PIFSC | Guam | 13.4847 | 144.6589 | 1004 | 20 | 2 |
| 6/30/2013 | 6c | PIFSC | Guam | 13.5526 | 144.7137 | 379 | 4 | 0 |
| 7/1/2013 | 11 | PIFSC | Guam | 13.4023 | 144.6097 | 1179 | 15 | 15 |
| 5/19/2014 | 4 | PIFSC | Guam | 13.4360 | 144.6175 | 719 | 21 | 12 |
| 5/25/2014 | 10 | PIFSC | Guam | 13.3789 | 144.6274 | 1047 | 20 | 1 |
| 6/16/2014 | 26 | PIFSC | Rota | 14.2159 | 145.3139 | 2102 | 41 | 13 |
| 6/17/2014 | 29 | PIFSC | Rota | 14.0544 | 145.2383 | 1558 | 35 | 6 |
| 6/18/2014 | 35 | PIFSC | Rota | 14.1674 | 145.0890 | 162 | 13 | 0 |
| | | | | | **Total:** | **13982** | **350** | **178** |

Table 9.-- Details of bottlenose dolphin encounters analyzed for individual photo-identification including the number of cataloged individuals identified during each encounter (including new individuals) and the number of new individuals added to the catalog after each encounter. The total number of cataloged individuals identified represents all encounters with cataloged individuals including resights. The total number of new cataloged individuals represents the current catalog size.

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 3/16/2007 | 111b | MISTCS | High Seas -south of CNMI EEZ | 10.1833 | 144.1167 | 3 | 0 | 0 |
| 3/18/2007 | 126b | MISTCS | High Seas -south of CNMI EEZ | 10.4667 | 142.0833 | 21 | 0 | 0 |
| 2/22/2011 | 5b | HDR | Guam | 13.5785 | 144.7613 | 90 | 3 | 3 |

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 8/29/2011 | 2 | PIFSC | Rota Bank | 13.7996 | 144.9539 | 158 | 9 | 9 |
| 9/9/2011 | 2 | PIFSC | Saipan | 15.1351 | 145.7456 | 307 | 8 | 5 |
| 9/10/2011 | 3 | PIFSC | Tinian | 15.0990 | 145.6365 | 222 | 7 | 0 |
| 3/24/2012 | 8 | HDR | Saipan | 15.2619 | 145.7347 | 134 | 3 | 3 |
| 5/29/2012 | 5 | PIFSC | Rota | 14.1621 | 145.1491 | 340 | 12 | 6 |
| 6/8/2012 | 14b | PIFSC | Aguijan | 14.7785 | 145.5184 | 116 | 4 | 4 |
| 6/26/2012 | 27 | PIFSC | Rota Bank | 13.7958 | 144.9563 | 141 | 5 | 1 |
| 6/29/2012 | 30 | PIFSC | Guam | 13.4410 | 144.6093 | 285 | 4 | 3 |
| 6/30/2013 | 6a | PIFSC | Guam | 13.4823 | 144.6507 | 67 | 3 | 1 |
| 7/6/2013 | 14b | PIFSC | Rota | 14.1405 | 145.1260 | 3 | 0 | 0 |
| 7/9/2013 | 19 | PIFSC | Rota | 14.1470 | 145.1375 | 805 | 12 | 2 |
| 7/10/2013 | 21 | PIFSC | Rota | 14.1976 | 145.2267 | 337 | 11 | 0 |
| 7/15/2013 | 29a | PIFSC | Aguijan | 14.8576 | 145.5831 | 123 | 5 | 2 |
| 7/17/2013 | 30 | PIFSC | Saipan | 15.2505 | 145.7060 | 132 | 3 | 1 |
| 7/17/2013 | 31 | PIFSC | Saipan | 15.2041 | 145.6968 | 447 | 6 | 5 |
| 7/23/2013 | 39 | PIFSC | Saipan | 15.2989 | 145.7068 | 200 | 5 | 0 |
| 4/16/2014 | 7a | PIFSC | Aguijan | 14.8378 | 145.5424 | 703 | 9 | 2 |
| 5/21/2014 | 5b | PIFSC | Guam | 13.63255 | 144.7348 | 83 | 2 | 2 |
| 6/12/2014 | 23b | PIFSC | Tinian | 14.99084 | 145.5301 | 46 | 1 | 1 |
| 6/12/2014 | 23c | PIFSC | Tinian | 15.12367 | 145.5593 | 524 | 13 | 2 |
| 6/20/2014 | 36a | PIFSC | Rota | 14.19217 | 145.2926 | 77 | 2 | 0 |
| | | | | | **Total:** | **5364** | **127** | **52** |

Table 10.-- Details of spinner dolphin encounters analyzed for individual photo-identification including the number of cataloged individuals identified during each encounter (including new individuals) and the number of new individuals added to the catalog

after each encounter. The total number of cataloged individuals identified represents all encounters with cataloged individuals including resights. The total number of new cataloged individuals represents the current catalog size. TBD = To Be Determined.

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 2/17/2007 | 56 | MISTCS | Saipan | 15.3167 | 145.8333 | 22 | 0 | 0 |
| 2/9/2010 | 1 | PIFSC | Guam | 13.4080 | 144.6580 | 274 | 15 | 15 |
| 2/9/2010 | 2 | PIFSC | Guam | 13.4070 | 144.6580 | 167 | 12 | 0 |
| 2/10/2010 | 1 | PIFSC | Guam | 13.3970 | 144.6580 | 250 | 8 | 1 |
| 2/10/2010 | 2 | PIFSC | Guam | 13.3350 | 144.6430 | 353 | 7 | 7 |
| 2/11/2010 | 1 | PIFSC | Guam | 13.4050 | 144.6570 | 491 | 20 | 11 |
| 2/12/2010 | 1 | PIFSC | Guam | 13.3960 | 144.6580 | 505 | 28 | 9 |
| 2/13/2010 | 1 | PIFSC | Guam | 13.4080 | 144.6560 | 240 | 19 | 0 |
| 2/14/2010 | 1 | PIFSC | Guam | 13.4070 | 144.6570 | 78 | 7 | 4 |
| 2/22/2010 | 1 | PIFSC | Saipan | 15.2487 | 145.7023 | 72 | 2 | 2 |
| 2/22/2010 | 2 | PIFSC | Marpi Reef | 15.4392 | 145.8839 | 187 | 7 | 7 |
| 2/23/2010 | 1 | PIFSC | Saipan | 15.2655 | 145.8346 | 34 | 2 | 2 |
| 2/23/2010 | 2 | PIFSC | Saipan | 15.1791 | 145.7890 | 232 | 4 | 4 |
| 2/23/2010 | 3 | PIFSC | Saipan | 15.1063 | 145.7575 | 186 | 3 | 3 |
| 2/18/2011 | 1 | HDR | Guam | 13.3898 | 144.6422 | 565 | 20 | 10 |
| 2/20/2011 | 2 | HDR | Guam | 13.4142 | 144.6449 | 102 | 3 | 3 |
| 2/21/2011 | 4 | HDR | Guam | 13.4883 | 144.7618 | 336 | 8 | 2 |
| 2/22/2011 | 6 | HDR | Guam | 13.5155 | 144.7940 | 101 | 9 | 1 |
| 3/1/2011 | 8 | HDR | Guam | 13.4032 | 144.6564 | 136 | 3 | 0 |
| 3/1/2011 | 9 | HDR | Guam | 13.3932 | 144.6521 | 252 | 6 | 1 |
| 08/28/2011 | 1 | PIFSC | Guam | 13.5159 | 144.7951 | 266 | 9 | 1 |
| 08/29/2011 | 1 | PIFSC | Rota Bank | 13.7955 | 144.9532 | 428 | 15 | 15 |
| 08/30/2011 | 1 | PIFSC | Guam | 13.2720 | 144.7571 | 320 | 11 | 8 |

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 09/01/2011 | 1 | PIFSC | Guam | 13.5630 | 144.9430 | 439 | 18 | 13 |
| 9/7/2011 | 2 | PIFSC | Aguijan | 14.8557 | 145.5823 | 615 | 22 | 19 |
| 9/8/2011 | 4 | PIFSC | Marpi Reef | 15.4110 | 145.8704 | 343 | 13 | 9 |
| 9/9/2011 | 1 | PIFSC | Saipan | 15.2680 | 145.7790 | 696 | 14 | 10 |
| 9/10/2011 | 1 | PIFSC | Tinian | 14.9790 | 145.6681 | 480 | 3 | 3 |
| 9/10/2011 | 2 | PIFSC | Tinian | 14.9202 | 145.6415 | 27 | 1 | 0 |
| 9/14/2011 | 2 | PIFSC | Rota | 14.1095 | 145.1775 | 315 | 14 | 14 |
| 9/15/2011 | 2 | PIFSC | Rota | 14.1156 | 145.1243 | 142 | 5 | 5 |
| 9/17/2011 | 2 | PIFSC | Rota | 14.1953 | 145.2935 | 462 | 9 | 1 |
| 9/18/2011 | 1 | PIFSC | Rota | 14.1839 | 145.2938 | 338 | 5 | 2 |
| 9/18/2011 | 2 | PIFSC | Rota | 14.1279 | 145.2310 | 212 | 9 | 0 |
| 9/19/2011 | 1 | PIFSC | Rota | 14.1306 | 145.1409 | 262 | 7 | 1 |
| 9/19/2011 | 2 | PIFSC | Rota | 14.1832 | 145.2947 | 205 | 7 | 0 |
| 9/24/2011 | 1 | PIFSC | Marpi Reef | 15.4328 | 145.8862 | 391 | 11 | 3 |
| 9/25/2011 | 1 | PIFSC | Saipan | 15.1926 | 145.7849 | 373 | 6 | 2 |
| 9/25/2011 | 2 | PIFSC | Saipan | 15.0922 | 145.7532 | 69 | 1 | 1 |
| 9/25/2011 | 3 | PIFSC | Saipan | 15.1200 | 145.6864 | 26 | 1 | 0 |
| 3/21/2012 | 5 | HDR | Guam | 13.4034 | 144.6572 | 319 | 7 | 0 |
| 5/25/2012 | 1 | PIFSC | Guam | 13.6085 | 144.9086 | 374 | 8 | 2 |
| 6/4/2012 | 9 | PIFSC | Rota | 14.1831 | 145.2920 | 27 | 2 | 1 |
| 6/8/2012 | 12 | PIFSC | Saipan | 15.1765 | 145.6872 | 399 | 6 | 5 |
| 6/8/2012 | 13 | PIFSC | Aguijan | 14.8525 | 145.5788 | 119 | 1 | 0 |
| 6/9/2012 | 15 | PIFSC | Marpi Reef | 15.4218 | 145.8792 | 706 | 22 | 5 |
| 6/11/2012 | 18 | PIFSC | Saipan | 15.2292 | 145.6915 | 326 | 4 | 3 |
| 6/11/2012 | 19 | PIFSC | Saipan | 15.2896 | 145.8181 | 177 | 4 | 1 |
| 6/16/2012 | 21 | PIFSC | Saipan | 15.2730 | 145.8341 | 673 | 8 | 0 |
| 6/16/2012 | 22 | PIFSC | Saipan | 15.1631 | 145.7994 | 22 | 1 | 0 |

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID’d | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 6/24/2012 | 24 | PIFSC | Marpi Reef | 15.4210 | 145.8763 | 104 | 1 | 0 |
| 6/26/2012 | 28 | PIFSC | Rota Bank | 13.7950 | 144.9584 | 189 | 12 | 3 |
| 6/29/2012 | 31 | PIFSC | Guam | 13.5140 | 144.7942 | 215 | 15 | 2 |
| 6/30/2012 | 32 | PIFSC | Guam | 13.3473 | 144.6346 | 346 | 3 | 0 |
| 7/2/2012 | 33 | PIFSC | Guam | 13.3277 | 144.6481 | 440 | 4 | 1 |
| 7/2/2012 | 34 | PIFSC | Guam | 13.2775 | 144.6607 | 987 | 29 | 14 |
| 7/2/2012 | 35 | PIFSC | Guam | 13.4779 | 144.7144 | 360 | 13 | 0 |
| 7/3/2012 | 37 | PIFSC | Guam | 13.4862 | 144.7475 | 796 | 11 | 0 |
| 06/23/2013 | 2 | PIFSC | Guam | 13.4007 | 144.6595 | 520 | 19 | 5 |
| 06/28/2013 | 5 | PIFSC | Guam | 13.4845 | 144.7543 | 381 | 12 | 0 |
| 06/30/2013 | 7 | PIFSC | Guam | 13.6514 | 144.8784 | 95 | 1 | 0 |
| 06/30/2013 | 8 | PIFSC | Guam | 13.6140 | 144.9079 | 421 | 12 | 3 |
| 06/30/2013 | 9 | PIFSC | Guam | 13.5673 | 144.9506 | 432 | 14 | 10 |
| 07/07/2013 | 16 | PIFSC | Rota | 14.1673 | 145.2878 | 392 | 10 | 6 |
| 07/09/2013 | 18 | PIFSC | Rota | 14.1389 | 145.1287 | 34 | 1 | 0 |
| 07/12/2013 | 22 | PIFSC | Saipan | 15.2661 | 145.7792 | 538 | 10 | 5 |
| 07/12/2013 | 23 | PIFSC | Saipan | 15.2725 | 145.8340 | 406 | 14 | 12 |
| 07/12/2013 | 24 | PIFSC | Saipan | 15.1164 | 145.7585 | 313 | 8 | 6 |
| 07/13/2013 | 26 | PIFSC | Saipan | 15.2283 | 145.7057 | 565 | 13 | 3 |
| 07/14/2013 | 27 | PIFSC | Saipan | 15.2054 | 145.6808 | 45 | 2 | 0 |
| 07/15/2013 | 28 | PIFSC | Aguijan | 14.8625 | 145.5803 | 463 | 11 | 7 |
| 07/18/2013 | 33 | PIFSC | Marpi Reef | 15.4135 | 145.8752 | 616 | 18 | 6 |
| 07/19/2013 | 34 | PIFSC | Saipan | 15.2179 | 145.6702 | 239 | 2 | 1 |
| 07/21/2013 | 36 | PIFSC | Saipan | 15.2104 | 145.6957 | 511 | 7 | 2 |
| 07/21/2013 | 37 | PIFSC | Saipan | 15.1734 | 145.6914 | 44 | 2 | 0 |
| 07/24/2013 | 40 | PIFSC | Saipan | 15.1923 | 145.6830 | 404 | 10 | 0 |
| 07/24/2013 | 41 | PIFSC | Tinian | 14.9912 | 145.6727 | 664 | 18 | 10 |

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 07/27/2013 | 42 | PIFSC | Aguijan | 14.8593 | 145.5817 | 449 | 13 | 5 |
| 04/11/2014 | 1 | PIFSC | Saipan | 15.2347 | 145.6905 | 118 | TBD | TBD |
| 04/12/2014 | 2 | PIFSC | Tinian | 14.9912 | 145.6733 | 357 | TBD | TBD |
| 04/14/2014 | 3 | PIFSC | Saipan | 15.2279 | 145.6929 | 303 | TBD | TBD |
| 04/14/2014 | 4 | PIFSC | Saipan | 15.2282 | 145.7126 | 388 | TBD | TBD |
| 04/15/2014 | 5 | PIFSC | Marpi Reef | 15.4321 | 145.8854 | 746 | TBD | TBD |
| 04/16/2014 | 6 | PIFSC | Aguijan | 14.8640 | 145.5801 | 405 | TBD | TBD |
| 04/25/2014 | 11 | PIFSC | Guam | 13.4851 | 144.7331 | 188 | TBD | TBD |
| 04/26/2014 | 13 | PIFSC | Guam | 13.4082 | 144.6571 | 318 | TBD | TBD |
| 04/27/2014 | 14 | PIFSC | Guam | 13.4859 | 144.7595 | 188 | TBD | TBD |
| 5/15/2014 | 1 | PIFSC | Guam | 13.4864 | 144.7446 | 530 | Initial sorting completed | TBD |
| 5/22/2014 | 6 | PIFSC | Guam | 13.4697 | 144.6937 | 293 | Initial sorting completed | TBD |
| 5/23/2014 | 7 | PIFSC | Guam | 13.4862 | 144.7585 | 475 | Initial sorting completed | TBD |
| 5/23/2014 | 8 | PIFSC | Guam | 13.5110 | 144.7885 | 530 | Initial sorting completed | TBD |
| 5/26/2014 | 11 | PIFSC | Guam | 13.3665 | 144.6406 | 122 | TBD | TBD |
| 5/30/2014 | 12 | PIFSC | Saipan | 15.2638 | 145.7760 | 389 | Initial sorting completed | TBD |
| 6/5/2014 | 15 | PIFSC | Saipan | 15.2283 | 145.6909 | 695 | Initial sorting in completed | TBD |

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 6/6/2014 | 16 | PIFSC | Marpi Reef | 15.4251 | 145.8682 | 1168 | Initial sorting in completed | TBD |
| 6/7/2014 | 17 | PIFSC | Saipan | 15.2307 | 145.6832 | 640 | TBD | TBD |
| 6/7/2014 | 18 | PIFSC | Aguijan | 14.8563 | 145.5815 | 935 | TBD | TBD |
| 6/8/2014 | 19 | PIFSC | Saipan | 15.2231 | 145.6990 | 776 | TBD | TBD |
| 6/11/2014 | 20 | PIFSC | Saipan | 15.2578 | 145.7480 | 778 | TBD | TBD |
| 6/11/2014 | 21 | PIFSC | Saipan | 15.2746 | 145.8312 | 688 | TBD | TBD |
| 6/11/2014 | 22 | PIFSC | Saipan | 15.2381 | 145.8107 | 190 | TBD | TBD |
| 6/14/2014 | 24 | PIFSC | Aguijan | 14.8625 | 145.5797 | 571 | TBD | TBD |
| 6/16/2014 | 27 | PIFSC | Rota | 14.1649 | 145.1487 | 99 | TBD | TBD |
| 6/18/2014 | 31 | PIFSC | Rota | 14.1391 | 145.1311 | 149 | TBD | TBD |
| 6/20/2014 | 36b | PIFSC | Rota | 14.1905 | 145.2947 | 721 | Initial sorting completed | TBD |
| | | | | | **Total:** | **37841** | **712** | **307** |

Table 11.-- Details of false killer whale encounters analyzed for individual photo-identification including the number of cataloged individuals identified during each encounter (including new individuals) and the number of new individuals added to the catalog after each encounter. The total number of cataloged individuals identified represents all encounters with cataloged individuals including resights. The total number of new cataloged individuals represents the current catalog size.

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 2/16/2007 | 52 | MISTCS | West Mariana Ridge | 16.1167 | 142.3833 | 56 | 0 | 0 |
| 2/19/2007 | 66 | MISTCS | CNMI EEZ - southeast | 14.5500 | 147.4667 | 3 | 0 | 0 |
| 2/20/2007 | 68b | MISTCS | CNMI EEZ - southeast | 13.7500 | 146.2833 | 12 | 0 | 0 |
| 2/25/2007 | 90 | MISTCS | CNMI EEZ - south central | 13.4833 | 144.4333 | 6 | 1 | 1 |
| 3/13/2007 | 99 | MISTCS | High Seas- south of CNMI EEZ | 11.5500 | 147.5333 | 3 | 0 | 0 |
| 3/13/2007 | 101 | MISTCS | High Seas- south of CNMI EEZ | 11.2833 | 147.3000 | 24 | 0 | 0 |
| 3/17/2007 | 112 | MISTCS | CNMI EEZ - south | 11.7667 | 143.7500 | 2 | 0 | 0 |
| 6/22/2013 | 1 | PIFSC | Guam | 13.5310 | 144.6114 | 28 | 2 | 2 |
| 7/6/2013 | 14a | PIFSC | Rota | 14.1405 | 145.1260 | 2161 | 13 | 13 |
| 7/7/2013 | 17 | PIFSC | Rota | 14.1143 | 145.0680 | 1162 | 14 | 14 |
| 5/21/2014 | 5a | PIFSC | Guam | 13.5533 | 144.7059 | 1227 | 10 | 3 |
| 6/12/2014 | 23a | PIFSC | Tinian | 14.9908 | 145.5301 | 955 | 9 | 7 |
| | | | | | **Total:** | **5639** | **49** | **40** |

Table 12.-- Details of pygmy killer whale encounters analyzed for individual photo-identification including the number of cataloged individuals identified during each encounter (including new individuals) and the number of new individuals added to the catalog after each encounter. The total number of cataloged individuals identified represents all encounters with cataloged individuals including resights. The total number of new cataloged individuals represents the current catalog size.

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 6/25/2013 | 4 | PIFSC | Guam | 13.4744 | 144.6402 | 578 | 6 | 6 |
| 4/26/2014 | 12 | PIFSC | Guam | 13.2370 | 144.6299 | 212 | 6 | 0 |
| | | | | | **Total:** | **790** | **12** | **6** |

Table 13.-- Details of rough-toothed dolphin encounters analyzed for individual photo-identification including the number of cataloged individuals identified during each encounter (including new individuals) and the number of new individuals added to the catalog after each encounter. The total number of cataloged individuals identified represents all encounters with cataloged individuals including resights. The total number of new cataloged individuals represents the current catalog size.

| Date | Sighting | Research Group | Location | Latitude | Longitude | No. Photos | No. Cataloged Individuals ID'd | No. New Cataloged Individuals |
|---|---|---|---|---|---|---|---|---|
| 7/15/2013 | 29b | PIFSC | Aguijan | 14.8567 | 145.5820 | 297 | 6 | 6 |
| 7/20/2013 | 35 | PIFSC | Saipan | 15.2340 | 145.6200 | 299 | 4 | 0 |
| 4/16/2014 | 7b | PIFSC | Aguijan | 14.8359 | 145.5420 | 703 | 4 | 0 |
| | | | | | **Total:** | **1299** | **14** | **6** |

## Figures

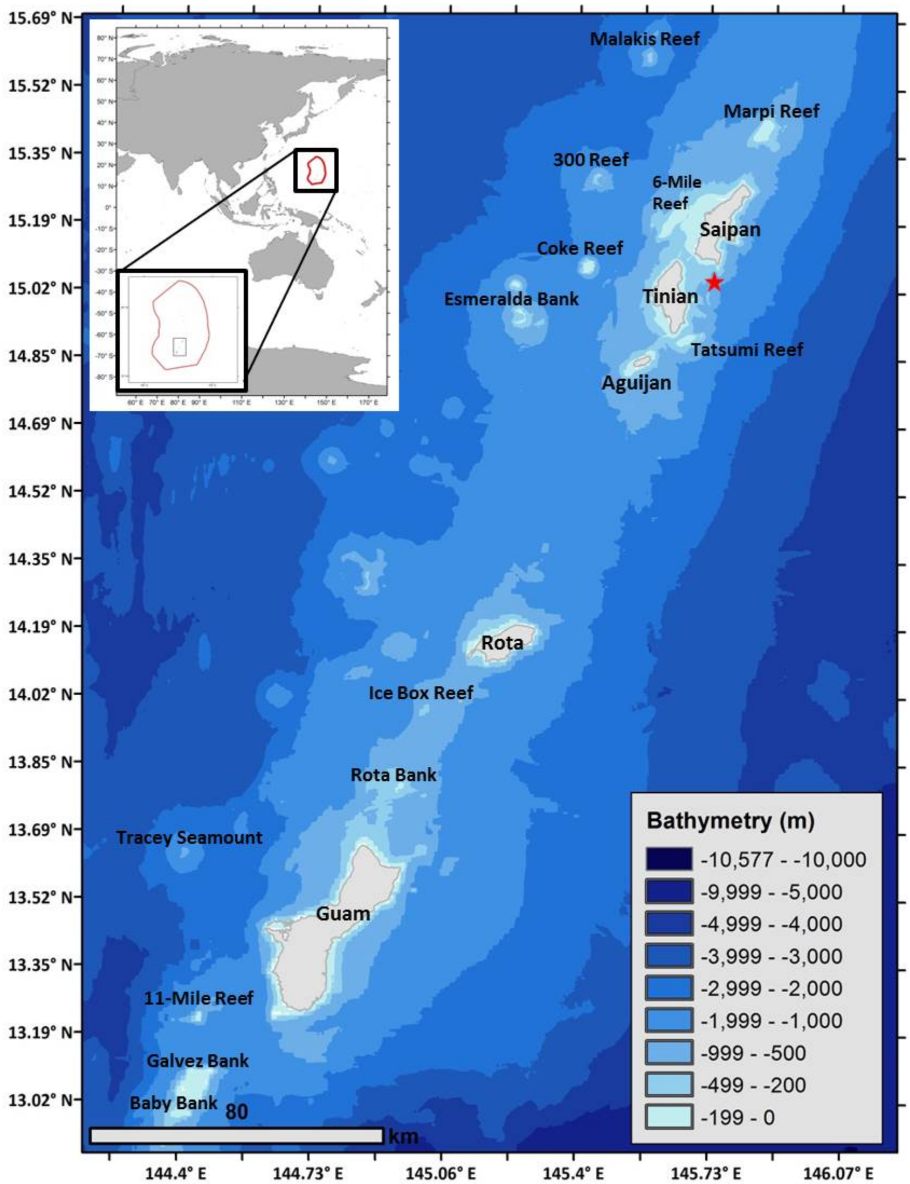


Figure 1.-- Survey area within the southern portion of the Mariana Archipelago. The red star indicates the location of the 2013-14 Tinian HARP.

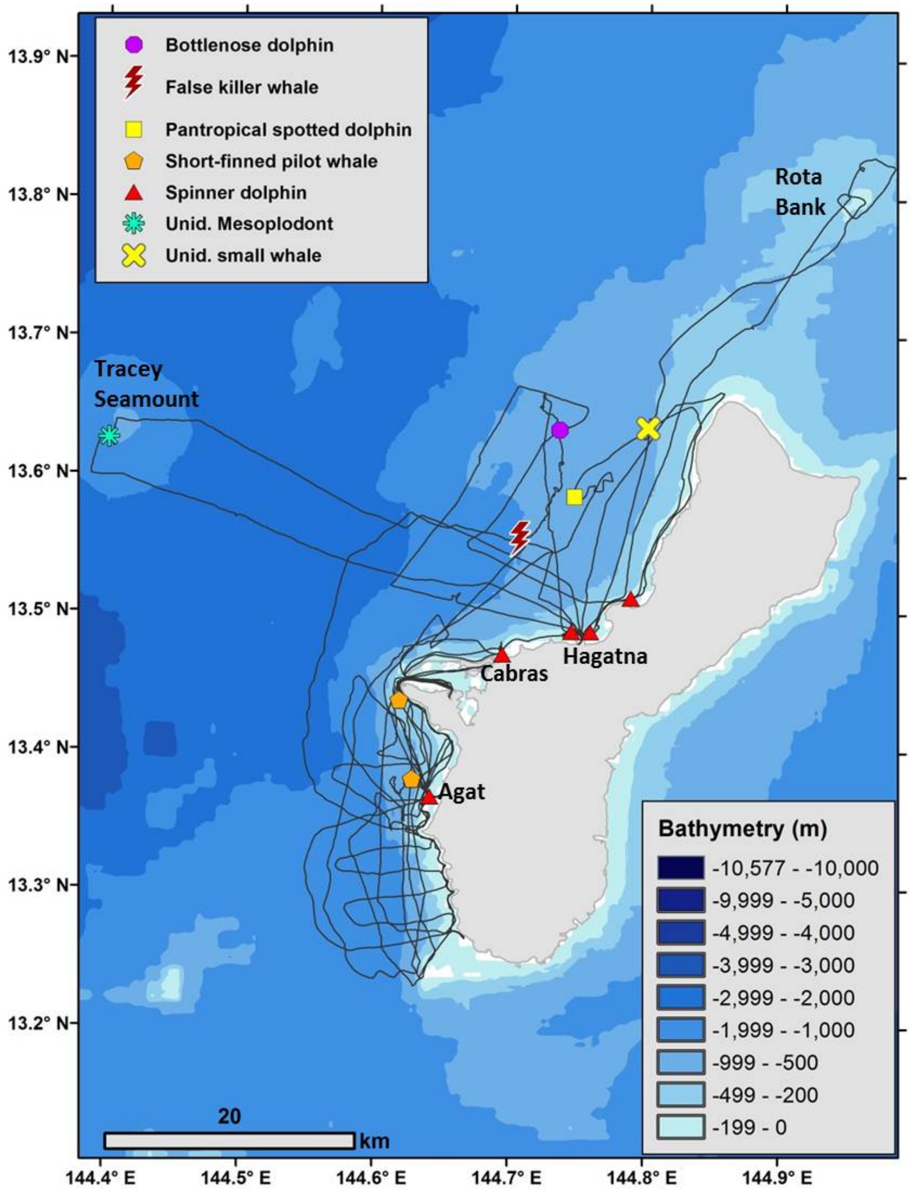


Figure 2.-- Visual survey tracklines and cetacean encounters off Guam (15-27 May 2014).

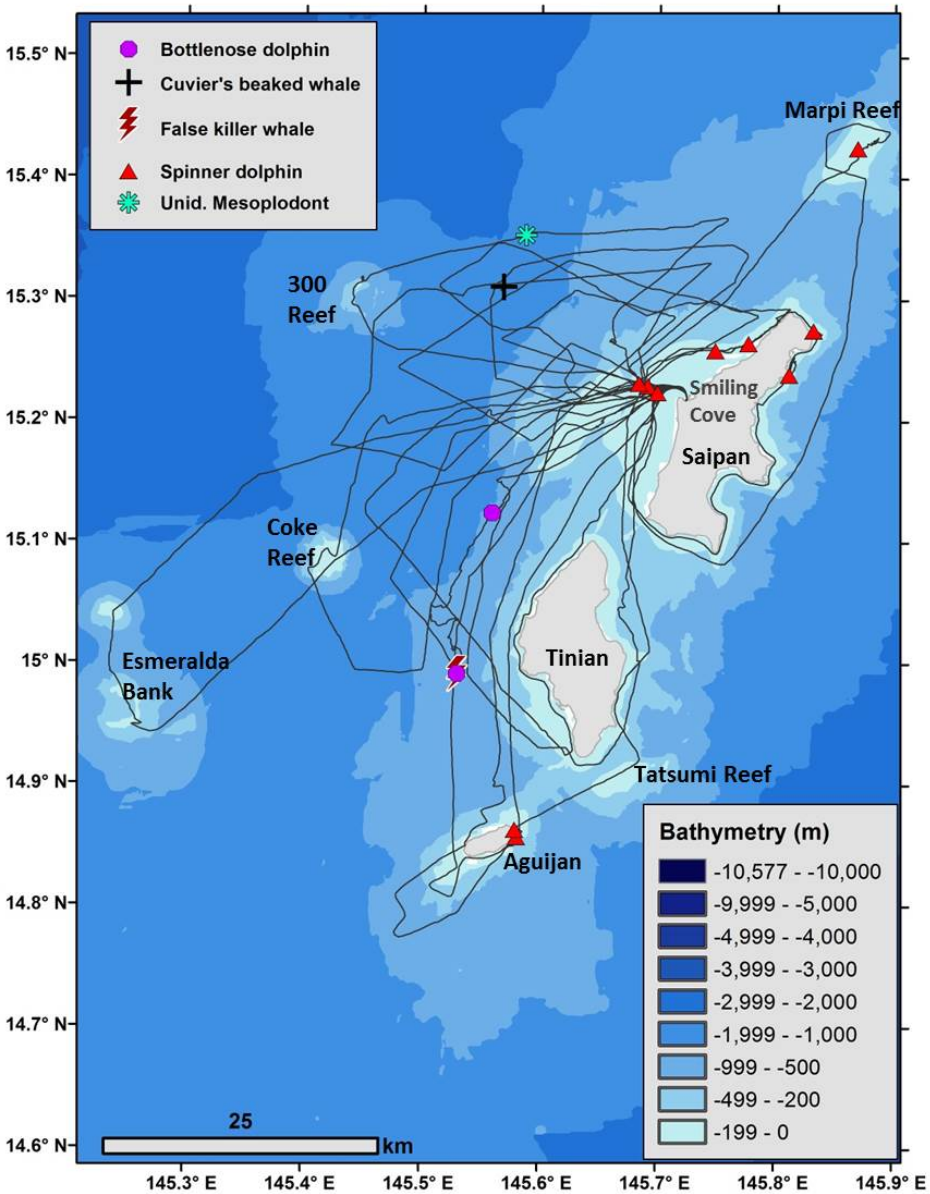


Figure 3.-- Visual survey tracklines and cetacean encounters off Saipan, Tinian, and Aguijan (30 May - 14 June 2014).

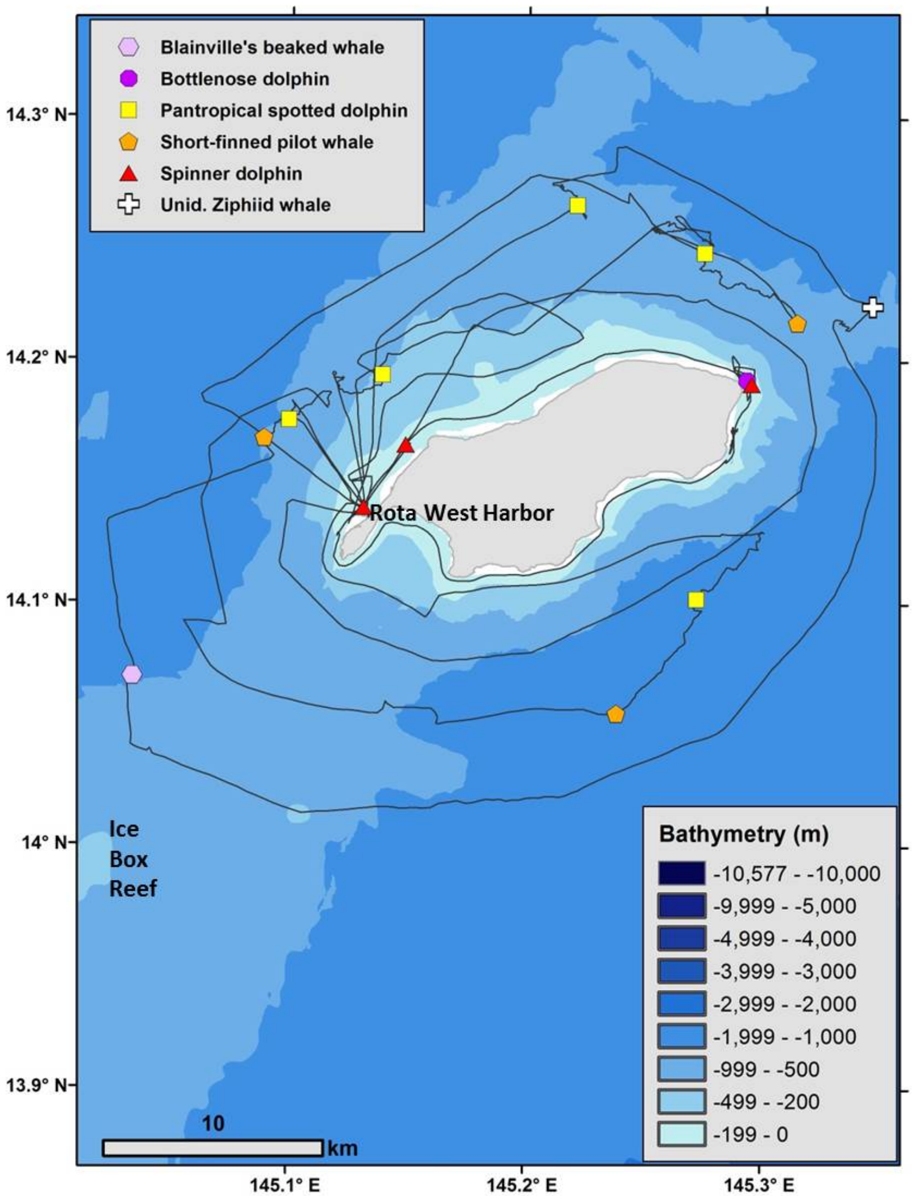


Figure 4.-- Visual survey tracklines and cetacean encounters off Rota (16 - 20 June 2014).

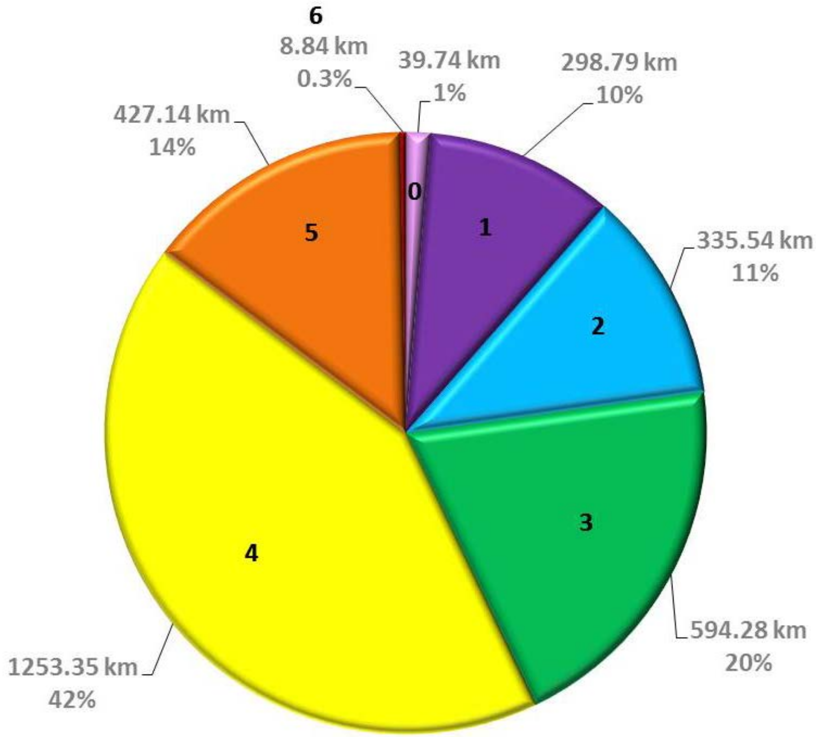


Figure 5.-- Survey effort by Beaufort Sea State for May-June 2014 visual survey.

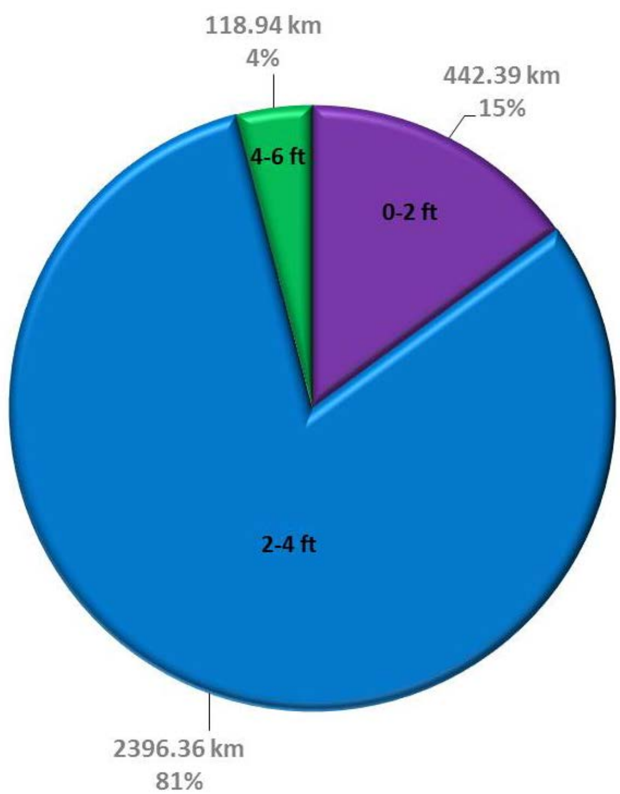


Figure 6.-- Survey effort by swell height (ft) for May-June 2014 visual survey.

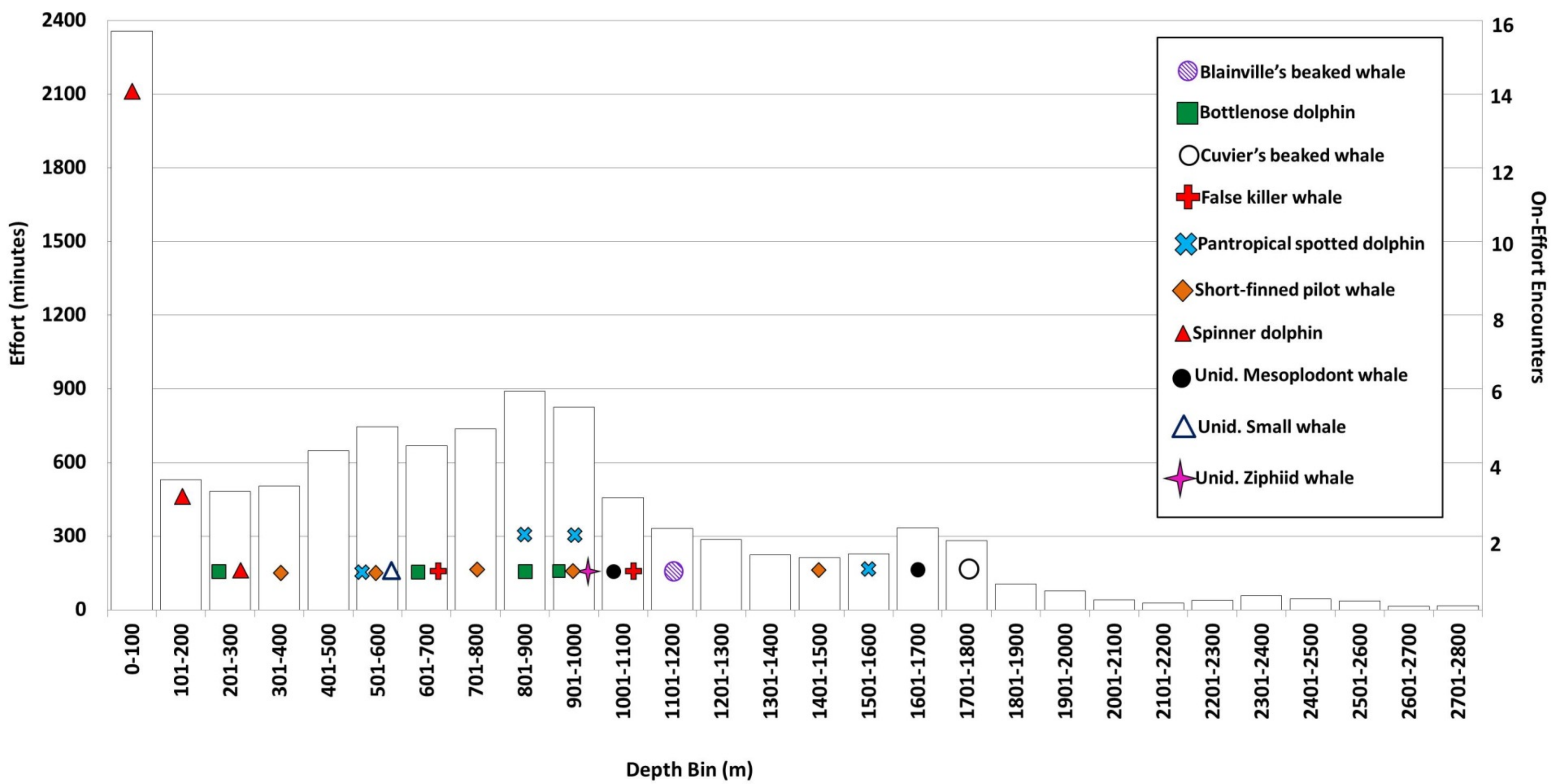


Figure 7.-- Survey effort and cetacean encounters by depth during the May-June 2014 visual survey. Total on-effort survey time was 186.6 hours (11,196 minutes).

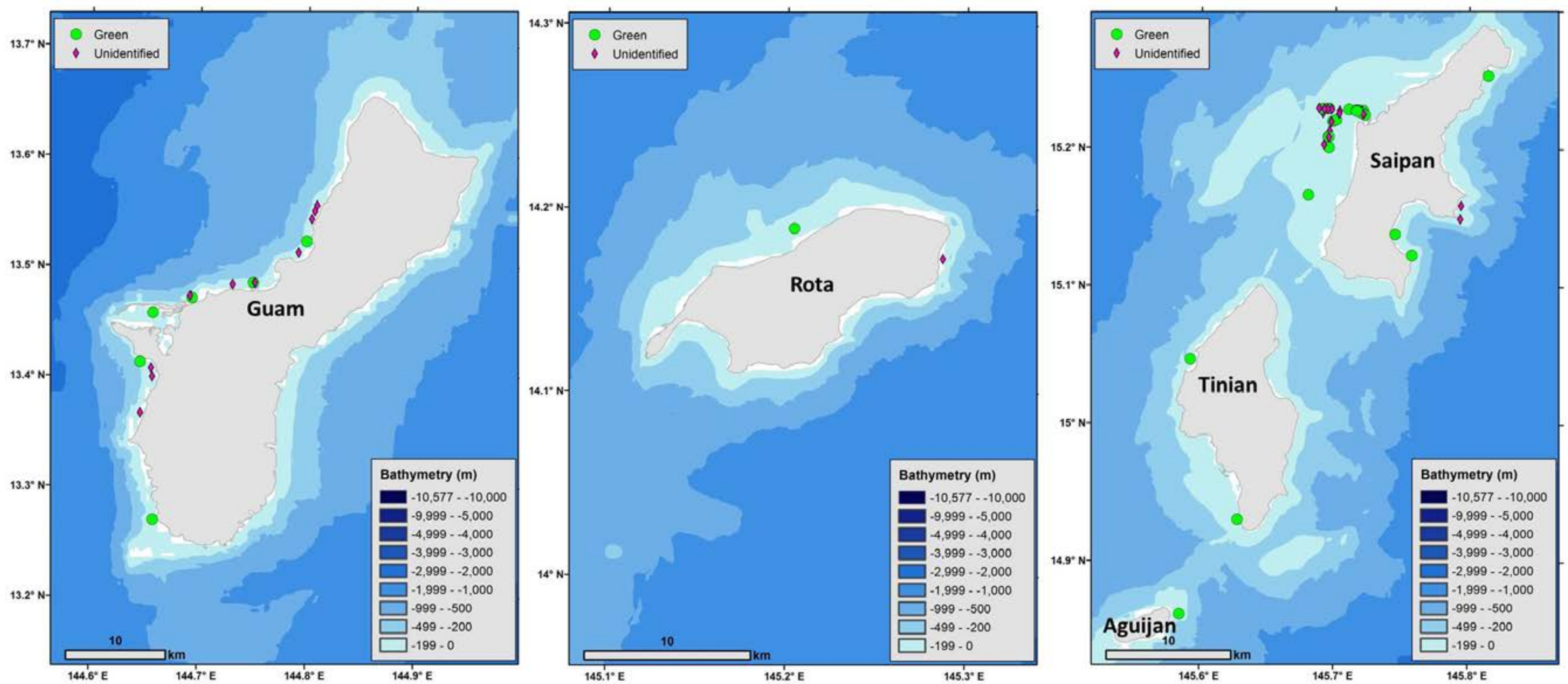


Figure 8.-- Sea turtles observed during the cetacean visual surveys off the islands within the southern Mariana Archipelago (15 May - 20 June 2014).

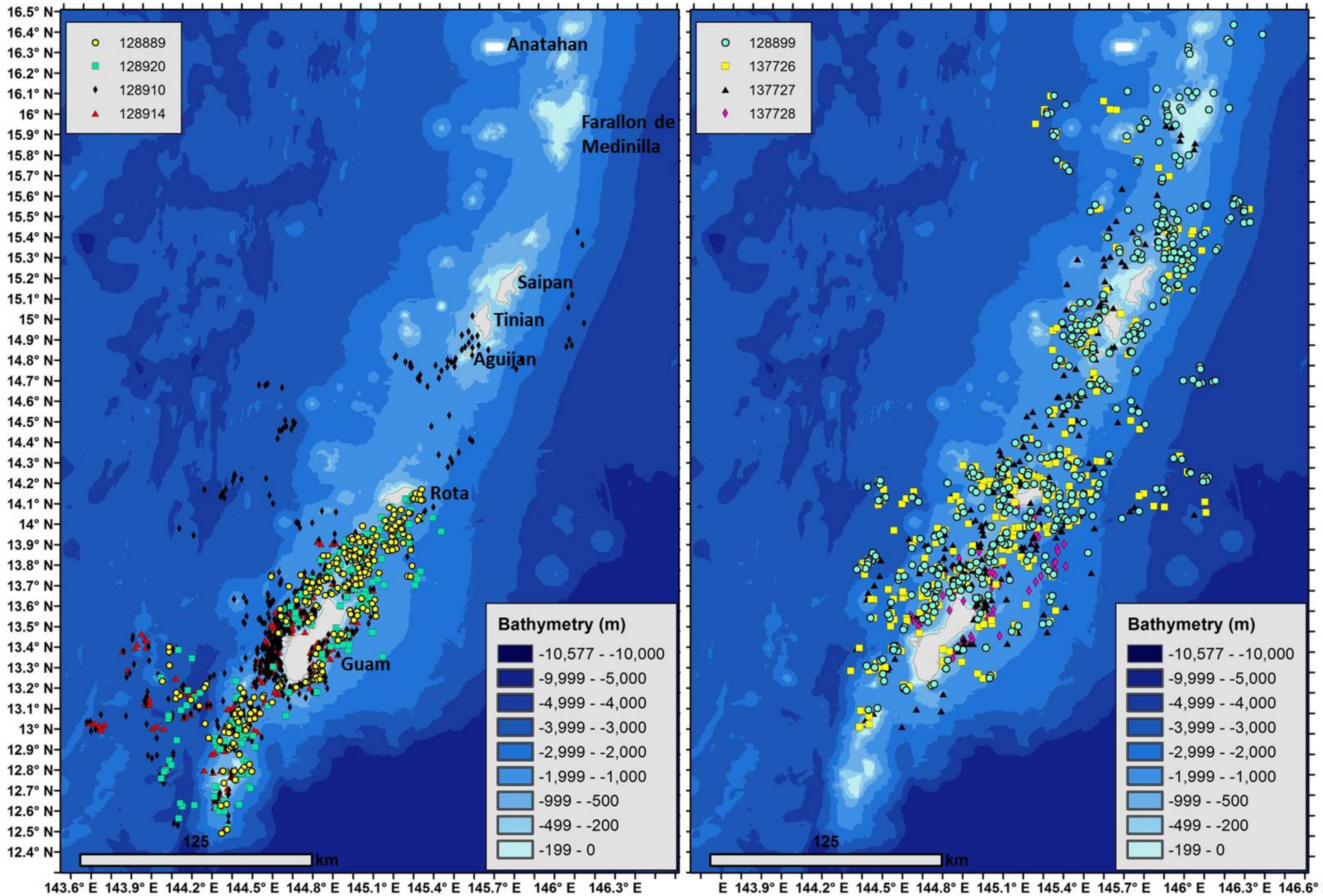


Figure 9.-- Douglas Argos filtered satellite locations for tags deployed on short-finned pilot whales. Left panel: tags 128889, 128920, 128910, 128914 deployed on individuals encountered off Guam (19 and 25 May 2014) with island locations labeled. Deployment durations were 34.7 d, 39.7 d, 35.3 d, 62.4 d respectively. Right panel: tags 128899, 137726, 137727, 137728 deployed on individuals encountered off Rota (16 and 17 June 2014). Deployment durations were 83.5 d, 50.9 d, 94.6 d, 10.5 d respectively.

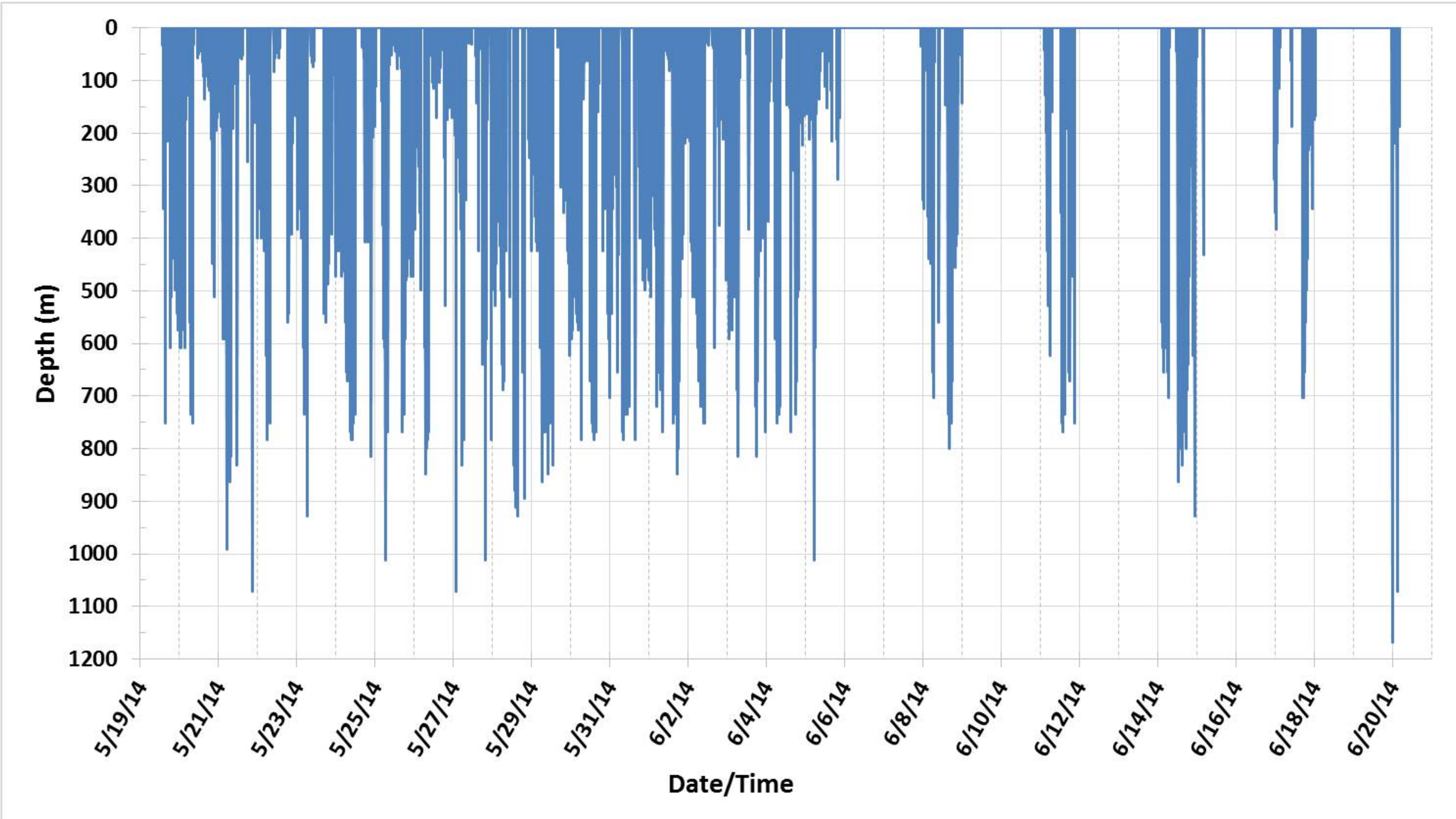


Figure 10: Maximum dive depths for each of the 1321 dives recorded from the short-finned pilot whale with SPLASH10 satellite tag ID 128889. Apparent gaps in dive data are due to tag duty-cycling (see Methods for details).

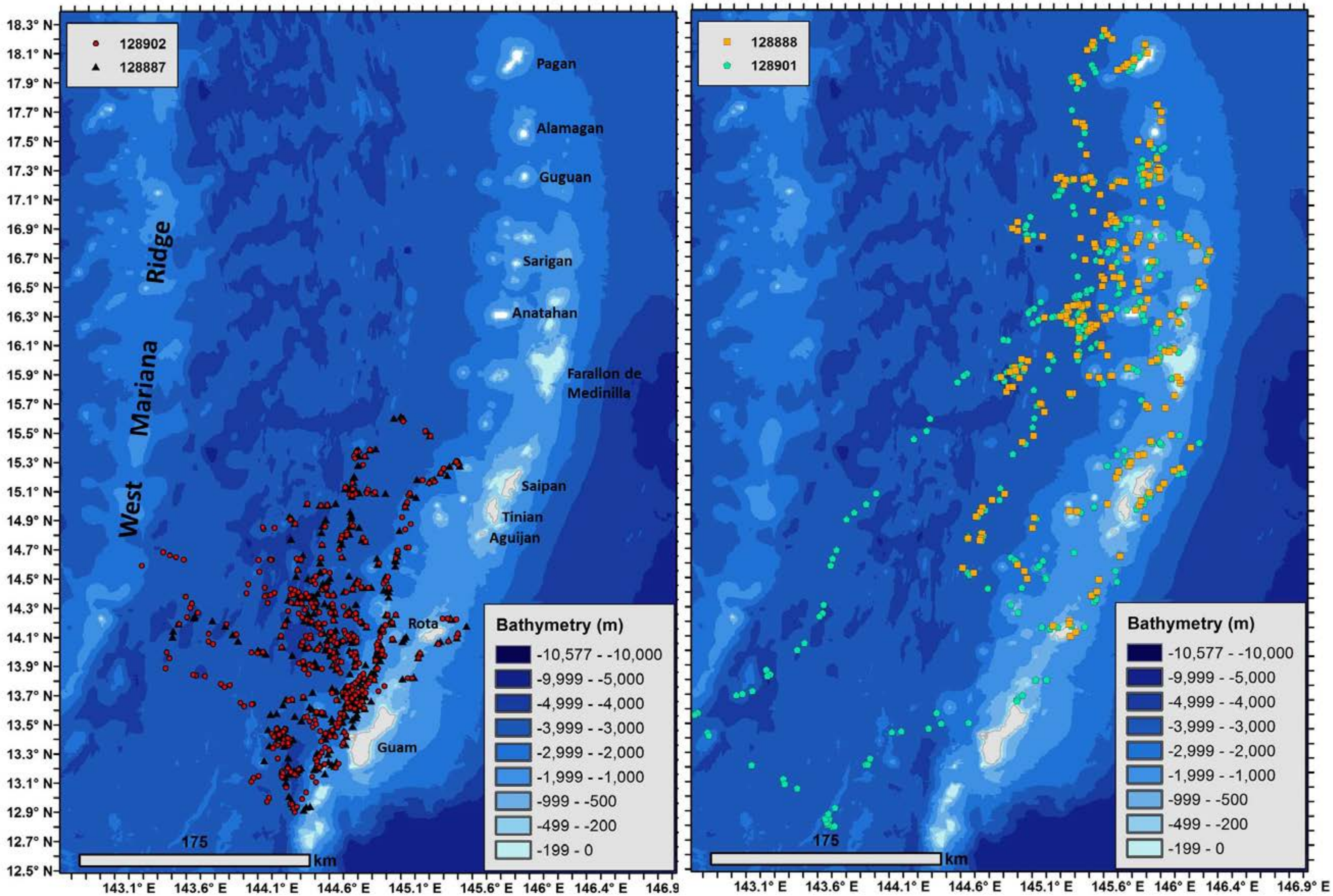


Figure 11.-- Douglas Argos filtered satellite locations from tags deployed on false killer whales. Left panel: tags 128887 and 128902 deployed on individuals encountered off Guam (21 May 2014) with island locations labeled. Deployment durations were 31.4 d and 39.0 d respectively. Right panel: tags 128888 and 128901 deployed on individuals off Tinian (12 June 2014). Deployment durations were 22.3 d and 30.7 d respectively.

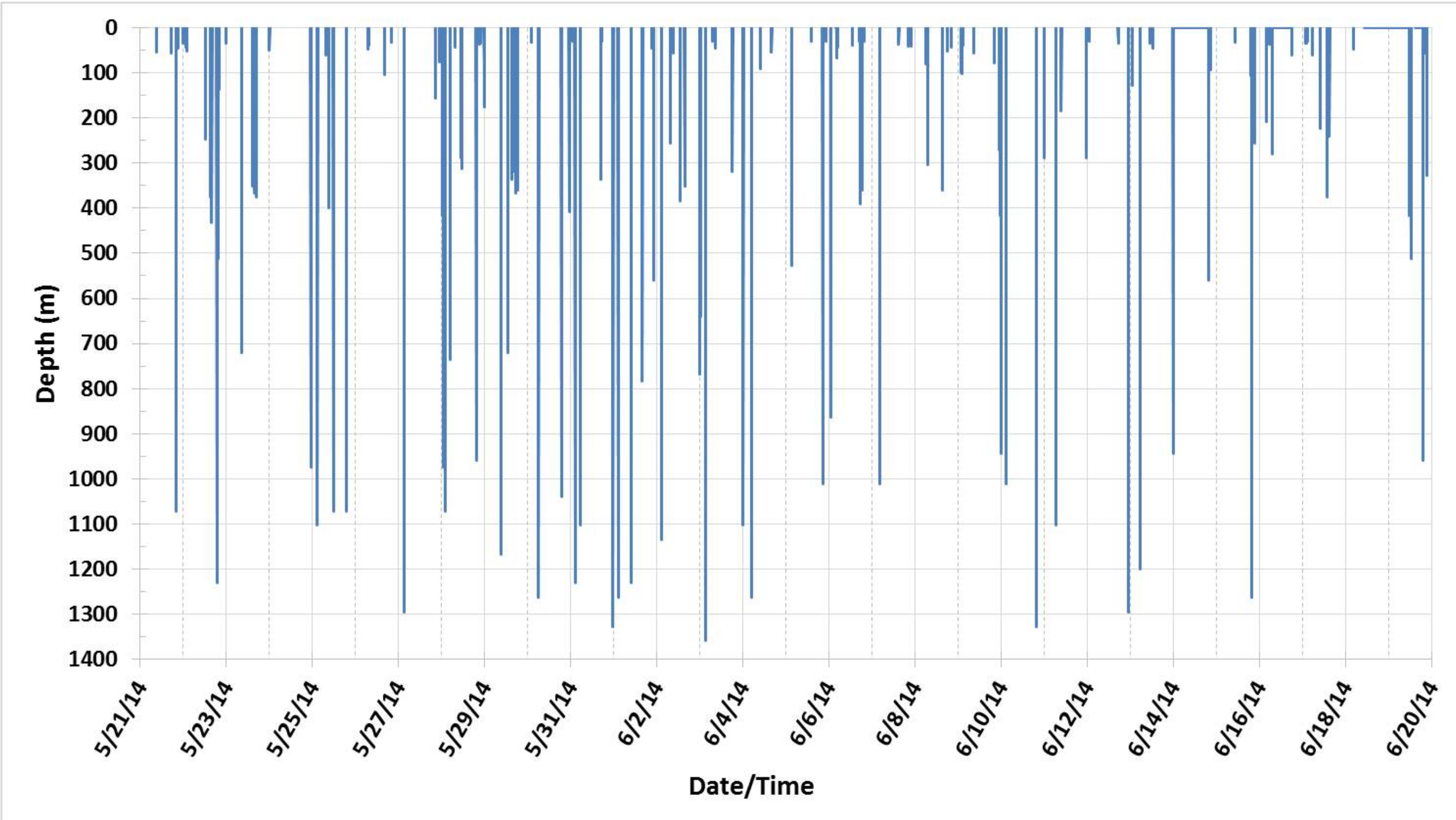


Figure 12: Maximum dive depths for each of the 167 dives recorded from the false killer whale with SPLASH10 satellite tag ID 128887, deployed off Guam. Apparent gaps in dive data are due to tag duty-cycling (see Methods for details).

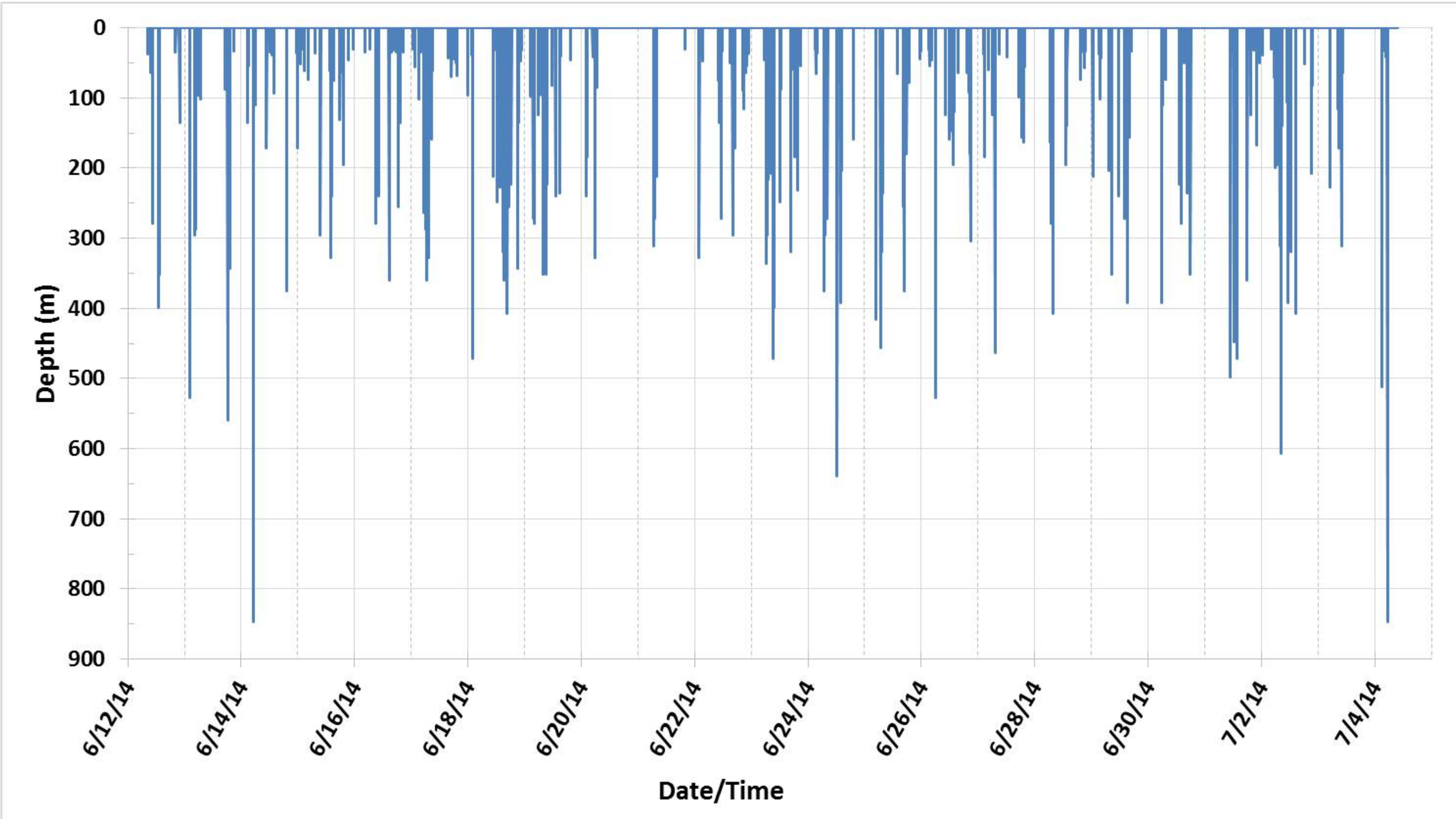


Figure 13: Maximum dive depths for each of the 332 dives recorded from the false killer whale with SPLASH10 satellite tag ID 128888, deployed off Tinian. Apparent gaps in dive data are due to tag duty-cycling (see Methods for details).

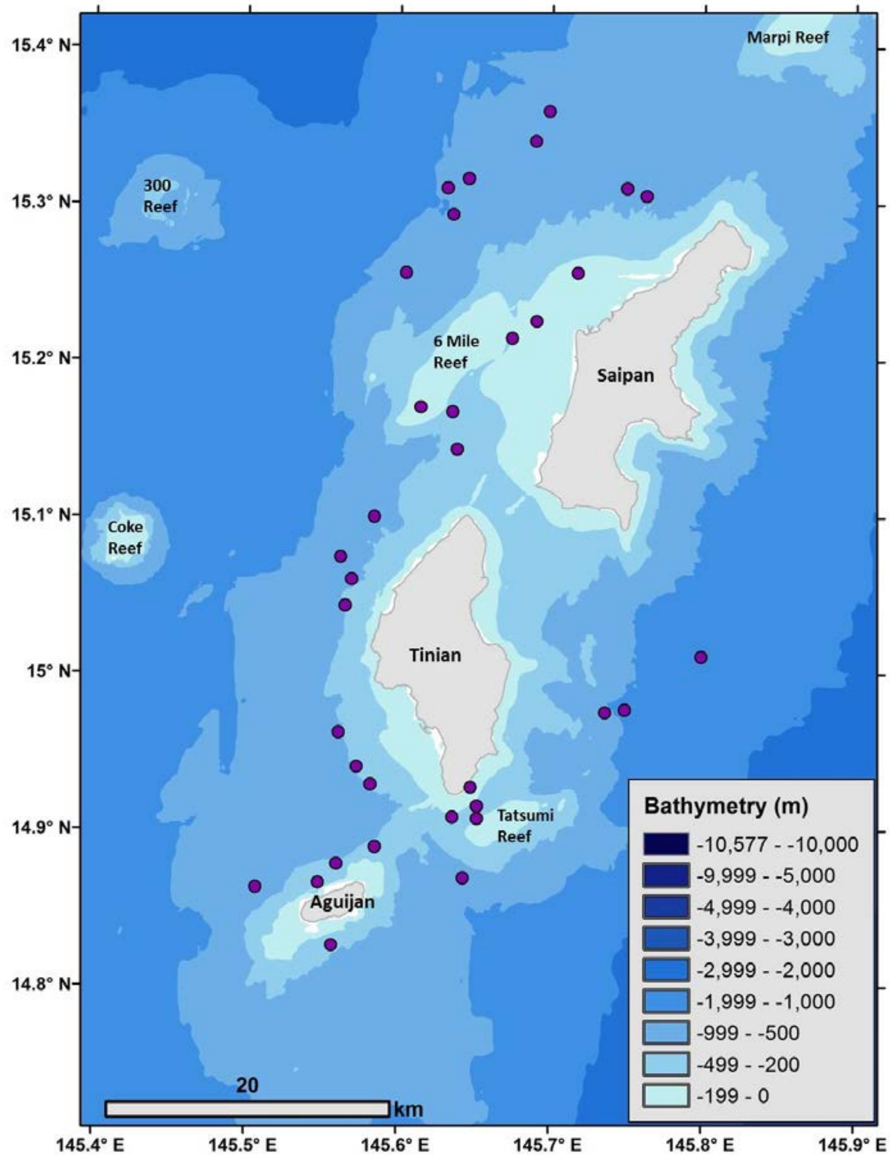


Figure 14.-- Douglas Argos filtered satellite locations from tag 128912 deployed on a bottlenose dolphin off the west side of Saipan and Tinian (12 June 2014). Deployment duration was 3.7 d.

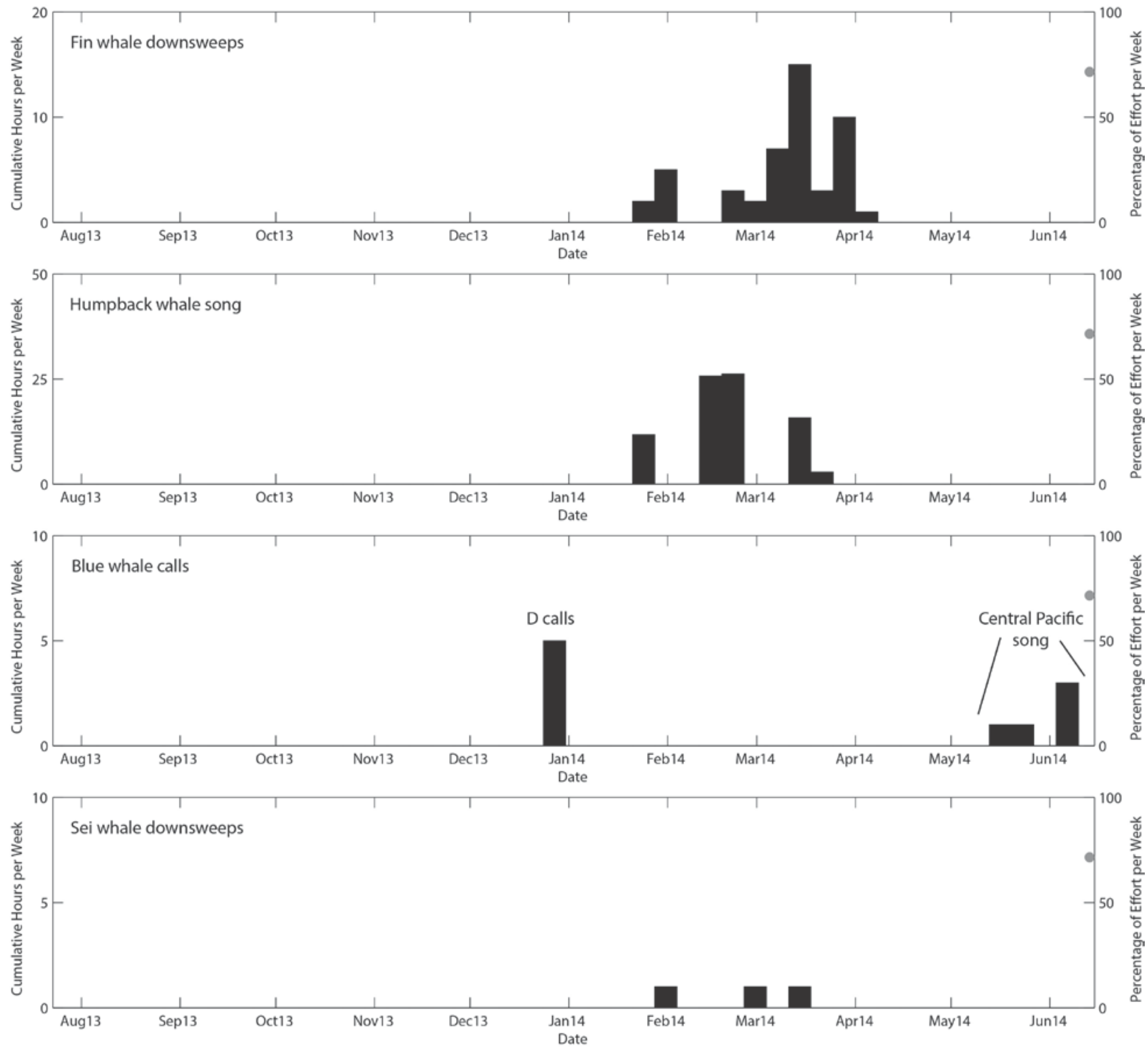


Figure 15.—Acoustic detections of baleen whale calls within the 2013-14 Tinian HARP dataset. Baleen whale calls are marked in hourly bins, not as individual calls or calling bouts, such that detection of a single or multiple calls within an hour is counted as one hour of detection. Y-axis scaling varies among plots. The light gray dot represents recording effort during the final monitoring week. Recording effort was 71.4% (5 minutes every 7 minutes).

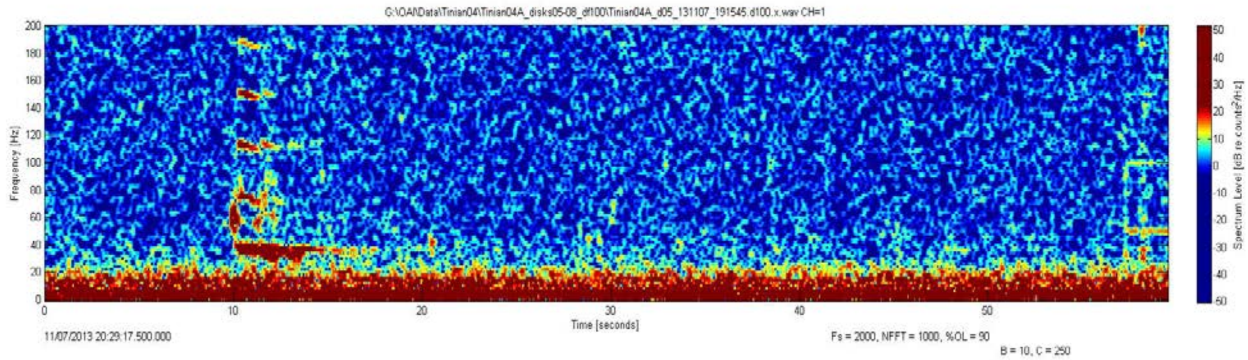


Figure 16. – Spectrogram of unidentified whale "tonal" call within the 2013-14 Tinian HARP dataset. This sound is similar to calls previously recorded from Bryde's whales in the eastern tropical Pacific (type Be3; Oleson et al. 2003), though is higher frequency and shorter duration. Bryde's whale calls have not been recorded in the Marianas to allow for comparison to detected sounds and definitive identification.

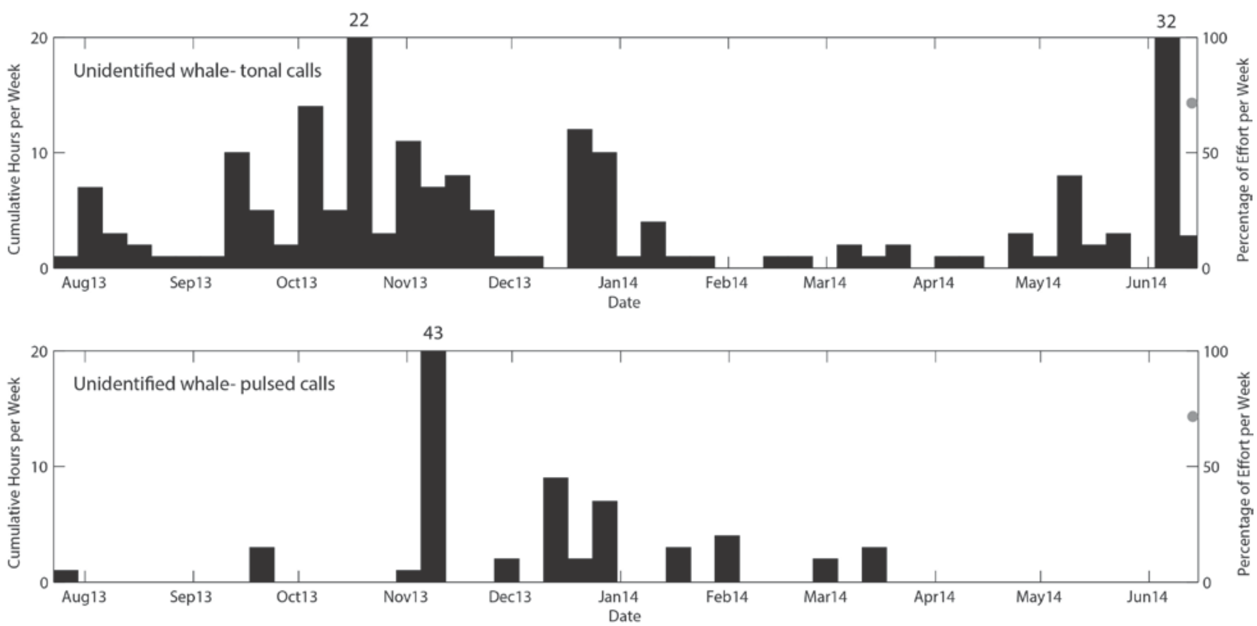


Figure 17. -- Acoustic detections of unidentified whale calls within the 2013-14 Tinian HARP dataset. Baleen whale calls are marked in hourly bins, not as individual calls or calling bouts, such that detection of a single or multiple calls within an hour is counted as one hour of detection. Values noted above the upper axis indicate cumulative hourly counts greater than the axis maximum. Y-axis scaling varies among plots. The light gray dot represents recording effort during the final monitoring week. Recording effort was 71.4% (5 minutes every 7 minutes).

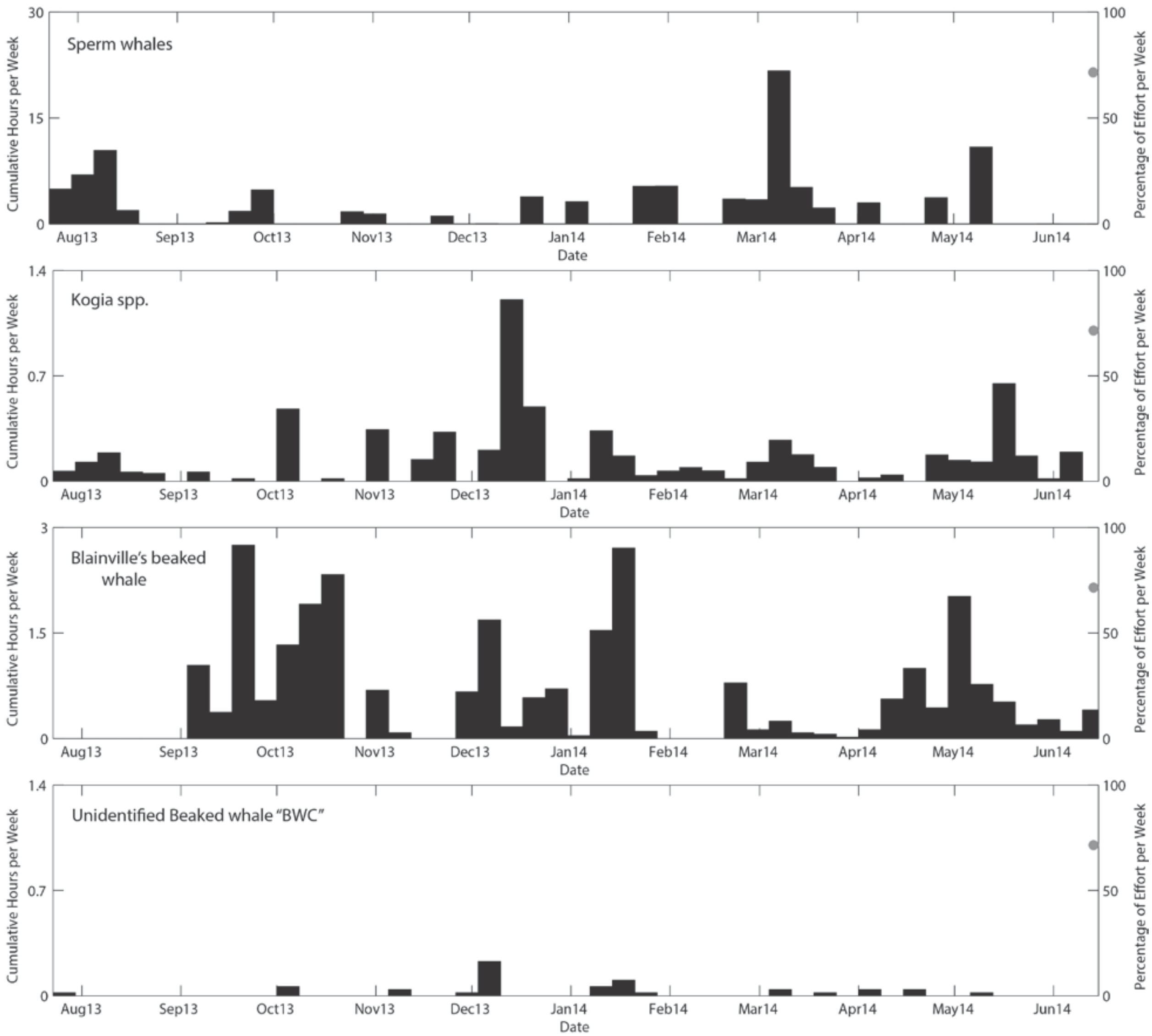


Figure 18.-- Acoustic detections of sperm whales (including *Kogia* spp.) and beaked whales within the 2013-14 Tinian HARP dataset. Sperm whale and *Kogia* occurrence are noted as calling bouts such that cumulative bout duration represents the total amount of time these species were heard during each weekly bin. Beaked whale calls were automatically detected and manually classified to species, and bout duration was measured following these detection and classification steps. BWC refers to the unidentified beaked whale described in Baumann-Pickering et al. (2013). Y-axis scaling varies among plots. The light gray dot represents recording effort during the final monitoring week. Recording effort was 71.4% (5 minutes every 7 minutes).

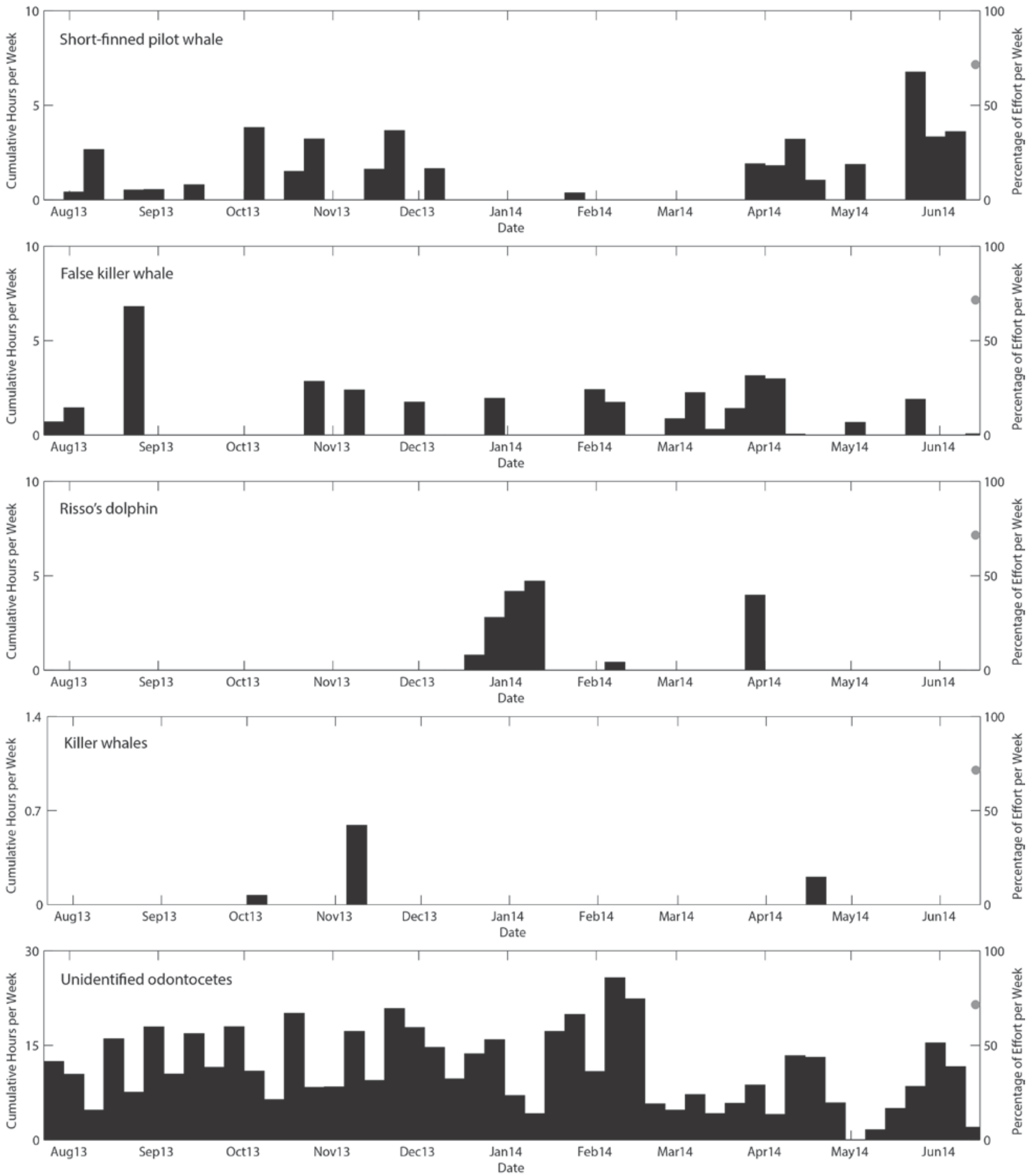


Figure 19. -- Acoustic detections of short-finned pilot whales, false killer whales, Risso's dolphins, killer whales, and unidentified odontocetes within the 2013-14 Tinian HARP dataset. Odontocete species occurrence is noted based on calling bouts such that cumulative bout duration represents the total amount of time each species were heard during each weekly bin. Y-axis scaling varies among plots. The light gray dot represents recording effort during the final monitoring week. Recording effort was 71.4% (5 minutes every 7 minutes).

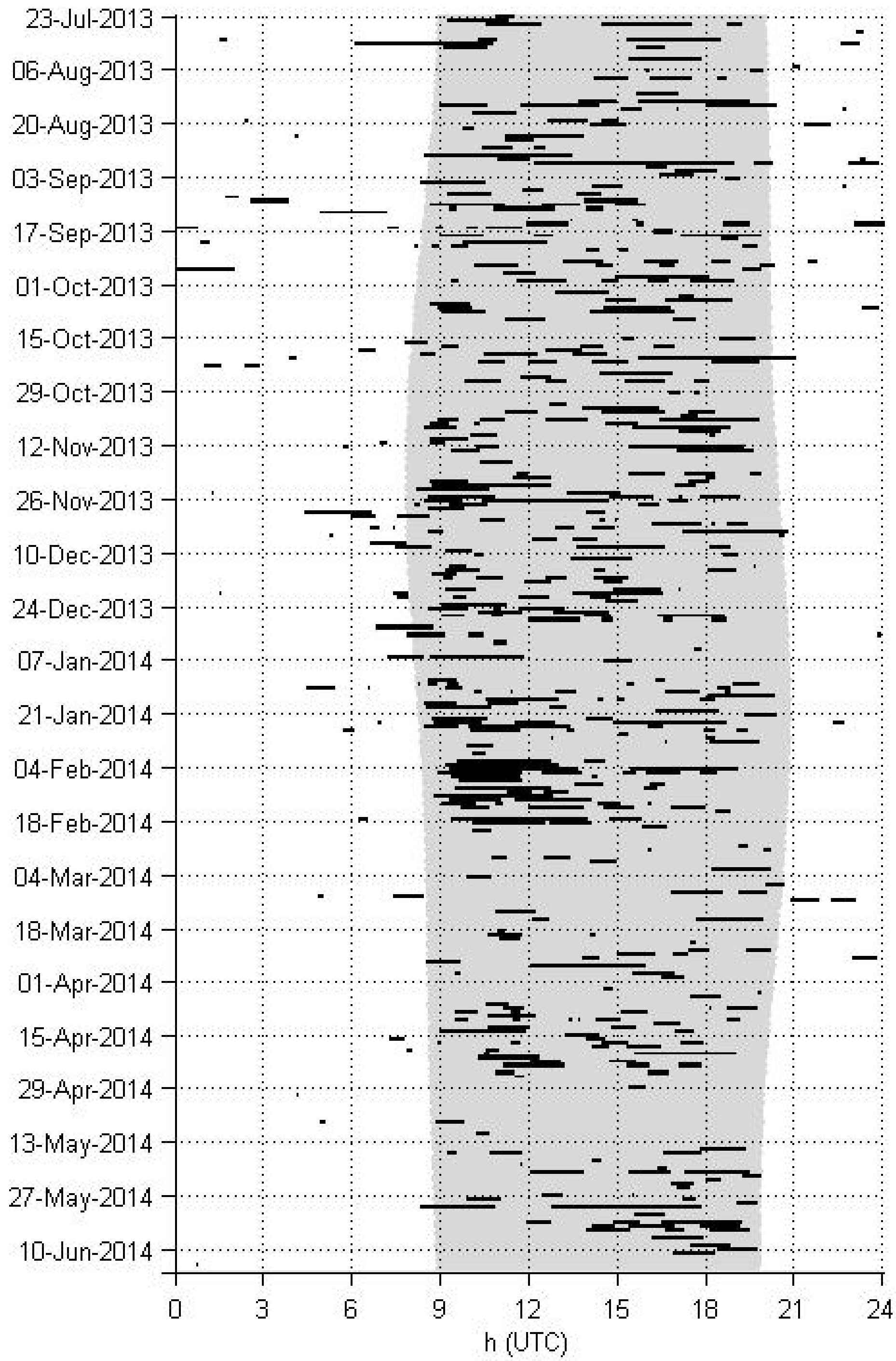


Figure 20. – Occurrence of unidentified odontocete sounds in one minute bins throughout the 2013-14 Tinian HARP dataset. Gray shading indicates nighttime.

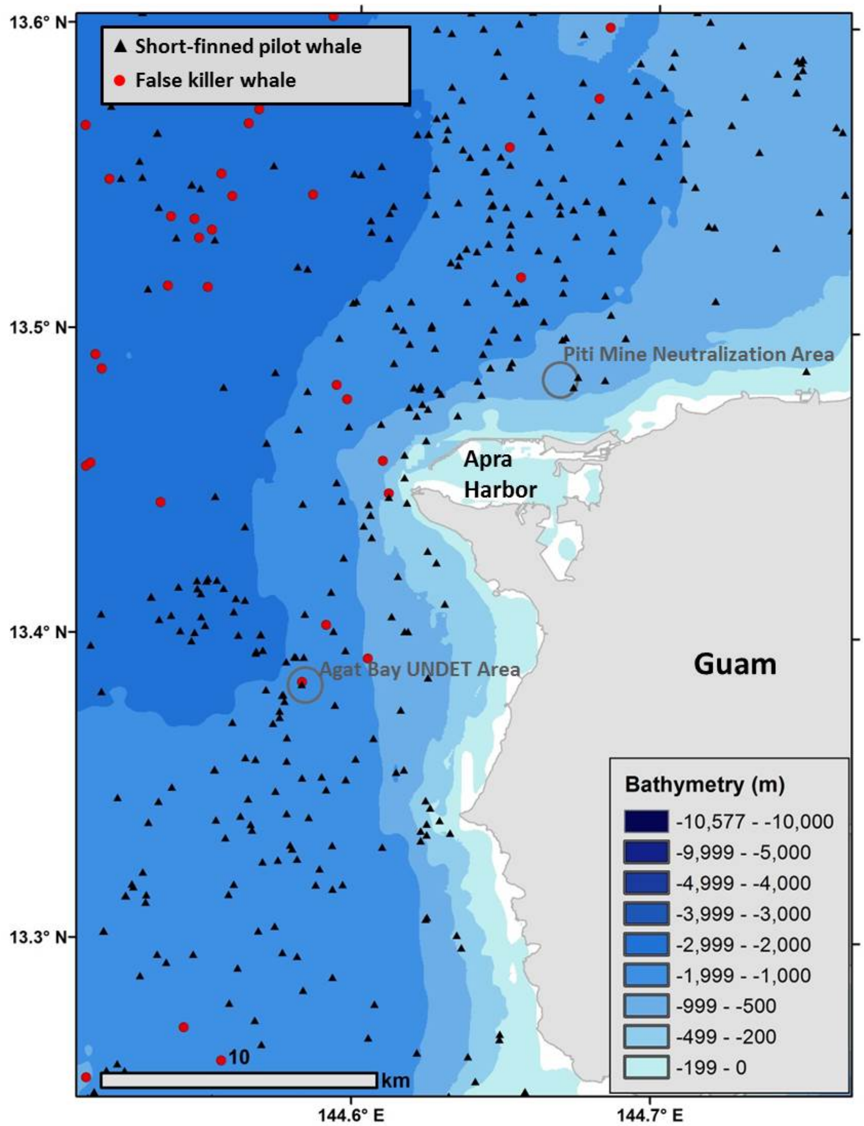


Figure 21.-- Navy underwater detonation and explosive ordinance areas and short-finned pilot whale and false killer whale filtered satellite tag locations. The circles at the Piti Floating Mine Neutralization Area and the Agat Bay UNDET Area represent the 640 m exclusion zone around the detonation site.

# Appendix I: Introgressive hybridization of Fraser's dolphin mitochondrial and nuclear DNA into Mariana Islands bottlenose dolphins

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## Abstract

We used mitochondrial sequence and nuclear microsatellite loci to examine introgression of Fraser's dolphin DNA into the Mariana Islands population of bottlenose dolphins. By comparing the nuclear genotypes of the Mariana Islands samples to those of 'pure' bottlenose dolphins and Fraser's dolphins, we estimate that the Mariana Islands animals derive approximately 14% of their nuclear ancestry from Fraser's dolphins. The fact that every Mariana Islands sample showed evidence of nuclear introgression, combined with the fact that those exhibiting mitochondrial introgression all share the same Fraser's dolphin haplotype, suggests that there was a single hybridization event far enough in the past to allow Fraser's dolphin nuclear DNA to permeate the population. The Mariana Islands samples exhibited low genetic diversity compared to other bottlenose dolphin populations, suggesting that they represent a small, genetically isolated population.

## Introduction

Most species concepts assume a complete lack of interbreeding between species. However, there is increasing evidence that interspecific hybridization is relatively common (Arnold 1992; Bernatchez et al. 1995; Seehausen et al. 2002; Shaw 2002). Introgressive hybridization, in which genetic material from one species persists in the genome of another species following hybridization, can result in gene trees that do not match species trees and seriously mislead phylogenetic studies. This is particularly true in studies based solely on mitochondrial DNA, as introgression of maternally-inherited genomes is predicted to occur far more rapidly and persist longer than introgression of nuclear genomes (Chan and Levin 2005).

Cetacean species are known to exhibit an unusually high rate of interspecific hybridization. Isolated hybridization events have been documented both in wild populations and among captive animals, and do not always involve sister species (Bérubé 2002; Kingston et al. 2009). Introgressive hybridization has long been suspected as a source of taxonomic confusion in the Delphinidae (Kingston et al. 2009). The bottlenose dolphin population in Shark Bay, Western Australia, contains haplotypes from both common (*Tursiops truncatus*) and Indo-Pacific (*T. aduncus*) bottlenose dolphins, suggesting a hybrid origin for the population (Krützen et al. 2004). The Clymene dolphin (*Stenella clymene*) is believed to have originated as a result of hybridization between spinner dolphins (*S. longirostris*) and striped dolphins (*S. coeruleoalba*)(Amaral et al. 2014).

Martien et al. (2014b) found that five out of 15 common bottlenose dolphin samples collected around the southern islands of the Mariana Archipelago possessed haplotypes characteristic of Fraser's dolphins (*Lagenodelphis hosei*). Photographs confirmed that the samples came from five different individuals, all of which appeared to be morphologically normal bottlenose dolphins. Martien et al. also conducted a search of genetic data available online and found two additional samples collected in China and identified as *T. truncatus* that possess the same Fraser's dolphin haplotype that they detected in the Mariana Islands bottlenose dolphin population.

In this study, we use mitochondrial DNA sequence data and nuclear microsatellite genotype data to further investigate the extent and origin of hybrid ancestry in Mariana Islands bottlenose dolphins. We compare the Mariana Islands samples to bottlenose dolphin samples from elsewhere in the western Pacific and the Hawaiian Archipelago and to Fraser's dolphin samples from throughout the Pacific and Indian Oceans. Our results provide insight into the degree of Fraser's dolphin introgression into the nuclear genomes of the Mariana Islands animals and the evolutionary history of hybridization into the population.

## Methods

### *Samples*

The focus of our study was 15 samples collected around the southern islands of the Mariana Archipelago. The samples came from animals that appeared morphologically to be bottlenose dolphins, yet five of them possessed Fraser's dolphin haplotypes (Martien et al. 2014b). We also analyzed 169 bottlenose dolphin samples collected outside the Mariana Archipelago (Figure 1). Most of these (n=159) were collected within the U.S. Exclusive Economic Zone surrounding the Hawaiian Archipelago (Hawaiʻi EEZ samples) between 1999 and 2013, primarily during research surveys conducted by the Southwest and Pacific Islands Fisheries Science Centers and during dedicated small-boat surveys conducted by Cascadia Research Collective. The remaining bottlenose dolphin samples were biopsies and strandings from other areas of the North Pacific (Figure 1). We consider the Hawaiʻi EEZ samples to represent 'pure' bottlenose dolphins (i.e., not hybridized with Fraser's dolphins), while the western Pacific samples could, given their proximity to the Mariana Archipelago, exhibit some degree of hybrid ancestry. We therefore only used the Hawaiʻi EEZ samples in analyses that required *a priori* stratification.

Our sample set also included 47 tissue samples collected from Fraser's dolphins between 1973 and 2009. These samples were primarily from animals stranded in the Philippines, with the remainder consisting of biopsies and strandings from around the Pacific and Indian Oceans (Figure 1). Examining population structure within Fraser's dolphin was not a goal of this study, nor did we have enough samples to stratify the Fraser's dolphin data set. Therefore, in analyses that included the Fraser's dolphin samples, we treated all Fraser's dolphin samples as a single stratum.

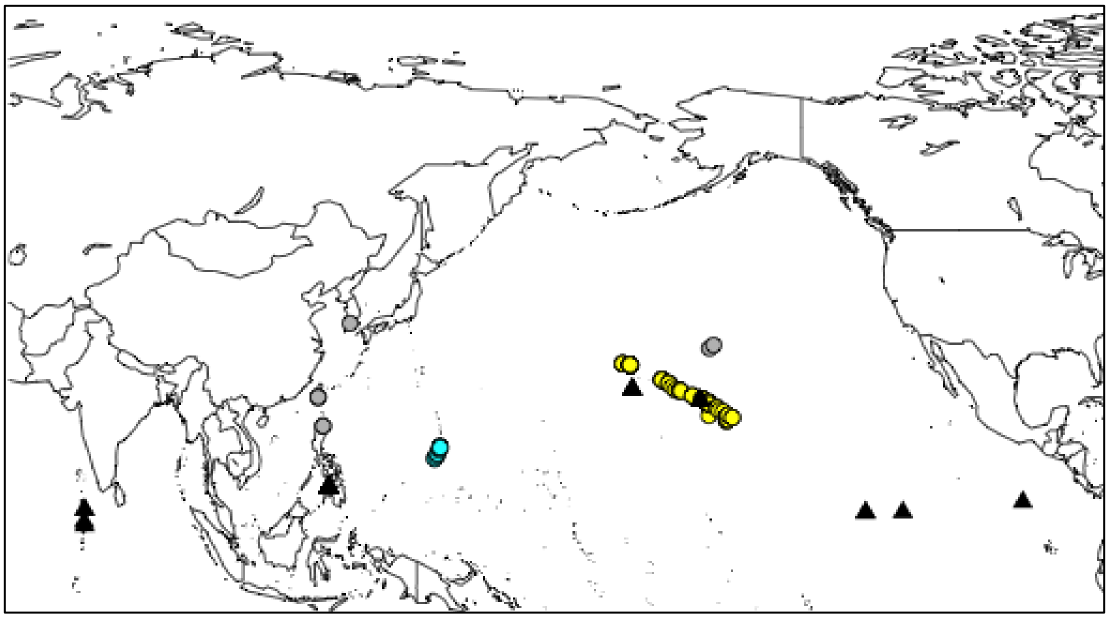

Figure 1. Distribution of bottlenose dolphin (circles) and Fraser's dolphin (black triangles) samples. Bottlenose dolphin samples from CNMI are in blue, those from the Hawai'i EEZ are in yellow, and all other samples are in gray.

***Laboratory analyses***

DNA extractions were performed using either a silica-based filter purification (Qiaxtractor, DX reagents; Qiagen) or a sodium chloride protein precipitation (Miller et al. 1988). Standard protocols were used for PCR amplification, as well as for mitochondrial DNA (mtDNA) sequencing (Saiki et al. 1988; Sambrook et al. 1989; Palumbi et al. 1991). A 400 basepair region of the 5' end of the hypervariable mtDNA control region was amplified using primers D (5'- CCTGAAGTAAGAACCAGATG- 3'; Rosel et al. 1994) and TRO (5'- CCTCCCTAAGACTCAAGG-3'; developed at SWFSC). The PCR cycling profile for mtDNA sequencing consisted of 94 °C for 2.5 min, followed by 35 cycles of 94 °C for 45 sec, 1 min at 56 °C annealing temperature, and 72 °C for 1.5 min, then a final extension at 72 °C for 5 min. Both the forward and reverse strands of the amplified DNA product were sequenced as mutual controls on the Applied Biosystems Inc. (ABI) 3730 DNA Analyzer. All sequences were aligned using Sequencer v4.1 software (Gene Codes Corp., 2000).

We genotyped all samples at fourteen microsatellite loci, all of which were dinucleotide repeats. Ten of the loci (KWM1b, KWM2a, KWM2b, KWM12a, D5, Ttr11, Ttr34, Ttr48, TexVet7, and D08) were also used in Martien et al.'s (2012) analysis. One locus used by Martien et al. (D8) did not amplify reliably in Fraser's dolphins, and so was excluded from our study. In order to increase the precision of our estimates of nuclear ancestry we used four additional loci (Ttr58, TexVet5, EV94, SL125), which were chosen because initial screening showed them to be highly polymorphic in Fraser's dolphins. Control samples from Martien et al.'s study were included on every genotyping plate in order to ensure consistent scoring of alleles across the two studies.

Primer sets for loci KWM1b, KWM2a, KWM2b, and KWM12a were derived from killer whales (Orcinus orca; Hoelzel et al. 1998), locus D5 from beluga whales (Delphinapterus leucas; Buchanan et al. 1996), loci Ttr11, Ttr34, Ttr48, Ttr58 (Rosel et al. 2005), TexVet5 and TexVet7 (Rooney et al. 1999), locus D08 (Shinohara et al. 1997) were all derived from bottlenose dolphins (*Tursiops* sp.), locus EV94 from Humpback whales (*Megaptera novaeangliae*; Valsecchi and Amos 1996), and locus SL125 spinner dolphins (*Stenella* sp.; Galver 2002). Extracted DNA was amplified using a 25 µL reaction of 1x PCR buffer (50 mM KCl, 10 mM Tris-HCl, pH 8.3, and 1.5 mM $MgCl_2$), 0.15 mM of each dNTP, 0.3 µM of each primer, 0.5 units of Taq DNA polymerase, and approximately 10ng of DNA. The PCR cycling profile consisted of 90 °C for 2.5 min, followed by 35 cycles of 94 °C for 45 sec, 1 min at annealing temperature, and 72 °C for 1.5 min, then a final extension at 72 °C for 5 min. The optimal annealing temperature was 55 °C for the loci D08, TexVet5, TexVet7, Ttr48, Ttr11, and SL125, 45 °C for loci KWM1b, KWM2a, KWM2b, and KWM12a, 57 °C for loci D5 and Ttr34, 52 °C for locus EV94 and 60 °C for locus Ttr58, respectively.

The amplifications were assessed electrophoretically on a 2 % agarose gel for quality and size before loading onto the ABI 3730 DNA Analyzer. ABI Genemapper v4.0 was used along with an internal standard marker, Genescan-500 ROX, Applied Biosystems Inc., to determine allele fragment size.

Samples were genetically sexed by amplification and Real-Time PCR (Stratagene) of the zinc finger (ZFX and ZFY) genes (Morin et al. 2005).

***Data review***

Prior to analysis, the mtDNA and nucDNA data sets were reviewed for quality using the standards described in Martien et al. (2014a) and Morin et al. (Morin et al. 2010). This included 10% random replication, re-sequencing of unique haplotypes, having all allele size calls reviewed by two independent genotypers, and eliminating samples deemed to be of poor quality.

For the bottlenose dolphin data set, we assessed each microsatellite locus for deviations from Hardy-Weinberg equilibrium (HWE) and linkage equilibrium as a means of ensuring that the loci were amplifying correctly (e.g., no null alleles) and that we had not included genetically differentiated populations into a single stratum. We tested for deviations from HWE using tests for heterozygote deficiency (Raymond and Rousset 1995) and exact tests of HWE (Guo and Thompson 1992), as implemented in strataG (available upon request from F.I. Archer), a package for the statistical program language R (R Development Core Team 2011). We used the same software to evaluate linkage disequilibrium for each pair of loci using Fisher's method and the Markov chain method. All HWE and linkage disequilibrium tests were conducted using 1,000 dememorization steps, 10,000 batches, 1,000 iterations per batch. The tests were conducted separately for CNMI and the Hawai'i EEZ and combined across the two strata to calculate a global *P*-value for each locus (Fisher 1935). The jackknife procedure described in Morin et al. (2009a) was used to identify samples that were highly influential (i.e., log-odds greater than two) in deviations from HWE. The genotypes identified by the jackknife procedure were removed from the data set. HWE and linkage disequilibrium analyses were not conducted for Fraser's dolphin data set, as there were not enough samples in that data set to stratify into putative populations, and equilibrium is not expected when samples from multiple populations are combined into a single stratum.

Pairs of samples that matched in sex, mtDNA haplotype, and microsatellite genotype were considered duplicate samples. When available, photo-identification data were also used to identify duplicate samples from the same individual. The program DROPOUT (McKelvey and Schwartz 2005) was used to identify additional pairs of samples whose genotypes differed at four or fewer loci. These pairs could represent duplicate samples with genotyping errors. One sample from each duplicate pair was removed prior to analysis. We also used DROPOUT to calculate the probability of two randomly selected individuals sharing an identical genotype.

***Analyses***

We incorporated into our analyses data published by Martien et al. (2012) on bottlenose dolphins sampled from the main Hawaiian Islands. Martien et al.'s data set included mitochondrial control region sequences from 119 animals and genotypes from 116 animals at ten of the 14 microsatellite loci used in this study. We included the data from Martien et al. in all of our mtDNA analyses. However, we did not include Martien et al.'s nucDNA data since doing so would have precluded us from using some of the loci that were most polymorphic for Fraser's dolphins and therefore most useful for estimating the proportion of Fraser's dolphin ancestry.

We calculated haplotypic diversity (*h*) and nucleotide diversity ($\pi$) for the mtDNA data set using *strataG*. These calculations were made both including and excluding the five CNMI individuals that possessed Fraser's dolphin haplotypes, as including haplotypes from two different species in the same stratum results in a strong upward bias in diversity estimates, particularly for nucleotide diversity. The mtDNA diversity analysis was the only analysis for which these individuals were excluded. For the nucDNA data set, we used *strataG* to calculate average number of alleles per locus, expected and observed heterozygosity, and allelic richness. The nucDNA diversity estimates include all individuals, regardless of haplotype.

We tested the null hypothesis of no population structure between CNMI and the Hawai'i EEZ for both the mtDNA and nucDNA data sets by conducting a $\chi^2$ test (Rolf and Bentzen 1989), as implemented in *strataG*. We estimated the magnitude of genetic differentiation between CNMI and Hawai'i EEZ using the statistics $F_{ST}$ (Wright 1931) and $\Phi_{ST}$ (Excoffier et al. 1992) for the mtDNA data set and $F_{ST}$ and $F'_{ST}$ (Meirmans 2006) for the nucDNA data set. To get a sense of the relative nuclear differentiation of the CNMI animals from Fraser's dolphins and all other bottlenose dolphins, we also used the nucDNA data set to estimate pairwise genetic differentiation between the CNMI animals, all non-CNMI bottlenose dolphins, and Fraser's dolphins.

To estimate the proportion of the nuclear ancestry of the CNMI animals that comes from bottlenose and Fraser's dolphins, we used the Bayesian clustering program STRUCTURE (Pritchard et al. 2000; Falush et al. 2003; Hubisz et al. 2009). We first used STRUCTURE to analyze all bottlenose dolphin samples, clustering them into *k*=1 to 6 groups using an admixture model with correlated allele frequencies and no prior information on group membership. We then re-ran the same analysis, but included the Fraser's dolphin samples and examined values of *k* from 1 to 4.

We next used STRUCTURE to look for individuals that had recent hybrid ancestry by labeling all bottlenose dolphin samples, including those from the CNMI, as bottlenose dolphins and all Fraser's dolphin samples as Fraser's dolphins. We then ran STRUCTURE with the USEPOPINFO option and had the analysis look for immigrant ancestry up two generations in the past, which is the longest time frame the analysis can examine. For this analysis, we assumed that allele frequencies were independent between the two species. Finally, we repeated this analysis but without assigning a species label to the CNMI samples. Thus, the analysis used an uninformative prior as to the species origin of the CNMI samples and estimated the proportion of their nuclear ancestry that came from each species.

All STRUCTURE analyses were run with a burn-in of 100,000 steps and a run length of 500,000 steps. We replicated each run 10 times and averaged the ancestry coefficients of individuals across replicate runs using the CLUMPP algorithm of Jakobsson and Rosenberg (2007). All STRUCTURE and CLUMPP analyses were conducted within the R package *strataG* (available upon request).

## Results

### *Data review*

Among the bottlenose dolphin samples, fifteen pairs of replicate samples were identified either genetically and photographically, all of which matched with respect to sex and mtDNA haplotype. One sample from each pair was therefore excluded from the final data set. In addition, twelve samples were found to be genetically identical to samples included in Martien et al.'s (2012) study. In these cases, the sample used by Martien et al. was excluded, as the newer samples had been genotyped at more loci. In all cases of replicate samples, both within our sample set and between our sample set and that of Martien et al., both samples were collected from the same Hawaiian island.

We excluded eight Fraser's dolphin samples from the mtDNA data set and 22 from the microsatellite data set due to poor sample quality. Only one bottlenose dolphin sample was excluded from the mtDNA data set and five from the nucDNA data set due to poor quality. After all exclusions our mtDNA dataset included 169 bottlenose dolphins and 39 Fraser's dolphins, while the nucDNA data set included 164 bottlenose dolphins and 25 Fraser's dolphins.

The jackknife analysis of the bottlenose dolphin data set identified one individual that was homozygous for a rare allele at locus SL125t and was therefore having a disproportionate effect on HWE at that locus. That individual's genotype at SL125t was treated as missing data for all microsatellite analyses. Three loci were identified as being out of HWE for the Hawaiʻi EEZ samples, while none were out of HWE in the CNMI samples. However, the Hawaiʻi EEZ is known to contain multiple populations (Martien et al. 2012). When the HWE analysis was re-run separately for each of the four populations identified by Martien et al., none of the loci were out of HWE. Similarly, while seven pairs of loci were found to be out of linkage equilibrium in the data set overall, none of them were out of equilibrium within any of the populations identified by Martien et al. Therefore, all 14 loci were retained.

***Diversity***

We resolved 28 unique haplotypic sequences among the bottlenose dolphin samples we analyzed, 13 of which were also identified by Martien et al. (2012). There were seven haplotypes identified within the Hawaiʻi EEZ by Martien et al. that we did not detect. Thus, the final combined data set included 35 haplotypes, including the single Fraser's dolphin haplotype (LH11) detected in CNMI. All mtDNA analyses were conducted on this combined data set (Table 1). We resolved 26 unique haplotypes among the Fraser's dolphin samples (Table 2). Five Fraser's dolphin samples – three from the Philippines and two from Hawaiʻi – possessed the same haplotype (Lh11) detected in the CNMI bottlenose dolphin samples.

Both haplotypic and nucleotide diversity of bottlenose dolphins were low in CNMI when the individuals possessing Fraser's dolphin haplotypes were excluded (Table 3). Including these individuals resulted in substantially higher diversity estimates, as would be expected when combining haplotypes from two different species in a single stratum, but haplotypic diversity was still lower than for the Hawaiʻi EEZ, entire bottlenose dolphin data set as a whole, and the Fraser's dolphin data set. Estimates of nuclear genetic diversity were also lower in CNMI than for any other stratum (Table 4).

Table 1. Bottlenose dolphin haplotype frequencies by location. Sample sizes are given in parentheses. Haplotypes are numbered to be consistent with Martien et al. 2012. Haplotypes marked with an asterisk were only found by Martien et al. (2012), not in the new samples analyzed for this paper. Haplotypes 21-25 have only been detected at Palmyra Atoll, which is not part of our study area, and so are omitted from the table. Haplotype Lh11 is the Fraser's dolphin haplotype detected in five CNMI bottlenose dolphins.

| Haplotype | CNMI (15) | Philippines (2) | Taiwan (4) | Korea (1) | Hawai'i EEZ (267) | NE Pacific (2) |
|---|---|---|---|---|---|---|
| 1 | | | | | 62 | |
| 2 | | | | | 34 | |
| 3 | | | | | 23 | |
| 4 | | | | | 46 | |
| 5 | | | | | 5 | |
| 6 | | | | | 30 | |
| 7 | | | | | 2 | |
| 8 | | | | 1 | 2 | |
| 9* | | | 1 | | 5 | |
| 10* | | | | | 1 | |
| 11* | | | | | 1 | |
| 12 | | | | | 17 | |
| 13 | | | 1 | | 15 | |
| 14* | | | | | 1 | |
| 15* | | | | | 1 | |
| 16* | | | | | 1 | |
| 17 | | | | | 3 | |
| 18* | | | | | 1 | |
| 19 | | | | | 6 | |
| 20 | | | | | 3 | |
| 26 | | | | | 3 | |
| 27 | | | | | 1 | |
| 28 | | | | | 1 | |
| 29 | | | | | | 1 |
| 30 | | | | | | 1 |
| 31 | | | | | 1 | |
| 32 | 7 | 1 | | | | |
| 33 | 1 | | | | | |
| 34 | 1 | 1 | | | | |
| 35 | | | 1 | | | |
| 36 | | | 1 | | | |
| 37 | | | | | 1 | |
| 38 | | | | | 1 | |
| 39 | 1 | | | | | |
| Lh11 | 5 | | | | | |

Table 2. Fraser's dolphin haplotype frequencies by location. Sample sizes are given in parentheses.

| Haplotype | Maldives (4) | Philippines (25) | Taiwan (3) | Hawai'i (3) | North Pacific (3) | ETP (1) |
|---|---|---|---|---|---|---|
| Lh1 | | 2 | | | | |
| Lh2 | 1 | 3 | 1 | | | |
| Lh3 | | 1 | | | | |
| Lh4 | | 3 | | | | |
| Lh5 | | | | | | 1 |
| Lh6 | | 2 | | | | |
| Lh7 | | 1 | | | | |
| Lh8 | | 1 | | | | |
| Lh9 | | 2 | | | | |
| Lh10 | | 1 | | | | |
| Lh11 | | 3 | | 2 | | |
| Lh12 | | 1 | | | | |
| Lh13 | | 1 | | | | |
| Lh14 | | 1 | | | | |
| Lh15 | | | | 1 | | |
| Lh16 | | 1 | | | | |
| Lh17 | | 1 | | | | |
| Lh18 | 1 | | | | | |
| Lh19 | | | | | 1 | |
| Lh20 | | | | | 1 | |
| Lh21 | | | | | 1 | |
| Lh22 | | 1 | | | | |
| Lh23 | | | 1 | | | |
| Lh24 | | | 1 | | | |
| Lh25 | 1 | | | | | |
| Lh26 | 1 | | | | | |

Table 3. Diversity estimates for the mtDNA data sets.

| | Sample Size | Number of Haplotypes | Haplotype Diversity | Nucleotide Diversity |
|---|---|---|---|---|
| CNMI – no Fraser's haps | 10 | 4 | 0.533 | 0.004 |
| CNMI – all | 15 | 5 | 0.705 | 0.029 |
| Hawai'i EEZ | 267 | 26 | 0.874 | 0.026 |
| All bottlenose dolphins | 286 | 34 | 0.893 | 0.022 |
| All Fraser's dolphins | 39 | 26 | 0.965 | 0.017 |

Table 4. Diversity estimates for the nucDNA data sets. Allelic richness was calculated for a minimum sample size of 14.

| | Sample Size | Num. alleles | $H_e$ | $H_o$ | $A_R$ |
|---|---|---|---|---|---|
| CNMI | 14 | 5.86 | 0.689 | 0.658 | 5.857 |
| Hawai'i EEZ | 144 | 8.79 | 0.746 | 0.743 | 6.332 |
| All bottlenose dolphins | 164 | 9.43 | 0.752 | 0.737 | 6.550 |
| All Fraser's dolphins | 25 | 7.79 | 0.726 | 0.737 | 6.561 |

***Differentiation***

CNMI was significantly differentiated from the Hawai'i EEZ in both the mtDNA ($F_{ST}$ = 0.192, $\Phi_{ST}$ = 0.166, $\chi^2$ *p*-value < 0.0001) and nucDNA ($F_{ST}$ = 0.070, $F'_{ST}$ = 0.251, $\chi^2$ *p*-value < 0.0001) data sets. The magnitude of differentiation in the nucDNA data set, as measured by both $F_{ST}$ and $F'_{ST}$, was more than double between CNMI and Fraser's dolphins than it was between CNMI and all non-CNMI bottlenose dolphins, and was comparable to the differentiation between Fraser's and bottlenose dolphins (Table 5).

Table 5. Estimates of genetic differentiation between CNMI animals, bottlenose dolphins not from CNMI, and Fraser's dolphins.

| Comparison | $F_{st}$ | $F'_{st}$ | $\chi^2$ *P* value |
|---|---|---|---|
| CNMI vs. bottlenose | 0.067 | 0.245 | <0.0001 |
| CNMI vs. Fraser's | 0.176 | 0.605 | <0.0001 |
| Bottlenose vs. Fraser's | 0.160 | 0.615 | <0.0001 |

When we used the program STRUCTURE to cluster all bottlenose dolphin samples, including those from CNMI, the model with the highest support was the one with two groups. Under this model, the CNMI samples had an average assignment probability of 91.2% to group 1, the other western Pacific samples had an average assignment probability of 86.1% to group 1, and the Hawai'i EEZ samples had an average assignment probability of 61.3% to group 2 (Figure 2a). When we included the Fraser's dolphin samples in the analysis, the best model was the one with three groups, and the bottlenose dolphin samples were much more clearly separated into a two groups. Under this model, the CNMI had 88.1% assignment to group 1, the western Pacific and Hawai'i EEZ bottlenose dolphin samples had average assignments to group 2 of 73.0% and 95.8%, respectively, and the Fraser's dolphins had an average assignment of 99.3% to group 3 (Figure 2b).

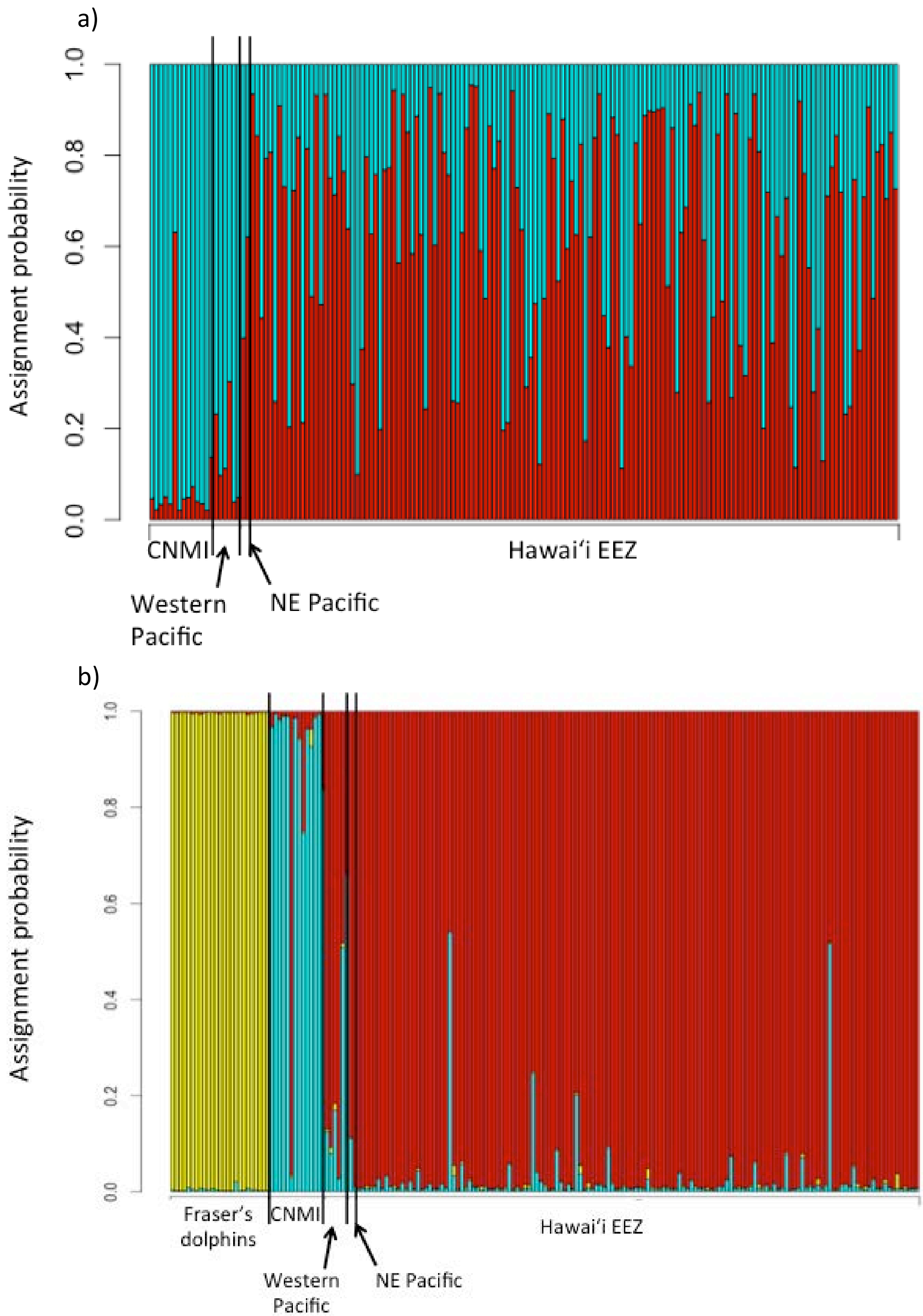


Figure 2. Graphical representation of STRUCTURE results. Each vertical bar represents an individual and is shaded as to the proportion of the individual's ancestry that is attributable to each of the groups defined by STRUCTURE. When only bottlenose dolphins were included in the analysis (a), the model with two groups was favored, while when both bottlenose and Fraser's dolphins were included (b), the model with three groups was favored.

When we used the USERPOPINFO option to look for evidence of recent hybrid ancestry among the CNMI samples, we found that, on average, 5.7% of the nucDNA ancestry of the CNMI samples was derived from Fraser's dolphins. The percent of Fraser's dolphin ancestry increased to 16.1% when we did not use an uninformative prior as to the species origin of the CNMI samples. In contrast, all other bottlenose dolphin samples and Fraser's dolphin samples were estimated to have received, on average, over 99% of their nucDNA ancestry from bottlenose dolphins and Fraser's dolphins, respectively. When the species origin of the CNMI animals was treated as unknown, all but two were estimated to have obtained more than 5% of their nucDNA ancestry from Fraser's dolphins (Table 6).

Table 6. Summary of STRUCTURE results for the CNMI samples.

| | | | % ancestry from | |
|---|---|---|---|---|
| Sample # | Sex | Haplotype | Fraser's | Bottlenose |
| 104035 | M | 32 | 0.062 | 0.938 |
| 104066 | F | Lh11 | 0.079 | 0.921 |
| 104067 | M | 34 | 0.187 | 0.813 |
| 104070 | M | 32 | 0.041 | 0.959 |
| 108172 | M | 32 | 0.128 | 0.872 |
| 108183 | M | 39 | 0.064 | 0.936 |
| 108207 | F | Lh11 | 0.147 | 0.853 |
| 108208 | F | Lh11 | 0.255 | 0.745 |
| 116858 | F | 32 | 0.103 | 0.897 |
| 116866 | M | 32 | 0.077 | 0.923 |
| 116867 | M | Lh11 | 0.526 | 0.474 |
| 116868 | M | Lh11 | 0.317 | 0.683 |
| 116869 | M | 32 | 0.238 | 0.762 |
| 116881 | M | 33 | 0.028 | 0.972 |

## Discussion

Our results indicate that the Fraser's dolphin introgression that Martien et al. (2014b) detected into the mitochondrial genomes of CNMI bottlenose dolphins is also present in their nuclear genomes. Nearly all of the CNMI animals, including those with bottlenose dolphin haplotypes, show greater than 5% Fraser's ancestry, with some individuals showing as much as 50% Fraser's ancestry. This result is consistent with either ongoing hybridization or a hybridization event that occurred enough generations in the past to allow the Fraser's dolphin alleles to spread throughout the population.

Though we cannot distinguish between past versus ongoing hybridization based on the nuclear DNA results, the pattern of mitochondrial introgression and photographic data suggest that past hybridization is more likely. Mitochondrial introgression can only occur if a female Fraser's dolphin mates with a male bottlenose dolphin and the resulting offspring then recruits into the paternal bottlenose dolphin population. This is a low probability event that is unlikely to have happened multiple times. Furthermore, given the relatively high haplotypic diversity we detected in the Fraser's dolphin data set, we would expect to detect more than one Fraser's dolphin haplotype in the CNMI animals if hybridization were ongoing. However, only one haplotype (LH11) was detected, and no Fraser's dolphin haplotypes were found in the other strata. Finally, photographs taken at the time of biopsy show that all individuals, regardless of haplotype, appear to be morphologically normal bottlenose dolphins (Martien et al. 2014b), reducing the likelihood that any are first generation hybrids. Thus, the mitochondrial and photographic data suggest that the widespread nuclear introgression we detected is due to a past hybridization event.

Because the Fraser's dolphin haplotype that we detected in the CNMI animals is identical to haplotypes found in Fraser's dolphins from both Hawai'i and the Philippines, it is not possible to estimate at what point in the past hybridization occurred. It is possible that sequencing the full mitochondrial genome or multiple nuclear genes from Fraser's dolphins and the CNMI animals would reveal mutations unique to the CNMI animals, in which case dating of the hybridization event might be possible. Full mitogenome sequences would also be helpful in pinpointing the Fraser's dolphin source population for the hybridization.

We did not detect Fraser's dolphins in any of the bottlenose dolphin samples from elsewhere in the western Pacific. Furthermore, we were unable to confirm the accuracy of the online genetic data suggesting that two bottlenose dolphins stranded in China possessed the same Fraser's dolphin haplotype detected in the CNMI bottlenose dolphins. It is possible that these represent Fraser's dolphins that were simply mis-identified as bottlenose dolphins. Thus, at this time the hybridization of bottlenose and Fraser's dolphins is not known to extend beyond the Mariana Islands.

The low genetic diversity of the CNMI population in both the mitochondrial and nuclear data sets indicate that it is a small population that does not receive substantial gene flow from neighboring populations. Haplotypic ($h$) and nucleotide ($\pi$) diversity among the CNMI samples is considerably lower than it is among island-associated populations around the main Hawaiian Islands ($h$ = 0.0779-0.892, $\pi$ = 0.018-0.022; Martien et al. 2012), indicating that the CNMI population is either considerably smaller or more genetically isolated than the Hawaiian populations. Thus, the data suggest that the CNMI animals represent an island-associated population with limited gene flow with offshore populations, though samples from the offshore waters near the Mariana Islands are needed to confirm this conclusion.

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# Appendix II: Mitogenome phylogeography of short-finned pilot whales in the North Pacific, with reference to the Mariana Islands

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## Abstract

Short finned pilot whales (SFPW) are a globally distributed temperate and tropical species. At least two morphotypes have been described in the western Pacific, and recent genetic analysis based on the mitochondrial control region indicates that those two types may be geographically segregated. Low diversity in the mitochondrial DNA, typical of social odontocetes, has made it difficult to determine the evolutionary significance and patterns of SFPW diversity. We have sequenced complete mitochondrial genomes from 99 SFPWs to infer evolutionary relationships and patterns in the Pacific. Results indicate that there are three major groups in the pilot whale phylogeny, corresponding to the two known morphotypes (called Naisa and Shiho based on original descriptions in Japan), and a third, widely distributed group that spans the range of the other two groups in the Pacific. These results suggest evolutionary divergence of multiple types of pilot whales. Global analysis of mitochondrial genomes and nuclear DNA is needed to determine the extent and patterns of differentiation among these types.

## Introduction

Although short-finned pilot whales (SFPWs) are described as a single species throughout their range, two morphotypes have been described around Japan (Kasuya et al. 1988). Based on their strong morphological and genetic differences, it has been proposed that these morphotypes may constitute separate subspecies. There is also evidence of a possible third morphologically and genetically distinct type around Japan (hereafter referred to as "stock 3"), though this evidence is weaker (Kasuya et al. 1988, Oremus et al. 2009). Although it has been suggested that the Japanese morphotypes have distributions corresponding to different habitats in the Pacific (e.g., different water temperature; Kasuya et al. 1988), little is known about the actual distributions because we have little data on morphology across the Pacific. It has been proposed that that the control region haplotypes may be diagnostic of the morphotypes (Oremus et al. 2009). Diagnosability cannot be fully tested, as we do not have morphological data from most specimens, but has been shown to be true for a subset of the samples near Japan. If the control region haplotypes are diagnostic, we can infer the distribution of morphotypes based on DNA sequences. Genetic data from pilot whales outside of Japan can be used as a proxy to infer the distributions of morphotypes based on unique mitochondrial DNA haplotypes identified in the animals of known morphotype.

Mitochondrial DNA (mtDNA) sequence data from all SFPWs collected in the Mariana Islands have been previously analyzed to investigate population structure of SFPWs in the Marianas (Martien et al. 2014).Within the Marianas, there was evidence of genetic differentiation between island groups, though this may reflect familial or social structure rather than population level differentiation. A majority of the Mariana Islands samples had haplotypes (A1, A2) previously found to be common in the South Pacific, Indian and Atlantic Oceans, though two samples had haplotypes similar to that identified in the Japanese "stock 3", which is intermediate to the Naisa and Shiho types and more similar to samples from the Atlantic and Indian Oceans (Oremus et al. 2009, Martien et al. 2014). A subset of the Mariana Islands samples were incorporated into a study aimed at determining the global distribution of the types described in Japan (Van Cise et al. Submitted). This latter study has revealed that the Shiho type is restricted to northern Japan and the eastern Pacific, while the Naisa type occurs in Hawaiʻi and the western and South Pacific, in addition to southern Japan.

However, the low genetic diversity in SFPWs is limiting our ability to resolve the relationships between these haplotypes and groups based on control region sequence alone. Phylogenetic relationships of unique control region haplotypes cannot be confidently determined with these short sequences. Some common haplotypes are widespread, suggesting genetic continuity, but this could be simply due to lack of diversity in the short control region. Previous studies have shown that globally common control region haplotypes in killer whales resolved to phylogenetically and geographically distinct ecotypes (and potentially subspecies or species) when longer DNA sequences were used (Morin et al. 2010). To improve our resolving power for SPFWs, we have sequenced the full mitochondrial genome of 99 SFPWs from across the Pacific and into the Indian Ocean in order to further examine the SFPW phylogeography and taxonomy.

**Methods**

Tissue samples were obtained from stranded dead animals and by remote biopsy of free-swimming short-finned pilot whales from locations across the Pacific Ocean and in the Indian Ocean, and stored in the Southwest Fisheries Science Center (SWFSC) tissue collection, either frozen at -80°C without preservative, or preserved in 20% DMSO saturated with NaCl, or in ethanol. DNA was extracted from tissue samples using either a silica-membrane method (Qiaxtractor® DX reagents, Qiagen, Valencia, CA, USA), or a simple salt-precipitation procedure (Miller et al. 1988). Detailed sample information is in Table 1, and sample locations are shown in Figure 1.

Mitogenome sequences were sequenced using multiplexed DNA libraries for capture enrichment and next-generation sequencing as described by Hancock-Hanser et al. (2013), using a previously published short-finned pilot whale mitogenome sequence (Accession No. HM060333; Morin et al. 2010) to design the capture-enrichment microarray. After capture enrichment, libraries were amplified and sequenced using single-end 100 base-pair (bp) sequencing on an Illumina HiSeq2000 Analyzer.

Assembly of reads to the reference mitogenome was done using custom scripts (Dryad data repository doi:10.5061/dryad.cv35b) in the R computing environment (R Development Core Team 2011) to iteratively run publicly available analysis packages for quality filtering (FASTX toolkit; http://hannonlab.cshl.edu/fastx_toolkit/), assembly (BWA; Li & Durbin 2009), multiple alignment (MAFFT; Katoh et al. 2005), and SNP detection (GATK; DePristo et al. 2011, Nielsen et al. 2011). The reference mitochondrial sequence (accession HM060333) was modified to improve assembly coverage at the "ends" of the linearized mitogenome by adding 40bp from each end to the opposite end (so that reads could map across the artificial break-point of the linearized sequence). All sequences were aligned and visually inspected in the program Geneious (V. 6.0.5, Biomatters, Auckland, New Zealand), and indels and unique variants were verified in the BAM files. Previously published control region sequences were aligned to the mitogenome sequences to identify the mitogenome haplotypes that contained previously known control region haplotype sequences.

We used the Bayesian phylogenetic approach implemented in BEAST 2 (Bouckaert et al. 2014) to estimate the tree based on the full, unpartitioned mitogenome sequences for 58 unique haplotypes identified from the 99 samples plus two previously published sequences (Morin et al. 2010, Vilstrup et al. 2011). We used a coalescent prior for the tree, with a strict clock. Posterior distributions of parameters were estimated using Markov chain Monte Carlo simulation, with samples drawn every $10^3$ steps over a total of $10^7$ steps. The first 10% of samples were discarded as burn-in, with the remaining samples checked for acceptable convergence and mixing. We used the program PopArt (http://popart.otago.ac.nz) to generate a median joining network (MJN; Bandelt et al. 1999) of the haplotypes.

**Results**

We obtained 99 complete mitochondrial genomes from the 101 samples sequenced. There were 56 unique sequences (haplotypes) among our new sequences, and two haplotypes from two previously published short-finned pilot whale mitogenomes (Morin et al. 2010, Vilstrup et al. 2011). Phylogenetic analysis of the 58 haplotypes yielded the unrooted phylogenetic tree shown in Figure 2. The median joining network is shown in Figure 3, with haplotype nodes colored to indicate whether the haplotypes contained the control region sequences previously identified for each of the three putative types of SFPW's (Oremus et al. 2009, Van Cise et al. Submitted).

**Discussion**

Although about 40% of all mitogenome haplotypes in this study did not contain control region sequences that have previously been found in morphologically identified Japanese morphotypes, the phylogenetic tree indicates that there are three major clades that correspond to the three described types, and that the geographic range of each is limited but overlapping with at least one of the other types. Clade 1 corresponds to the Naisa type in the central and western Pacific. Clade 2 contains all samples of the poorly known “stock 3”, but also closely related haplotypes that span the Pacific. Little is known about “stock 3”, but the wide geographical distribution of related haplotypes suggests that these could represent a widely distributed pelagic type that is separate from the two described morphotypes. Clade 3 corresponds closely to the Shiho type in the eastern Pacific and North Japan.

The distributions of mitogenome haplotypes (Figure 1a-b) for the three morphotypes or stocks of SFPW’s are consistent with the distributions of control region haplotypes described previously (Oremus et al. 2009, Van Cise et al. Submitted). Figure 1c-d uses the relationships inferred from the complete mitochondrial phylogeny to show the distribution of haplotypes from each of the 3 clades. Based on the mitogenome clade distributions, we confirm that the clade containing the Shiho type was found only in the eastern Pacific, and the clade containing Naisa type was found in Hawaiʻi, the western/southern Pacific, and the Indian Ocean. The three mitogenome haplotypes that contained the single control region sequence previously found in the putative “stock 3” from offshore southern Japan were found in the Mariana Islands, Samoa, and New Zealand. The clade containing this “stock 3” type was found across the tropical Pacific and in New Zealand. While we know little about this putative stock, it appears that it may be limited to the western and southern Pacific. The Mariana Islands fall within the geographic ranges of both the Naisa type (Van Cise et al. Submitted) and the putative “stock 3” from southern Japan (Clade 2, Figure 1d), and had a diverse set of haplotypes that were unique to these samples (i.e., not found anywhere else), but that were phylogenetically linked to others in both clades 1 and 2 (Figure 2).

In order to determine whether the mitochondrial genome phylogeny clades represent genetically distinct ecotypes or subspecies of SFPWs in the Pacific, further work is needed to expand the sampling of SFPWs globally, and to match haplotypes to morphologically identified whales. Additional analysis of the phylogenetic tree using sequences from other cetaceans could also be used to estimate the approximate time of divergence between these three groups.

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MMPA permit 14097 issued to the SWFSC and CNMI-DFW permit, license no. 02260-11 (2011 samples); NMFS MMPA permit 15240 issued to PIFSC and CNMI-DFW permit, license nos. 02444-12 and 02694-13 (2012 and 2013 samples).

## Figures and Tables

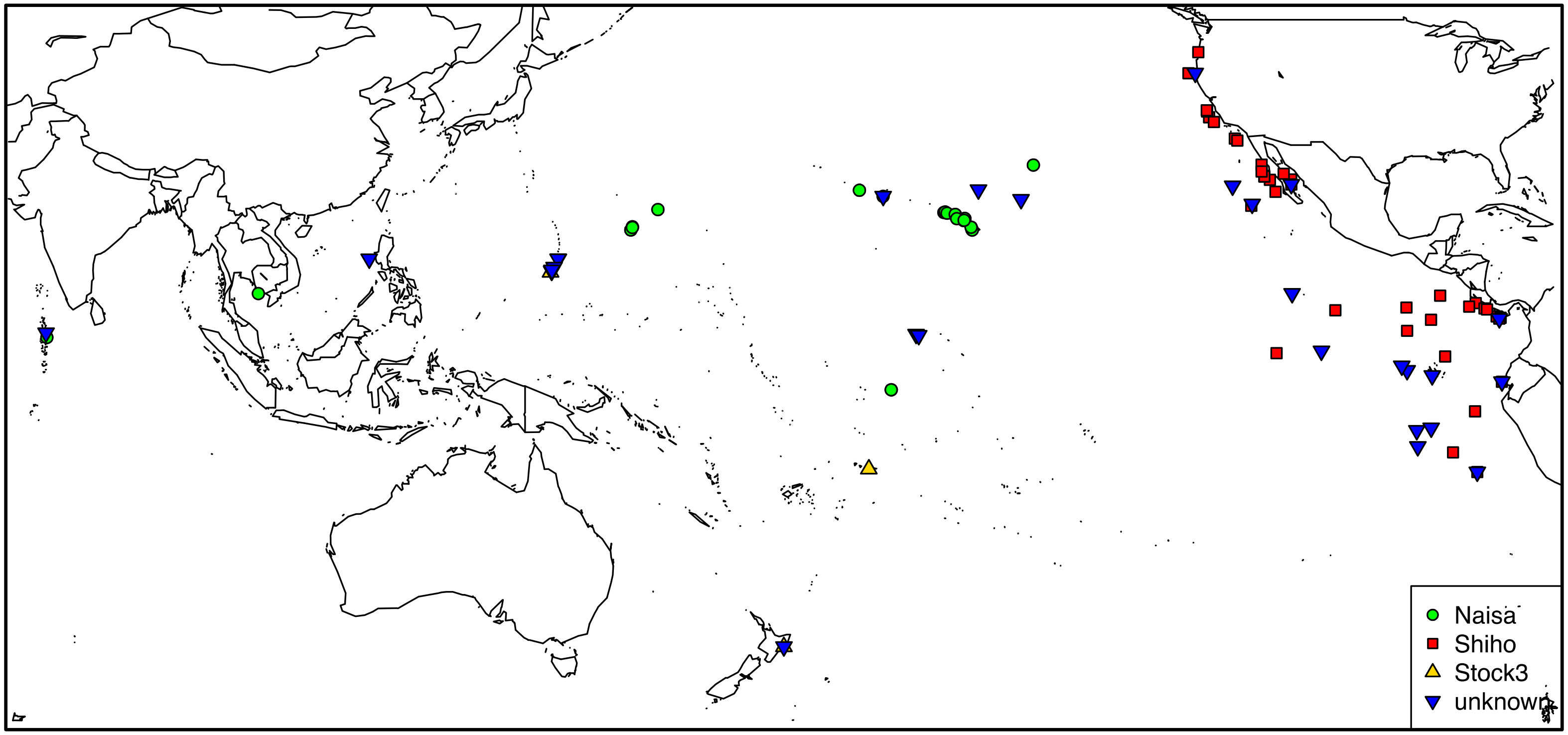
**Table 1.** Sample information

| SWFSC ID | haplotype | Broad strata | Fine strata | Long CR haplotype | Short Standard Haplotype | Type | phylogeny clade |
|---|---|---|---|---|---|---|---|
| 1297 | mtGen02 | NPAC | CALIFORNIA | E3 | E1 | Shiho | 3 |
| 1685 | mtGen02 | NPAC | CALIFORNIA | E3 | E1 | Shiho | 3 |
| 1739 | mtGen14 | NPAC | CALIFORNIA | 19 | E1 | unknown | 3 |
| 1864 | mtGen04 | NPAC | CALIFORNIA | E3 | E1 | Shiho | 3 |
| 4629 | mtGen15 | ETP | GULF OF CALIFORNIA | E3 | E1 | Shiho | 3 |
| 4642 | mtGen04 | ETP | GULF OF CALIFORNIA | E3 | E1 | Shiho | 3 |
| 4682 | mtGen16 | ETP | GULF OF CALIFORNIA | 9 | 9 | unknown | 3 |
| 4683 | mtGen02 | ETP | MEXICO IFS | E3 | E1 | Shiho | 3 |
| 4694 | mtGen02 | NPAC | CALIFORNIA | E3 | E1 | Shiho | 3 |
| 4986 | mtGen02 | NPAC | NPAC IFS | E3 | E1 | Shiho | 3 |
| 5766 | mtGen02 | NPAC | CALIFORNIA | E3 | E1 | Shiho | 3 |
| 7618 | mtGen04 | ETP | BAJA | E3 | E1 | Shiho | 3 |
| 8752 | mtGen02 | NPAC | CALIFORNIA | E3 | E1 | Shiho | 3 |
| 9850 | mtGen17 | INDIA | INDIA | A1 | A1 | unknown | 1 |
| 9871 | mtGen18 | INDIA | INDIA | K | K | Naisa | 1 |
| 11454 | mtGen19 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 11496 | mtGen20 | ETP | ETP IFS | 2 | 2 | unknown | 2 |
| 11515 | mtGen21 | ETP | BAJA | E3 | E1 | Shiho | 3 |
| 11526 | mtGen02 | ETP | BAJA | E3 | E1 | Shiho | 3 |
| 11873 | mtGen22 | ETP | EL SALVADOR | E3 | E1 | Shiho | 3 |
| 11943 | mtGen05 | ETP | COSTA RICA | E3 | E1 | Shiho | 3 |
| 11954 | mtGen06 | ETP | PANAMA | E3 | E1 | Shiho | 3 |
| 11977 | mtGen23 | ETP | CLIPPERTON IS. | 5 | 5 | unknown | 3 |
| 11985 | mtGen24 | ETP | ECUADOR | 2 | 2 | unknown | 2 |
| 12009 | mtGen25 | ETP | ECUADOR | 6 | 6 | unknown | 3 |
| 12029 | mtGen26 | ETP | ECUADOR | E3 | E1 | Shiho | 3 |
| 12030 | mtGen07 | ETP | ECUADOR | 7 | 7 | unknown | 3 |
| 12095 | mtGen02 | ETP | PANAMA | E3 | E1 | Shiho | 3 |
| 13367 | mtGen27 | PHILLIPINES | PHILLIPINES | 14 | 14 | unknown | 1 |
| 16047 | mtGen08 | ETP | COSTA RICA | E3 | E1 | Shiho | 3 |
| 16079 | mtGen28 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 16167 | mtGen06 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 17977 | mtGen02 | ETP | BAJA | E3 | E1 | Shiho | 3 |
| 17981 | mtGen29 | ETP | BAJA | E2 | E1 | Shiho | 3 |
| 18191 | mtGen02 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 18261 | mtGen08 | ETP | COSTA RICA | E3 | E1 | Shiho | 3 |
| 18293 | mtGen30 | ETP | PANAMA | E3 | E1 | Shiho | 3 |
| 18298 | mtGen31 | ETP | PANAMA | 2 | 2 | unknown | 2 |
| 18941 | mtGen01 | HI | LANAI | J | J | Naisa | 1 |
| 18953 | mtGen01 | HI | LANAI | J | J | Naisa | 1 |
| 23968 | mtGen32 | CAMBODIA | CAMBODIA | K | K | Naisa | 1 |
| 25546 | mtGen02 | NPAC | OREGON | E3 | E1 | Shiho | 3 |
| 30435 | mtGen33 | HI | NWHI | J | J | Naisa | 1 |
| 30439 | mtGen01 | HI | NWHI | J | J | Naisa | 1 |
| 30442 | mtGen34 | HI | NWHI | 12 | 12 | unknown | 1 |
| 30535 | mtGen35 | HI_IFS | HI IFS | 11 | 11 | unknown | 2 |
| 33294 | mtGen36 | NEW ZEALAND | NEW ZEALAND | A1 | A1 | unknown | 1 |
| 33295 | mtGen37 | NEW ZEALAND | NEW ZEALAND | C | C | Stock3 | 2 |
| 33798 | mtGen01 | HI | LANAI | J | J | Naisa | 1 |
| 33813 | mtGen38 | HI | LANAI | J | J | Naisa | 1 |
| 33814 | mtGen09 | HI | LANAI | J | J | Naisa | 1 |
| 33851 | mtGen01 | HI | OAHU | J | J | Naisa | 1 |
| 33852 | mtGen01 | HI |  | J |  | Naisa | 1 |

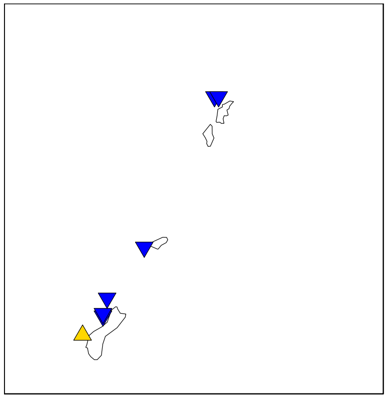
| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 33861 | mtGen03 | HI | OAHU | J | J | Naisa | 1 |
| 33879 | mtGen03 | HI | OAHU | J | J | Naisa | 1 |
| 33916 | mtGen01 | HI | OAHU | J | J | Naisa | 1 |
| 33941 | mtGen01 | HI | | J | | Naisa | 1 |
| 33981 | mtGen03 | HI | KAUAI | J | J | Naisa | 1 |
| 37746 | mtGen02 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 37752 | mtGen39 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 37753 | mtGen40 | ETP | ECUADOR | E3 | E1 | Shiho | 3 |
| 37766 | mtGen41 | ETP | ETP IFS | 10 | 10 | unknown | 3 |
| 37772 | mtGen42 | ETP | ETP IFS | 2 | 2 | unknown | 2 |
| 37781 | mtGen43 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 37783 | mtGen44 | ETP | ETP IFS | 8 | 8 | unknown | 3 |
| 37788 | mtGen45 | ETP | ETP IFS | E3 | E1 | Shiho | 3 |
| 37884 | mtGen05 | ETP | COSTA RICA | E3 | E1 | Shiho | 3 |
| 37896 | mtGen46 | ETP | MEXICO IFS | 3 | 3 | unknown | 2 |
| 37907 | mtGen02 | ETP | BAJA | E3 | E1 | Shiho | 3 |
| 38312 | mtGen47 | ETP | MEXICO IFS | E1 | E1 | Shiho | 3 |
| 38314 | mtGen48 | ETP | MEXICO IFS | 2 | 2 | unknown | 2 |
| 45934 | mtGen01 | HI | | J | | Naisa | 1 |
| 49063 | mtGen49 | KIRIBATI | KIRIBATI | 2 | | unknown | 2 |
| 49070 | mtGen50 | KIRIBATI | KIRIBATI | 20 | | unknown | 1 |
| 51029 | mtGen01 | HI | | J | | Naisa | 1 |
| 55234 | mtGen01 | HI | | J | | Naisa | 1 |
| 55239 | mtGen01 | HI | | J | | Naisa | 1 |
| 67152* | mtGen12 | ETP | ETP IFS | 10 | 10 | unknown | 3 |
| 67165* | mtGen13 | ETP | ETP IFS | 10 | 10 | unknown | 3 |
| 74708 | mtGen51 | HI_IFS | HI IFS | K | K | Naisa | 1 |
| 78786 | mtGen52 | KIRIBATI | KIRIBATI | K | | Naisa | 1 |
| 78787 | mtGen53 | KIRIBATI | KIRIBATI | K | K | Naisa | 1 |
| 79766 | mtGen54 | SAMOA | SAMOA | C | C | Stock3 | 2 |
| 79992 | mtGen01 | HI | | J | | Naisa | 1 |
| 88594 | mtGen03 | HI | | J | | Naisa | 1 |
| 92242 | mtGen09 | HI | | J | | Naisa | 1 |
| 102494 | mtGen01 | HI | | J | | Naisa | 1 |
| 104024 | mtGen10 | MARIANA_Is. | CNMI | A2 | | unknown | 1 |
| 104027 | mtGen10 | MARIANA_Is. | CNMI | A2 | A1 | unknown | 1 |
| 104051 | mtGen55 | MARIANA_Is. | CNMI | 18 | | unknown | 2 |
| 104055 | mtGen11 | MARIANA_Is. | CNMI | A1 | | unknown | 1 |
| 104078 | mtGen11 | MARIANA_Is. | CNMI | A1 | | unknown | 1 |
| 108166 | mtGen56 | MARIANA_Is. | CNMI | 17 | | unknown | 1 |
| 112652 | mtGen01 | HI | | J | | Naisa | 1 |
| 112653 | mtGen01 | HI | | J | | Naisa | 1 |
| 113653 | mtGen01 | HI | | J | | Naisa | 1 |
| 114348 | mtGen57 | HI_IFS | HI_IFS | 2 | | unknown | 2 |
| 114352 | mtGen01 | HI | | J | | Naisa | 1 |
| 114354 | mtGen01 | HI | | J | | Naisa | 1 |
| 114565 | mtGen03 | HI | | J | | Naisa | 1 |
| 116839 | mtGen58 | MARIANA_Is. | CNMI | C | | Stock3 | 2 |

* previously published, (Morin et al. 2010, Vilstrup et al. 2011)

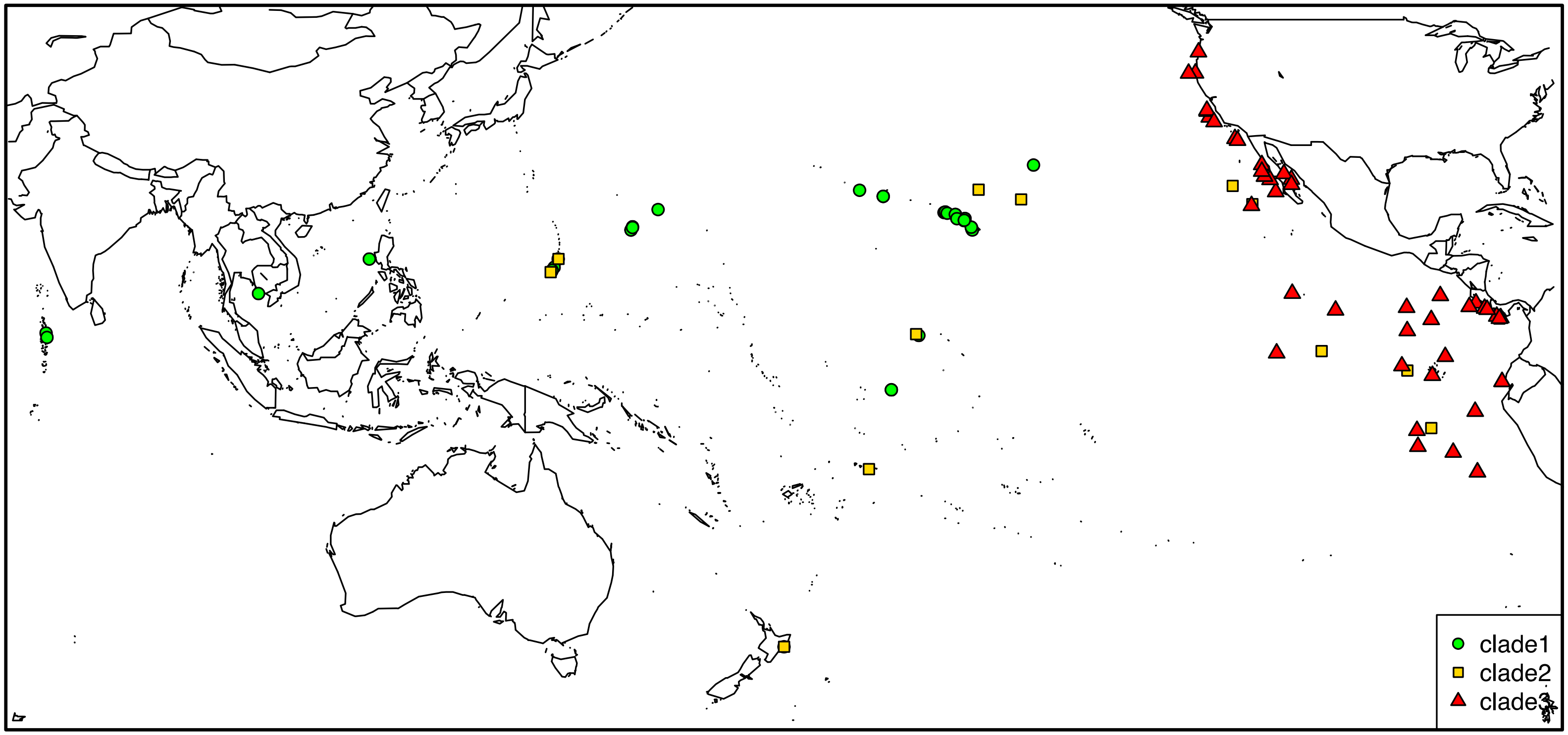
**Figure 1a**. Sample locations and types. The color indicates whether the haplotype contains the control region sequences previously identified by Oremus et al. (2009) as being found in the northern Japan ("Shiho", Red), southern Japan ("Naisa", Green), or putative third southern (stock 3) stocks (putatively containing Control Region haplotype C, Yellow). Blue triangles = haplotypes not previously identified from one of the types or stocks.




**1b**. Samples from the Mariana Islands. Symbols and colors identify types as in 1a.



1c. Samples showing samples colored by clades from the phylogenetic tree (Fig. 2).




1d. Samples from the Mariana Islands. Symbols and colors identify types as in 1c.

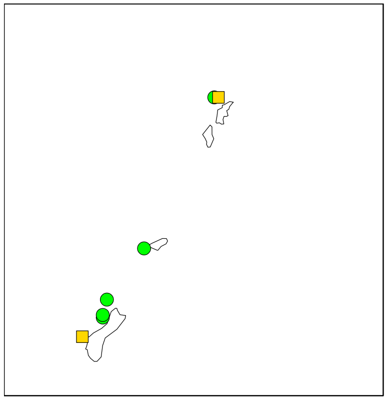


**Figure 2**. Phylogenetic tree of 58 mitogenome haplotypes. Colors are as described in Figure 1a.

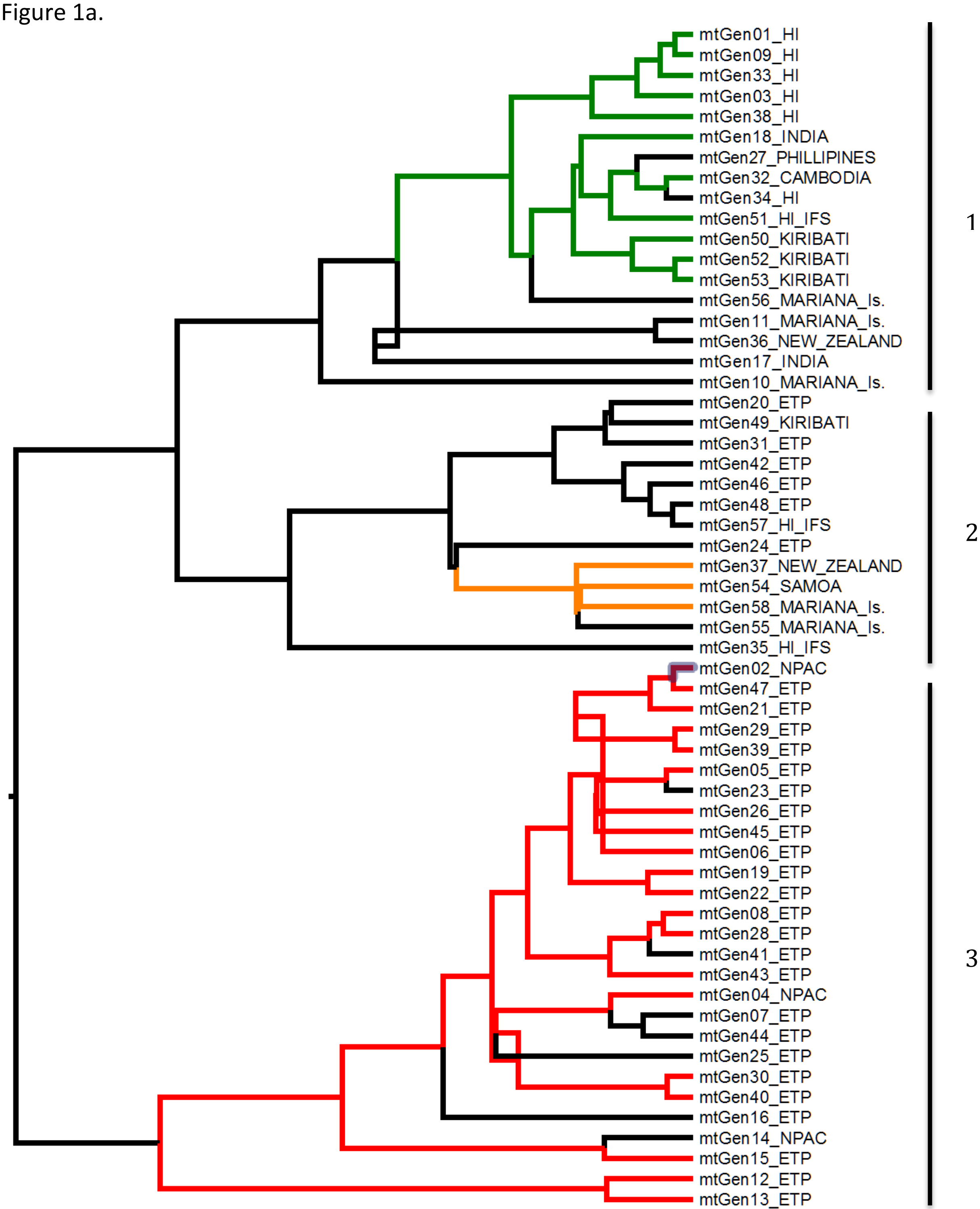
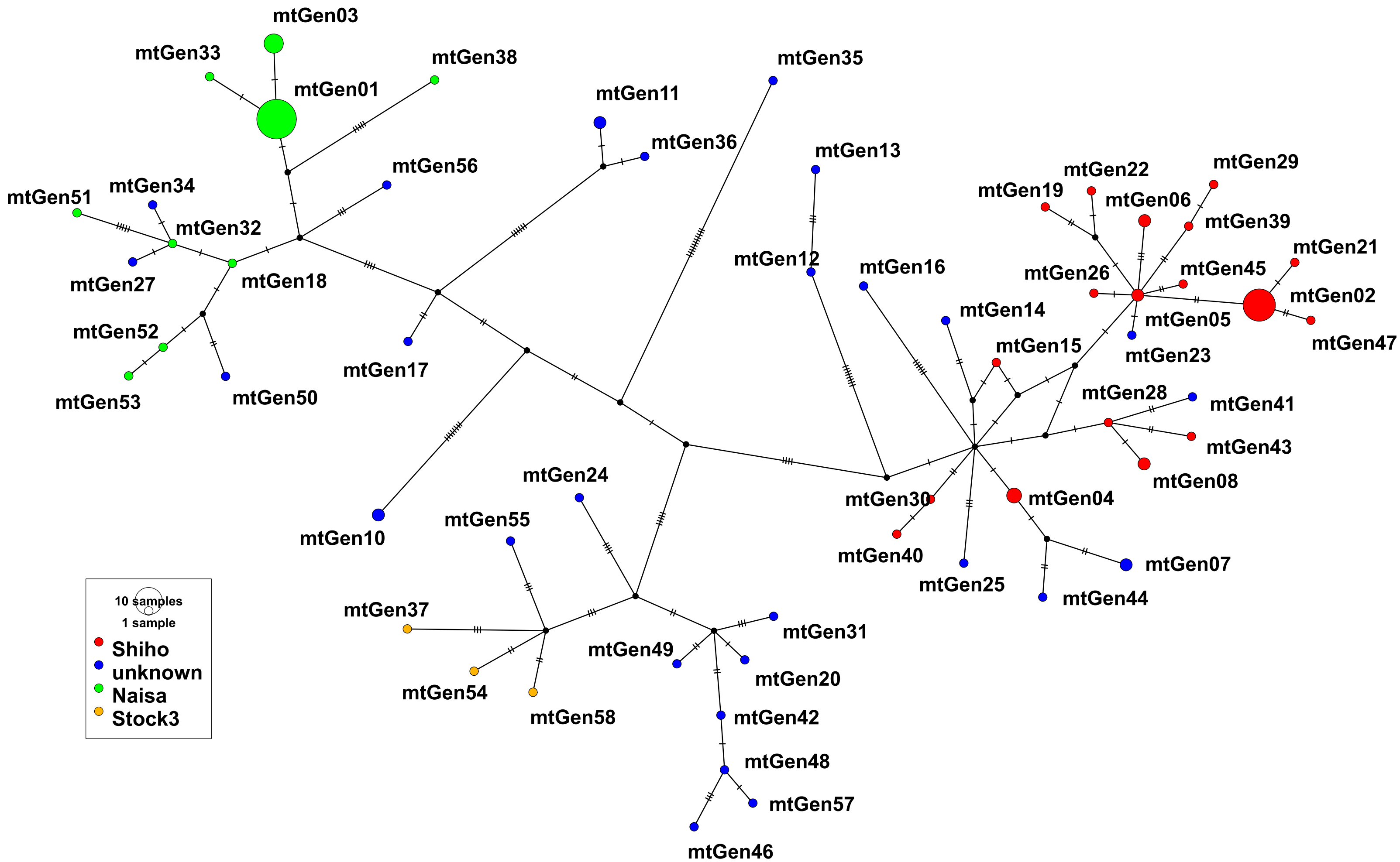


**Figure 3**. Median joining network of mitogenome haplotypes. The size of the circle is proportional to the number of samples with that haplotype. Colors are as described as in Figure 1a.



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