A list of MMTD publications is available through our online database. For more recent publications that may not be available yet in the database, please see below.

**Week of 5 November 2018**


*Abstract* – Recent exploration into the interactions and relationship between hosts and their microbiota has revealed a connection between many aspects of the host's biology, health and associated micro-organisms. Whereas amplicon sequencing has traditionally been used to characterize the microbiome, the increasing number of published population genomics data sets offers an underexploited opportunity to study microbial profiles from the host shotgun sequencing data. Here, we use sequence data originally generated from killer whale *Orcinus* orca skin biopsies for population genomics, to characterize the skin microbiome and investigate how host social and geographical factors influence the microbial community composition. Having identified 845 microbial taxa from 2.4 million reads that did not map to the killer whale reference genome, we found that both ecotypic and geographical factors influence community composition of killer whale skin microorganisms. Furthermore, we uncovered key taxa that drive the microbiome community composition and showed that they are embedded in unique networks, one of which is tentatively linked to diatom presence and poor skin condition. Community composition differed between Antarctic killer whales with and without diatom coverage, suggesting that the previously reported episodic migrations of Antarctic killer whales to warmer waters associated with skin turnover may control the effects of potentially pathogenic bacteria such as *Tenacibaculum dicentrarchi*. Our work demonstrates the feasibility of microbiome studies from host shotgun sequencing data and highlights the importance of metagenomics in understanding the relationship between host and microbial ecology.

**Week of 22 October 2018**

*Whale Photo-identification Guide* - developed by Jessica Taylor, Paula Olson, Jessica Fitzpatrick, Gianna Minton, and Jennifer Jackson with funding from the International Whaling Commission/Southern Ocean Research Partnership. This concise guide illustrating the photo-identification features for six species of whales (blue, fin, sei, humpback, right, and killer) was developed for distribution to naturalists and citizen scientists in the Antarctic region. Although focused on Southern Hemisphere populations, the guide is applicable for photo-ID efforts of these whales throughout their geographic ranges. Confirmed sightings in the Antarctic and sub-Antarctic will be incorporated into a global web-based photo-identification platform via happywhale.com. Images will be forwarded to relevant catalog curators and photographers will be informed of matches made from contributed images. Print and electronic versions are available at: [https://iwc.int/sorp](https://iwc.int/sorp). For more information contact Paula.Olson@noaa.gov.

**Week of 8 October 2018**


*Abstract*: Sea turtle research has received substantial focus worldwide. However, a larger proportion of research has focused on adults and the terrestrial life stages, while less attention has been given to the immature life stages. The latter is of particular importance, given that a large proportion of sea turtle populations comprises...
immature individuals. We set to identify the most important knowledge gaps in immature sea turtle research, and identify the main barriers hindering research in this field. We analyzed the perceptions of sea turtle experts through an online survey which gathered their opinion on the current state of knowledge of immature sea turtle research, including species and regions in need of further study, priority research questions, and barriers that have interfered with the advancement of research. Based on our gap analysis, a particular emphasis should be placed on future studies on immature individuals of the leatherback Dermochelys coriacea and hawksbill Eretmochelys imbricata turtles, and studies on all species based in the Indian, South Pacific and South Atlantic Oceans. Experts also perceived that studies in population ecology, namely survivorship and demographic studies, and habitat use and behavior, are needed to advance the state of knowledge of immature sea turtles. Our survey findings indicate the need for more inter-disciplinary research, collaborative efforts (e.g., data-sharing, joint field activities), improved communication among researchers, funding bodies, stakeholders, and decision-makers on the importance of supporting research on immature sea turtles.

**Week of 24 September 2018**


*No abstract*

**Week of 10 September 2018**


*No abstract*


*Abstract* — During their migrations, marine predators experience varying levels of protection and face many threats as they travel through multiple countries’ jurisdictions and across ocean basins. Some populations are declining rapidly. Contributing to such declines is a failure of some international agreements to ensure effective cooperation by the stakeholders responsible for managing species throughout their ranges, including in the high seas, a global commons. Here we use biologging data from marine predators to provide quantitative measures with great potential to inform local, national and international management efforts in the Pacific Ocean. We synthesized a large tracking data set to show how the movements and migratory phenology of 1,648 individuals representing 14 species—from leatherback turtles to white sharks—relate to the geopolitical boundaries of the Pacific Ocean throughout species’ annual cycles. Cumulatively, these species visited 86% of Pacific Ocean countries and some spent three-quarters of their annual cycles in the high seas. With our results, we offer answers to questions posed when designing international strategies for managing migratory species.

**Week of 13 August 2018**


**Week of 30 July 2018**

Abstract – Species’ foraging choices influence their somatic growth rates, age at maturity, and time spent in vulnerable early life stages. Thus, differences in population demographics are often attributed to variability either in diet type, quality, and/or quantity ingested. Knowledge of diet selection, though currently limited, can enhance our understanding of the roles of marine turtles in marine ecosystems and, at a finer scale, elucidate how nutrition and diet influence their growth and productivity. To investigate this relationship, we combined stable isotope analysis with a diet preference index to provide insights into the selection and plasticity of juvenile green turtle Chelonia mydas diet. The study was conducted at 2 sites (Bonefish Hole and South Bimini) in Bimini, Bahamas, in 2016. Habitat surveys were conducted to gather habitat data and determine resource availability. A dichotomy in diet was found between the sites: at Bonefish Hole, turtles exhibited a more generalist omnivorous diet, selecting for sessile filter feeders and green algae, whereas turtles in South Bimini had a more specialist herbivorous diet, primarily consuming seagrasses and selecting for red algae, when available. The foraging dichotomy found in this study expands our understanding of the spatial differences in green turtle biology in the Bahamas and provides novel information for turtle foraging in Bimini. Knowledge about differences in intra-specific diet, with a focus on diet selection and potential drivers, can shed light on the factors that influence critical life history traits and ultimately inform species management.


Abstract – Western gray whales (WGWs) are endangered and their range overlaps areas where several important commercial fisheries operate in the Russian Far East (RFE). Throughout their range, gray whales commonly become entangled or entrapped in fishing gear. In the western North Pacific, they have been killed in set nets and seen entangled with ropes and float lines. Signs of fishery interactions on 28 of 150 living whales photographed near Sakhalin Island were reported in a published study. We describe characteristics of RFE fisheries that might entangle WGWs, including fishing effort based on daily catch reports from 2010–2014. We make a preliminary qualitative assessment of entanglement risk taking into account factors including (1) evidence that the gear type has entangled large whales, (2) fishing effort, and (3) geographic and temporal overlap between WGWs and fishing activity. Fishing for salmonids with pelagic gillnets is no longer allowed in the RFE, and as long as the prohibition is being followed such fishing poses no risk to WGWs. In contrast, the coastal salmon set net fishery poses a high entanglement risk off northeastern Sakhalin and Kamchatka where WGWs feed very close to shore, and that situation should be mitigated. Bottom-set gillnet, demersal longline, snurrewad, and trap and pot fisheries overlap substantially with WGW distribution, and bycatch in those fisheries should at least be monitored. More rigorous risk assessment would require additional information on WGW distribution and movements.


Abstract – Habitat-based distribution modelling is an established method for predicting species distributions and is necessary for many conservation and management applications. Cetacean habitat models have primarily been developed using data from visual surveys. However, numerous techniques exist for detecting animal presence and each capture a portion of the true population. Combining detection data gathered from multiple survey methods, such as visual and acoustic surveys, may lead to a more robust picture of a species distribution and ecology. We compare habitat models for Dall’s porpoise built with visual versus acoustic survey data from a line-transect survey in the California Current and develop a combined model, utilizing both acoustic detections and visual sightings. Combining acoustic and visual detections increases sample size and allows for detections under a greater range of oceanographic conditions. Consequently, the combined model shows a modest expansion of predicted distribution of Dall’s porpoise compared to either single-source model. However, this study reveals that acoustic and visual methods appear to be more complementary, rather than directly additive. Models built with acoustic data display differences from those built with visual data. Different predictor variables were selected across models and the acoustic model predicts a distribution shifted slightly south of the visual distribution. Results from the current study show promise for incorporating acoustics into
habitat models but also identify discrepancies in population sampling between these two methods that should inform future population assessments and modelling efforts.

Week of 16 July 2018


Week of 2 July 2018


Abstract – This short note presents evidence for geographic concordance in phenotype with the genotype of eastern tropical Pacific (ETP) short-finned pilot whales (SFPWs). The phenotypic evidence is provided by body length data obtained from vertical aerial photographs taken during NOAA's SWFSC research cruises conducted in the ETP between 1988 and 2003. These data in combination with a review of the published literature allowed us to refine the known distribution of the two morphologically distinct forms of SFPW in the Pacific Ocean and to propose a boundary between the two. Additionally, this study provides additional clues to the evolutionary processes influencing SFPWs, including the role of potential barriers limiting animal movements (e.g. ocean current boundaries, glacial periods) and support for the hypothesis that the northern and southern forms of SFPWs are likely different subspecies.

Week of 25 June 2018


Abstract – Understanding drivers of ecosystem structure and function is a pervasive goal in academic and applied research. We used 24 synthetic ecosystem-level indices derived from trophic models, and independently derived data for Net Primary Productivity, to investigate drivers of ecosystem structure and function for 43 marine ecosystems distributed in all oceans of the world and including coastal, estuaries, mid-ocean islands, open-ocean, coral reef, continental shelf, and upwelling ecosystems. Of these indices, ecosystem Biomass, Primary Production, Respiration, the ratio of Biomass to Total System Throughput (sum of total energy flow into and out of an ecosystem as well as between ecosystem components), the ratio of Production to Biomass, Residence Time (mean time that a unit of energy remains in the ecosystem), Average Trophic Level, and Relative Ascendency (index of organization and complexity of a food web) displayed relationships with measures of Net Primary Productivity (NPP). Across all ecosystems, relationships were stronger with seasonal and interannual variability of NPP as compared to mean NPP. Both measures of temporal variability were combined into multivariate predictive relationships for each ecosystem index, with r² values ranging from 0.14 to 0.49 and Akaike’s information criteria values from - 8.44 to 3.26. Our results indicate that despite large geographic and environmental differences, temporal variability of NPP is strongly linked to the structure and function of marine ecosystems.


Abstract – Genetic analyses of nuclear DNA (e.g., microsatellites) are a primary tool for investigating mating systems in reptiles, particularly marine turtles. Whereas studies over the past two decades have demonstrated that polyandry (i.e., females mating with multiple males) is common in marine turtles, polygyny (i.e., males mating with multiple females) has rarely been reported. In this study we investigated the mating structure of Critically Endangered hawksbill turtles (Eretmochelys imbricata) at Bahia de Jiquilisco in El Salvador, one of
the largest rookeries in the eastern Pacific Ocean. We collected genetic samples from 34 nesting females and hatchlings from 41 clutches during the 2015 nesting season, including one nest from each of 27 females and two nests from seven additional females. Using six highly polymorphic microsatellite loci, we reconstructed the paternal genotypes for 22 known male turtles and discovered that seven (31.8%) sired nests from multiple females, which represents the highest polygyny level reported to date for marine turtles and suggests that this is a common mating structure for this population. We also detected multiple paternity in four (11.8%) clutches from the 34 females analyzed, confirming polyandrous mating strategies are also employed. Our findings of a high level of polygyny suggest there may be a limited number of sexually mature males at Bahía de Jiquilisco; a scenario supported by multiple lines of empirical evidence. Our findings highlight key management uncertainties, including whether polygynous mating strategies can compensate for potential ongoing feminization and the low number of adult males found at this and possibly other marine turtle populations.

**Week of 18 June 2018**


**Abstract** – Whale entanglements in US west coast fishing gear are largely represented by opportunistic sightings, and some reports lack species identifications due to rough seas, distance from whales, or a lack of cetacean identification expertise. Unidentified entanglements are often ignored in species risk assessments and thus, entanglement risk is underestimated. To address this negative bias, a species identification model was built from random forest (RF) classification trees using 199 identified entanglements (‘model data’). Humpback *Megaptera novaeangliae* and gray whales *Eschrichtius robustus* represented 92% of identified entanglements; the remaining 8% were minke whales *Balaenoptera acutorostrata*, fin whales *B. physalus*, blue whales *B. musculus*, and sperm whales *Physeter macrocephalus*. Predictor variables included year, gear type, location, season, sea surface temperature, water depth, and a multivariate El Niño index. Cross-validated species classifications were correct in 78% (155/199) of cases, significantly higher (p < 0.001, permutation test) than the 49% correct classification rate expected by chance. The RF model correctly classified 91% of humpback whale cases, 64% of gray whale cases, and 100% of sperm whale cases, but misclassified all minke, blue, and fin whale cases. The cross-validated RF classification-tree species model was used to classify 35 entanglements without species identifications (‘novel data’) and each case was assigned a probability of belonging to each of 6 model data species. This approach eliminates the negative bias associated with ignoring unidentified entanglements in species risk assessments. Applications to other wildlife studies where some detections are unidentified include fisheries bycatch, line-transect surveys, and large-whale vessel strikes.

**Week of 4 June 2018**


**Abstract** – Historical and archaeological evidence documents the importation of sea turtles from the eastern Pacific Ocean (Baja California) to California during the Gold Rush (1848–1855) and through the end of 19th century, but it is unknown whether these 19th century sea turtles foraged in similar ways to their modern counterparts. To identify the species of two Gold Rush-era sea turtle specimens recovered from archaeological deposits in San Francisco, California, we first analyze ancient DNA (aDNA). We then analyze carbon (δ13Ccol), nitrogen (δ15N), and hydrogen (δD) stable isotopes of bone collagen and carbon (δ13Cap) and oxygen (δ18Oap) stable isotopes of bone apatite to test if eastern Pacific sea turtle diets have changed over the past 160 years. Ancient DNA confirms that both archaeological specimens are green sea turtles (Chelonia mydas). The stable isotope values from the 19th-century specimens are statistically indistinguishable from the modern comparatives in both δ13Ccol and δ15N, suggesting that green sea turtle dietary intake has remained relatively unchanged since the 1850s. However, the values are unclear for δD and δ18Oap and require additional research.

Abstract – Estimating the number of dolphins in a group is a challenging task. To assess the accuracy and precision of dolphin group size estimates, observer estimates were compared to counts from large-format vertical aerial photographs. During 11 research cruises, a total of 2,435 size estimates of 434 groups were made by 59 observers. Observer estimates were modeled as a function of the photo count in a hierarchical Bayesian framework. Accuracy varied widely among observers, and somewhat less widely among dolphin species. Most observers tended to underestimate, and the tendency increased with group size. Groups of 25, 50, 100, and 500 were underestimated by <1%, 16%, 27%, and 47%, respectively, on average. Precision of group size estimates was low, and estimates were highly variable among observers for the same group. Predicted true group size, given an observer estimate, was larger than the observer estimate for groups of more than about 25 dolphins. Predicted group size had low precision, with coefficients of variation ranging from 0.7 to 1.9. Studies which depend on group size estimates will be improved if the tendency to underestimate group size and the high uncertainty of group size estimates are included in the analysis.


Abstract – Seafood is an essential source of protein for more than 3 billion people worldwide, yet bycatch of threatened species in capture fisheries remains a major impediment to fisheries sustainability. Management measures designed to reduce bycatch often result in significant economic losses and even fisheries closures. Static spatial management approaches can also be rendered ineffective by environmental variability and climate change, as productive habitats shift and introduce new interactions between human activities and protected species. We introduce a new multispecies and dynamic approach that uses daily satellite data to track ocean features and aligns scales of management, species movement, and fisheries. To accomplish this, we create species distribution models for one target species and three bycatch-sensitive species using both satellite telemetry and fisheries observer data. We then integrate species-specific probabilities of occurrence into a single predictive surface, weighing the contribution of each species by management concern. We find that dynamic closures could be 2 to 10 times smaller than existing static closures while still providing adequate protection of endangered nontarget species. Our results highlight the opportunity to implement near real-time management strategies that would both support economically viable fisheries and meet mandated conservation objectives in the face of changing ocean conditions. With recent advances in eco-informatics, dynamic management provides a new climate-ready approach to support sustainable fisheries.

Week of 21 May 2018


Abstract – On 22 February 2015, a single specimen of Caretta caretta was identified in surface waters about 45 nm west of Tofino, British Columbia. The animal’s carapace was covered with algae, but the specimen was identified based on shell shape, head size, and the color of its parietal and interparietal scales. This record confirms that 4 sea turtle species range into British Columbia’s coastal waters.


Abstract – Species conservation depends on robust population assessment. Data on population abundance, distribution, and connectivity are critical for effective management, especially as baseline information for newly documented populations. We describe a pygmy blue whale Balaenoptera musculus brevicauda population in New Zealand waters with year-round presence that overlaps with industrial activities. This population was investigated using a multidisciplinary approach, including analysis of survey data, sighting records, acoustic data, identification photographs, and genetic samples. Blue whales were reported during every month of the year in the New Zealand Exclusive Economic Zone, with reports concentrated in the South Taranaki Bight (STB) region, where foraging behavior was frequently observed. Five hydrophones in the STB recorded the New Zealand blue whale call type on 99.7% of recording days (January to December 2016). A total of 151 individuals were photo-identified between 2004 and 2017. Nine individuals were resighted across
multiple years. No matches were made to individuals identified in Australian or Antarctic waters. Mitochondrial DNA haplotype frequencies differed significantly between New Zealand (n = 53 individuals) and all other Southern Hemisphere blue whale populations, and haplotype diversity was significantly lower than all other populations. These results suggest a high degree of isolation of this New Zealand population. Using a closed capture-recapture population model, our conservative abundance estimate of blue whales in New Zealand is 718 (SD = 433, 95% CI = 279-1926). Our results fill critical knowledge gaps to improve management of blue whale populations in New Zealand and surrounding regions.


Abstract – Mitochondrial DNA has been heavily utilized in phylogeography studies for several decades. However, underlying patterns of demography and phylogeography may be misrepresented due to coalescence stochasticity, selection, variation in mutation rates and cultural hitchhiking (linkage of genetic variation to culturally-transmitted traits affecting fitness). Cultural hitchhiking has been suggested as an explanation for low genetic diversity in species with strong social structures, counteracting even high mobility, abundance and limited barriers to dispersal. One such species is the sperm whale, which shows very limited phylogeographic structure and low mtDNA diversity despite a worldwide distribution and large population. Here, we use analyses of 175 globally distributed mitogenomes and three nuclear genomes to evaluate hypotheses of a population bottleneck/expansion vs. a selective sweep due to cultural hitchhiking or selection on mtDNA as the mechanism contributing to low worldwide mitochondrial diversity in sperm whales. In contrast to mtDNA control region (CR) data, mitogenome haplotypes are largely ocean-specific, with only one of 80 shared between the Atlantic and Pacific. Demographic analyses of nuclear genomes suggest low mtDNA diversity is consistent with a global reduction in population size that ended approximately 125,000 years ago, correlated with the Eemian interglacial. Phylogeographic analysis suggests that extant sperm whales descend from maternal lineages endemic to the Pacific during the period of reduced abundance and have subsequently colonized the Atlantic several times. Results highlight the apparent impact of past climate change, and suggest selection and hitchhiking are not the sole processes responsible for low mtDNA diversity in this highly social species.

**Week of 14 May 2018**


Abstract – Little is known about global patterns of genetic connectivity in pelagic dolphins, including how circumtropical pelagic dolphins spread globally following the rapid and recent radiation of the subfamily delphininæ. In this study, we tested phylogeographic hypotheses for two circumtropical species, the spinner dolphin (*Stenella longirostris*) and the pantropical spotted dolphin (*Stenella attenuata*), using more than 3000 nuclear DNA single nucleotide polymorphisms (SNPs) in each species. Analyses for population structure indicated significant genetic differentiation between almost all subspecies and populations in both species. Bayesian phylogeographic analyses of spinner dolphins showed deep divergence between Indo-Pacific, Atlantic and eastern tropical Pacific Ocean (ETP) lineages. Despite high morphological variation, our results show very close relationships between endemic ETP spinner subspecies in relation to global diversity. The dwarf spinner dolphin is a monophyletic subspecies nested within a major clade of pantropical spinner dolphins from the Indian and western Pacific Ocean populations. Population-level division among the dwarf spinner dolphins was detected—with the northern Australia population being very different from that in Indonesia. In contrast to spinner dolphins, the major boundary for spotted dolphins is between offshore and coastal habitats in the ETP, supporting the current subspecies-level taxonomy.

**Week of 30 April 2018**


No abstract

No abstract

Week of 16 April 2018


Abstract – Seaborne trade continues to grow and is an important component of the global economy. Threats from shipping to marine ecosystems include oil spills and other water pollution, air pollution, anchor scouring, biological invasions, container loss, chronic noise, and collisions between ships and large whales. Shipping and its associated threats can be influenced by a suite of regulations and economic events. The dynamic nature of ship traffic can be characterized using ship tracking data from automatic identification system (AIS) technology. These data enhance our ability to analyze the ecological threats from commercial shipping as a component of spatially explicit risk assessments. We explore ship traffic variability using a case study in waters off California. AIS data from 2008 to 2015 were used to evaluate the role of vessel emission regulations and economic events on vessel routes and speeds. We document vessels navigating around emission control areas (ECAs) or reducing speed when traveling through them. Large freight vessels decreased speeds from 2008 to 2015 by about 3–6 knots in many areas, with lowered speeds observed in areas of both heavy and sparse vessel use. The timing and location of the speed reductions appear to be most influenced by state and international clean fuel standards, which required the use of more costly fuels. Therefore, the speed reductions may have provided a more cost-effective means of travel. We also found temporary speed increases off southern California when vessels used longer routes to avoid traveling through an ECA. We conclude that the establishment of ECAs had a profound influence on vessel routes and speeds, likely due to the higher costs of clean fuels. Proposals have come before the International Maritime Organization (IMO) to establish clean fuel requirements in various locations around the world to reduce air-borne emissions from vessels. Our research suggests such proposals, or other events that may affect marine fuel prices, can have key impacts on vessel behavior. Consequently, it is important to consider this variability when designing strategies to minimize threats from shipping to vulnerable biophysical systems.


Abstract – Climate change has exacerbated the occurrence of large-scale sea surface temperature anomalies, or marine heatwaves (MHWs)—extreme phenomena often associated with mass mortality events of marine organisms. Using a combination of citizen science and federal data sets, we investigated the causal mechanisms of the 2014/2015 die-off of Cassin’s Auklets (Ptychoramphus aleuticus), a small zooplanktivorous seabird, during the NE Pacific MHW of 2013–2015. Carcass deposition followed an effective reduction in the energy content of mesozooplankton, coincident with the loss of cold-water foraging habitat caused by the intrusion of the NE Pacific MHW into the nearshore environment. Models examining interannual variability in effort-controlled carcass abundance (2001–2014) identified the biomass of lipid-poor zooplankton as the dominant predictor of increased carcass abundance. In 2014, Cassin’s Auklets dispersing from colonies in British Columbia likely congregated into a nearshore band of cooler upwelled water and ultimately died from starvation following the shift in zooplankton composition associated with onshore transport of the NE Pacific MHW. For Cassin’s Auklets, already in decline due to ocean warming, large-scale and persistent MHWs might represent a global population precipice.


Abstract – Gorgona National Park (GNP) protects the only known feeding aggregation of juvenile green turtles Chelonia mydas on the Pacific coast of Colombia. This study was undertaken to compare the diet of the two
known *C. mydas* morphotypes (black and yellow), and to determine availability, selectivity, and quality of food resources at GNP. Oesophageal lavages and isotopic analysis of epidermal tissue were performed on turtles captured between February and December 2012. Food quantity was estimated by determining per cent cover in quadrats randomly placed on the reefs. Food quality of algae species was estimated by proximate analysis. Food selection was estimated using Ivlev’s electivity index, and the trophic level of sea turtles at GNP was calculated. A total of 30 black (mean = 63.9 cm SCL) and 47 yellow (mean = 54.3 cm SCL) morphotype turtles were lavaged. Eight invertebrate and nine algae food items were identified in oesophageal contents. The most frequently found and abundant items in lavages were terrestrial plants, plastic fibres, invertebrates and algae. A total of 27 items, including 15 algae species, were identified on the reefs, of which *Cladophora* sp. was selected by black turtles, and *Hypnea pannosa* and *Dictyota* sp. were selected by both morphotypes; the latter species had the highest protein and lipid content, and low lignin content. A trophic level of 3.5 for black and 3.4 for yellow turtles was calculated. No significant difference in diet between the two morphotypes could be determined through lavage or isotopic analysis.


**Abstract**—This paper considers fisheries bycatch reduction within the least-cost biodiversity impact mitigation hierarchy. It introduces conservatory offsets that are implemented earlier in the biodiversity impact mitigation hierarchy than conventional compensatory offsets used as instruments of last resort. The paper illustrates implementation in an on-going sea turtle conservation program by the International Seafood Sustainability Foundation.

**Week of 9 April 2018**


**Abstract**—The endangered population of Southern Resident killer whales (*Orcinus orca*) is hypothesized to be food limited, but uncertainty remains over if and when the availability of their primary prey, Chinook salmon (*Oncorhyncus tshawytscha*), is low enough to cause nutritional stress. To measure changes in body condition, we collected 1635 measurable images from a helicopter hovering 230-460 m above whales, and linked these to individuals with distinctive natural markings. Head width (HW), measured at 15% of the distance between the blowhole and the dorsal fin (BHDF), was measured from images of 59 individuals in 2008 (from a population of 84) and 66/81 individuals in 2013, enabling assessment of between-year changes for 44 individuals (26 females, 18 males). Of these, 11 had significant declines in HW/BHDF compared to five with significant increases. Two whales with declines died shortly after being photographed, suggesting a link between body condition and mortality. Most (8/11) of the significant declines in condition were from one social pod (“J-pod”), and all the whales that increased in condition were from K-pod (n=3) and L-pod (n=2). Notably, 11/16 whales that changed condition were reproductive-aged females and there were no adult males with significant changes. This likely reflects the increased energetic costs of lactation to reproductive females, and the nutritional help provided to adult males through prey sharing. These data demonstrate the utility of aerial photogrammetry as a non-invasive approach for providing quantitative data on body condition, and support monitoring the condition of reproductive females as key indicators of nutritional stress.

**Week of 2 April 2018**


**Abstract**—The marine mammal life history sample and data archive originated with the fishery observer program for the eastern tropical Pacific (ETP) yellowfin tuna purse-seine fishery. One goal of this observer program was to collect biological samples from individual dolphins that could contribute to the assessment of fishery impacts on dolphin populations. Subsequently, biological studies became an integral part of the marine mammal assessment process. Through time, these studies have expanded to include characterizing the health and ecology of marine mammal populations in addition to their life history. A broad suite of biological tissue
samples and data are collected for these studies. This document presents an overview of the current protocols and procedures used to collect and archive biological samples and data. A summary of past protocols is also included along with references to additional detail about the collection and preservation of biological samples for marine mammals.

2017 Annual Report of NOAA Fisheries' National Seabird Program

NOAA Fisheries' National Seabird Program (NSP) is a crosscutting group of managers and scientists who work domestically and internationally to protect and conserve seabirds. The program's activities are guided by statutes and emerging agency priorities (e.g., Ecosystem-Based Fishery Management Policy and Road Map, the National Marine Fisheries Service Climate Change Strategy, Annual Guidance Memoranda). Together, these form the basis for NSP’s two overarching goals: 1 - Mitigate bycatch; 2 - Promote seabirds as ecosystem indicators. The NSP works through representation on steering committees and working groups within and external to NOAA Fisheries, and through partnerships with other NOAA Line Offices, Fisheries Management Councils, the States, and other Federal agencies. The NSP is formally housed in the Office of Science and Technology, though NSP members work in all five NOAA Fisheries Regional Offices, six Science Centers, and Headquarters Offices of Protected Resources, Science and Technology, International Affairs, Sustainable Fisheries, Habitat Conservation, and General Counsel. As such, it is a nationally coordinated program that benefits from significant leveraging at the regional level. This annual report provides an overview of 2017 accomplishments (policy and management, research and fieldwork, presentations and meetings, publications, NSP funded projects). NSP team members are listed at the end of the report and include MMTDers Trevor Joyce, Annette Henry (NSP Coordinator), and Lisa T. Ballance (Chair). The report is posted on the NSP website.

Week of 12 March 2018


Abstract – The National Oceanic and Atmospheric Administration (NOAA)/National Park Service (NPS) Ocean Noise Reference Station (NRS) Network is an array of currently twelve calibrated autonomous passive acoustic recorders. The first NRS was deployed in June 2014, and eleven additional stations were added to the network during the following two years. The twelve stations record data that can be used to quantify baseline levels and multi-year trends in ocean ambient sound across the continental United States, Alaska, Hawaii, and island territories within and near to the United States Exclusive Economic Zone (U.S. EEZ). The network provides multi-year, continuous observations of low-frequency underwater sound between 10 Hz and 2000 Hz to capture anthropogenic, biological, and geophysical contributions to the marine soundscape at each location. Comparisons over time and among recording sites will provide information on the presence of calling animals and the prevalence of abiotic and anthropogenic activities that contribute to each soundscape. Implementation of the NRS Network advances broad-scale passive acoustic sensing capabilities within NOAA and the NPS and is an important tool for monitoring protected areas and marine species and assessing potential environmental impacts of anthropogenic noise sources. This analysis focuses on the first year of recordings and captures the wide variability of low-frequency sound levels among and within individual NRS sites over time. Continued data collection will provide information on long-term, low-frequency sound level trends within or near the U.S. EEZ and will be used to explore the value of using soundscape analysis to inform management and mitigation strategies.

Week of 20 February 2018

Abstract – While environmental pollutants have been associated with changes in endocrine health in cetaceans, efforts to link contaminant exposure with hormones have largely been limited to a list of known, targeted contaminants, overlooking minimally characterized or unknown compounds of emerging concern. To address this gap, we analyzed a suite of potential endocrine disrupting halogenated organic compounds (HOCs) in blubber from 16 male short-beaked common dolphins (Delphinus delphis) with known maturity status collected from fishery bycatch in the Southern California Bight. We employed a suspect screening mass spectrometry-based method to investigate a wide range of HOCs that were previously observed in cetaceans from the same region. Potential endocrine effects were assessed through the measurement of blubber testosterone. We detected 167 HOCs, including 81 with known anthropogenic sources, 49 of unknown origin, and 37 with known natural sources. The sum of 11 anthropogenic and 4 unknown HOC classes were negatively correlated with blubber testosterone. Evidence suggests that elevated anthropogenic HOC load contributes to impaired testosterone production in mature male D. delphis. The application of this integrative analytical approach to cetacean contaminant analysis allows for inference of the biological consequences of accumulation of HOCs and prioritization of compounds for future environmental toxicology research.

Week of 29 January 2018


Abstract – A maximum likelihood method is presented for estimating drift direction and speed of a directional sonobuoy given the deployment location and a time series of acoustic bearings to a sound source at known position. The viability of this method is demonstrated by applying it to two real-world scenarios: (1) during a calibration trial where buoys were independently tracked via satellite, and (2) by applying the technique to sonobuoy recordings of a vocalising Antarctic blue whale that was simultaneously tracked by photogrammetric methods. In both test cases, correcting for sonobuoy drift substantially increased the accuracy of acoustic locations.


Abstract – The East Pacific green turtle Chelonia mydas population is gradually recovering, yet much remains unknown about their long-term demographics and habitat use due to their inaccessibility for study. We present the first detailed characterization of age-at-settlement (~3-5 yr), age-at-maturity (~17-30 yr), and long-term resource use patterns for these turtles by combining skeletal chronology with stable carbon (δ13C) and nitrogen (δ15N) isotope analysis of annual bone growth layers. We studied dead green turtles stranding along the Baja California Peninsula at Playa San Lázaro in Mexico, where their deaths are presumed to be a result of regional fisheries bycatch. Our stable isotope results indicate that these turtles utilize resources differently than other regional, lagoon-foraging green turtle aggregations. Based on stable isotope values from multiple years for individual turtles, we propose these green turtles are long-term pelagic foragers in the coastal shelf habitat of the Gulf of Ulloa and consume a more carnivorous diet from the epipelagic zone, likely including fishery discards, similar to a sympatric group of foraging North Pacific loggerhead turtles. Thus, green turtles use the Gulf of Ulloa as more than a transit area between benthic lagoon foraging and/or breeding locations. This unexpected and prolonged use of a pelagic foraging area could benefit the turtles by facilitating increased somatic growth, but may be of conservation concern as this area also experiences high fisheries turtle bycatch rates. Our findings expand the current paradigm of green turtle life history and habitat use by demonstrating an unexpected exploitation of habitat and prey for post-oceanic stage turtles.

Week of 22 January 2018


Abstract – The California sea lion (Zalophus californianus) population in the United States has increased steadily since the early 1970s. The Marine Mammal Protection Act of 1972 (MMPA) established criteria for
management of marine mammals based on the concept of managing populations within the optimal sustainable population (OSP), defined as a range of abundance from the maximum net productivity level (MNPL) to carrying capacity (K). Recent declines in California sea lion pup production and survival suggest that the population may have stopped growing, but the status of the population relative to OSP and MNPL is unknown. We used a time series of pup counts from 1975-2014 and a time series of mark-release-resight-recovery data from 1987-2015 for survival estimates to numerically reconstruct the population and evaluate the current population status relative to OSP using a generalized logistic model. We demonstrated that the population size in 2014 was above MNPL and within its OSP range. However, we also showed that population growth can be dramatically decreased by increasing sea surface temperature associated with El Niño events or similar regional ocean temperature anomalies. In this analysis we developed a critical tool for management of California sea lions that provides a better understanding of the population dynamics and a scientific foundation upon which to base management decisions related to complex resource issues involving this species.

**Week of 16 January 2018**


**Summary** – Climate change affects species and ecosystems around the globe [1]. The impacts of rising temperature are particularly pertinent in species with temperature-dependent sex determination (TSD), where the sex of an individual is determined by incubation temperature during embryonic development [2]. In sea turtles, the proportion of female hatchlings increases with the incubation temperature. With average global temperature predicted to increase 2.6°C by 2100 [3], many sea turtle populations are in danger of high egg mortality and female-only offspring production. Unfortunately, determining the sex ratios of hatchlings at nesting beaches carries both logistical and ethical complications. However, sex ratio data obtained at foraging grounds provides information on the amalgamation of immature and adult turtles hatched from different nesting beaches over many years. Here, for the first time, we use genetic markers and a mixed-stock analysis (MSA), combined with sex determination through laparoscopy and endocrinology, to link male and female green turtles foraging in the Great Barrier Reef (GBR) to the nesting beach from which they hatched. Our results show a moderate female sex bias (65%–69% female) in turtles originating from the cooler southern GBR nesting beaches, while turtles originating from warmer northern GBR nesting beaches were extremely female-biased (99.1% of juvenile, 99.8% of subadult, and 86.8% of adult-sized turtles). Combining our results with temperature data show that the northern GBR green turtle rookeries have been producing primarily females for more than two decades and that the complete feminization of this population is possible in the near future.

**Week of 8 January 2018**


**Abstract** - Details are provided on 17 previously unreported catches of blue whales, and 93 catches of North Pacific right whales, all taken illegally by the former USSR. The blue whale catches were made between mid-July and mid-September 1972 in the eastern North Pacific at distances of from 96 to 626 nautical miles from the US west coast (Oregon and Washington); they highlight the inadequacy of the International Observer Scheme, as implemented in 1972, to report or detect illegal whaling. These previously unknown blue whale catches bring the Soviet total to 1,638 for the period 1948–1972. The 93 right whale catches were made during the period 1951–62 around the Kuril Islands, which brings the known total of takes of this species from 1935–1971 to 775 (including 10 taken for scientific research and officially reported at the time).


**Abstract** - For over a century, the Ross Sea killer whale (RSKW; Orcinus orca, Antarctic type C), a fish-eating ecotype, has been com-monly reported in McMurdo Sound (McM), Ross Sea, Antarctica. However, a significant population decline reported at Ross Island after 2006 has been linked to a commercial fishery that
began in the Ross Sea in 1996–1997 and targets large Antarctic toothfish (*Dissostichus mawsoni*)—the presumed primary prey of RSKW. We assessed RSKW population abundance and trends using photo-identification data collected in McM during seven summers from 2001–2002 to 2014–2015. We identified 352 individual RSKWs and estimated an average annual population of 470 distinctly marked whales. Using a Bayesian mark–recapture model, we identified two population clusters: ‘regulars’ showed strong inter- and intra-annual site fidelity and an average annual abundance of 73 distinctive individuals (95% probability: 57–88); ‘irregulars’ were less frequently encountered but comprised a larger population with an annual estimate of 397 distinctive individuals (287–609). The number of seasonally resident regulars appeared to be stable over the period of purported RSKW decline, with the estimated annual number of deaths (6; 95% probability: 1–22) offset by the number of recruits (6; 2–19). As an alternative to the decline-due-to-fishery hypothesis, we suggest that the presence of mega-iceberg B-15 at Ross Island during the “iceberg years” (2000–2001 to 2005–2006) could have temporarily disrupted normal RSKW movement patterns, resulting in an apparent decline. Continued population monitoring of toothfish and their predators will be important for assessing ecosystem impacts of commercial fishing in the Ross Sea.


**Abstract** — Climate-related shifts in marine mammal range and distribution have been observed in some populations; however, the nature and magnitude of future responses are uncertain in novel environments projected under climate change. This poses a challenge for agencies charged with management and conservation of these species. Specialized diets, restricted ranges, or reliance on specific substrates or sites (e.g., for pupping) make many marine mammal populations particularly vulnerable to climate change. High-latitude, predominantly ice-obligate, species have experienced some of the largest changes in habitat and distribution and these are expected to continue. Efforts to predict and project marine mammal distributions to date have emphasized data-driven statistical habitat models. These have proven successful for short time-scale (e.g., seasonal) management activities, but confidence that such relationships will hold for multi-decade projections and novel environments is limited. Recent advances in mechanistic modeling of marine mammals (i.e., models that rely on robust physiological and ecological principles expected to hold under climate change) may address this limitation. The success of such approaches rests on continued advances in marine mammal ecology, behavior, and physiology together with improved regional climate projections. The broad scope of this challenge suggests initial priorities be placed on vulnerable species or populations (those already experiencing declines or projected to undergo ecological shifts resulting from climate changes that are consistent across climate projections) and species or populations for which ample data already exist (with the hope that these may inform climate change sensitivities in less well observed species or populations elsewhere). The sustained monitoring networks, novel observations, and modeling advances required to more confidently project marine mammal distributions in a changing climate will ultimately benefit management decisions across time-scales, further promoting the resilience of marine mammal populations.

**Week of 18 December 2017**


**Abstract** — Population genetic studies of non-model organisms often rely on initial ascertainment of genetic markers from a single individual or a small pool of individuals. This initial screening has been a significant barrier to beginning population studies on non-model organisms (Aitken et al., Mol Ecol 13:1423–1431, 2004; Morin et al., Trends Ecol Evol 19:208–216, 2004). As genomic data become increasingly available for non-model species, SNP ascertainment from across the genome can be performed directly from published genome contigs and short-read archive data. Alternatively, low to medium genome coverage from shotgun NGS library sequencing of single or pooled samples, or from reduced-representation libraries (e.g., capture enrichment; see Ref. “Hancock-Hanser et al., Mol Ecol Resour 13:254–268, 2013”) can produce sufficient new data for SNP discovery with limited investment. We describe protocols for assembly of short read data to reference or related species genome contig sequences, followed by SNP discovery and filtering to obtain an optimal set of SNPs for population genotyping using a variety of downstream high-throughput genotyping methods.

Book launch and signing will take place on 19 December 2017, 7 pm at the San Diego Natural History Museum. 22 cetacean and 5 pinniped species accounts were authored/co-authored by MMTD scientists:


Cetaceans:
Gray whale, *Eschrichtius robustus* (migrant)
Minke whale, *Balaenoptera acutorostrata*
Bryde's whale *Balaenoptera* cf. brydei (vagrant)
Blue whale, *Balaenoptera musculus*
Fin whale, *Balaenoptera physalus*
Humpback whale, *Megaptera novaeangliae*
North Pacific right whale - *Eubalaena japonica* (vagrant)
Short-beaked common dolphin, *Delphinus delphis*
Long-beaked common dolphin, *Delphinus capensis*
Short-finned pilot whale, *Globicephala macrorhynchus*
Risso's dolphin, *Grampus griseus*
Pacific white-sided dolphin, *Lagenorhynchus obliquidens*
Northern right whale dolphin, *Lissodelphis borealis*
Killer whale, *Orcinus Orca*
False killer whale, *Pseudorca crassidens* (vagrant)
Striped dolphin, *Stenella coeruleoalba*
Common bottlenose dolphin, *Tursiops truncatus*
Dall's porpoise - *Phocoenoides dalli*
Harbour porpoise - *Phocoena phocoena*
Pygmy sperm whale - *Kogia breviceps*
Sperm whale - *Physeter macrocephalus*
Hubbs' beaked whale, *Mesoplodon carlhubbsi*
Ginkgo-toothed beaked whale, *Mesoplodon ginkgodens*
Perrin's beaked whale, *Mesoplodon perrini*
Stejneger's beaked whale, *Mesoplodon stejnegeri*
Cuvier's beaked whale, *Ziphius cavirostris*
Pinnipeds:
Guadalupe fur seal, *Arctocephalus townsendi*
Northern fur seal, *Callorhinus ursinus*
California sea lion, *Zalophus californianus*
Northern elephant seal, *Mirounga angustirostris*
Harbor seal, *Phoca vitulina*


*Abstract* – Measurements of body size and mass are fundamental to pinniped population management and research. Manual measurements tend to be accurate but are invasive and logistically challenging to obtain. Ground-based photogrammetric techniques are less invasive, but inherent limitations make them impractical for many field applications. The recent proliferation of unmanned aerial systems (UAS) in wildlife monitoring has provided a promising new platform for the photogrammetry of free ranging pinnipeds. Leopard seals (*Hydrurga leptonyx*) are an apex predator in coastal Antarctica whose body condition could be a valuable indicator of ecosystem health. We aerially surveyed leopard seals of known body size and mass to test the precision and
accuracy of photogrammetry from a small UAS. Flights were conducted in January and February of 2013 and 2014 and 50 photogrammetric samples were obtained from 15 unrestrained seals. UAS-derived measurements of standard length were accurate to within 2.01 ± 1.06 %, and paired comparisons with ground measurements were statistically indistinguishable. An allometric linear mixed effects model predicted leopard seal mass within 19.40 kg (4.4% error for a 440 kg seal). Photogrammetric measurements from a single, vertical image obtained using UAS provide a noninvasive approach for estimating the mass and body condition of pinnipeds that may be widely applicable.


Abstract - The vaquita is a critically endangered species of porpoise. It produces echolocation clicks, making it a good candidate for passiveacoustic monitoring. A systematic grid of sensors has been deployed for 3 months annually since 2011; results from 2016 are reported here. Statistical models (to compensate for non-uniform data loss) show an overall decline in the acoustic detection rate between 2015 and 2016 of 49% (95% credible interval 82% decline to 8% increase), and total decline between 2011 and 2016 of over 90%. Assuming the acoustic detection rate is proportional to population size, approximately 30 vaquita (95% credible interval 8–96) remained in November 2016.


34 encyclopedia chapters were authored/co-authored by MMTD scientists:

- Atlantic Spotted Dolphin (Stenella frontalis) – W.F. Perrin
- Blue Whale (Balaenoptera musculus) – W.F. Perrin
- Bryde’s Whale (Balaenoptera edeni) – W.F. Perrin
- Cetacean Ecology – L.T. Ballance
- Cetacean Life History – S.J. Chivers
- Clymene Dolphin (Stenella clymene) – T.A. Jefferson
- Coloration – W.F. Perrin
- Common Dolphin (Delphinus delphis) – W.F. Perrin
- Dall’s Porpoise (Phocoenoides dalli) – T.A. Jefferson
- Delphinids, Overview – T.A. Jefferson, and R.G. LeDuc
- Fraser’s Dolphin (Lagenodelphis hosei) – M.L. Dolar
- Genetics for Management – P.A. Morin and A.E. Dizon
- Geographic Variation – W.F. Perrin
- History of Marine Mammal Research – W.F. Perrin
- Humpback Dolphins (Sousa spp.) – G.J. Parra and T.A. Jefferson
- Management – J. Barlow
- Mating Systems – S.L. Mesnick and K. Ralls
- Melon-headed Whale (Peponocephala electra) – W.L. Perryman and K. Danil
- Mesoplodon Beaked Whales: Mesoplodon spp. – R.L. Pitman
- Minke Whales (Balaenoptera acutorostrata, B. bonaerensis) - W.F. Perrin, R.L. Brownell Jr., and S.D. Mallete
- The Ocean Environment – P. Fiedler
- Pantropical Spotted Dolphin (Stenella attenuata) – W.F. Perrin
- Pilot Whales (Globicaphala spp.) – P.A. Olson
- Predation on Marine Mammals – D.W. Weller
- Right whale Dolphins (Lissodephis spp.) - J.D. Lipsky and R.L. Brownell Jr.
- Rough-toothed Dolphin (Steno bredanensis) – T.A. Jefferson
- Sexual Dimorphism – S.L. Mesnick and K. Ralls
- Spinner Dolphin (Stenella longirostris) – W.F. Perrin
Abstract – Stable isotope analysis (SIA) has rapidly become a useful tool to study the ecology of wild animal populations, especially for elusive, wide-ranging predators like marine mammals. The development of projectile biopsy techniques resulted in the collection of thousands of cetacean tissue samples that were archived in a dimethyl sulfoxide (DMSO) solution for long-term, multi-decadal preservation. Here we examine the influence of DMSO preservation on carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) values by comparing a set of paired delphinid skin samples stored frozen without preservative and in DMSO for up to 22 yr. Treatment of paired frozen and DMSO-preserved skin in a 2:1 chloroform:methanol solution yielded similar $\delta^{13}C$ and $\delta^{15}N$ values, revealing that DMSO and lipid contamination have similar isotopic effects on skin, and that these effects can be removed using routine lipid-extraction methods. Further, amino acid concentrations in DMSO-preserved and frozen skin tissue were similar, providing independent evidence of minimal protein alteration due to preservation. Access to a rich archive of skin samples preserved in DMSO will expand our ability to examine temporal and spatial variability in the isotope values of cetaceans, which will aid of understanding of how their ecology has been influenced by historical changes in environmental conditions.

Abstract – Stable isotopic compositions in animal tissues have been widely used to gain insight into trophic dynamics, especially of mobile aquatic predators whose behavior and dietary preferences are difficult to directly measure. Olive ridley sea turtles (Lepidochelys olivacea) range across $>3$ million km$^2$ of the tropical and subtropical eastern Pacific Ocean and their trophic ecology in open ocean areas has not yet been adequately described. Individuals feed within biogeographic regions where varying nutrient cycling regimes result in phytoplankton with distinct $\delta^{13}C$ and $\delta^{15}N$ values that are assimilated by the turtles. We sampled 346 turtles at-sea between 2003 and 2009 and used bulk tissue (n = 346) and amino acid compound specific isotope analysis (AA-CSIA, n = 31) to empirically support the conventional understanding that olive ridleys are omnivores. Bulk $\delta^{15}N$ values did not significantly vary with carapace length, a proxy for age, or with putative sex of adults. We therefore hypothesize that trophic position (TP) does not vary across age or sex. In line with other isotopic studies of this biogeographic scale in the same region, we observed a trend of bulk tissue $^{15}N$ enrichment with increasing latitude. Using AA-CSIA to account for $\delta^{15}N$ baseline shifts among food webs (space), we estimated the TP of adult foragers using two methods. We found that across their eastern Pacific range, olive ridley $\delta^{13}C$ and $\delta^{15}N$ niche area varied, but median TP of adults remained constant ($\sim 3.1$). Using a two-amino acid TP estimation method, we detected a small but notable elevation of TP for olive ridleys on the Costa Rica Dome. This study underscores the value of large-scale in-water olive ridley sea turtle research across oceanic foraging habitats to confirm or challenge anecdotal understanding of trophic roles, susceptibility to environmental change, and critical habitats. Further, it improves our understanding of why this species is now abundant in the eastern Pacific Ocean. A prey generalist with plenty of suitable foraging habitat can recover from the brink of extinction despite the presence of major threats. However, such foraging characteristics may require dynamic open ocean management approaches to meet conservation objectives if threats persist and/or increase.

R.H. Defran, David W. Weller, Nicholas M. Kellar and Susan J. Chivers. 2017. Research on coastal bottlenose dolphins (Tursiops truncatus), including a photo-identification catalog, following the 2015 Refugio Beach Oil Spill in
Abstract – On 19 May 2015, NOAA was notified of an oil spill that occurred near Refugio Beach in Santa Barbara County, California (34°27.74’N, 120°5.21’W). This Technical Memorandum (TM) summarizes the analysis of photo-identification data collected on coastal bottlenose dolphins during boat-based and shore-based surveys conducted in the coastal waters of Santa Barbara following the Refugio Beach Oil Spill. As part of this work, a digital photo-identification catalog was created containing images of the 66 dolphins identified during the study period. This catalog appears as Appendix 2 of the TM and was created as: (1) a resource for stranding and rescue organizations to determine if a given specimen is an individual dolphin known to have been in the spill related area, and (2) a resource for scientists that study bottlenose dolphins off the California and Baja coast to determine if a given sighting is of an individual dolphin known to have been in the spill related area.

Week of 6 November 2017


Abstract – Eastern North Pacific gray whales make one of the longest annual migrations of any mammal, traveling from their summer feeding areas in the Bering and Chukchi Seas to their wintering areas in the lagoons of Baja California, Mexico. Although a significant body of knowledge on gray whale biology and behavior exists, little is known about their vocal behavior while migrating. In this study, we used a sparse hydrophone array deployed offshore of central California to investigate how gray whales behave and use sound while migrating. We detected, localized, and tracked whales for one full migration season, a first for gray whales. We verified and localized 10,644 gray whale M3 calls and grouped them into 280 tracks. Results confirm that gray whales are acoustically active while migrating and their swimming and acoustic behavior changes on daily and seasonal time scales. The seasonal timing of the calls verifies the gray whale migration timing determined using other methods such as counts conducted by visual observers. The total number of calls and the percentage of calls that were part of a track changed significantly over both seasonal and daily time scales. An average calling rate of 5.7 calls/whale/day was observed, which is significantly greater than previously reported migration calling rates. We measured a mean speed of 1.6 m/s and quantified heading, direction, and water depth where tracks were located. Mean speed and water depth remained constant between night and day, but these quantities had greater variation at night. Gray whales produce M3 calls with a root mean square source level of 156.9 dB re 1 μPa at 1 m. Quantities describing call characteristics were variable and dependent on site-specific propagation characteristics.


Abstract – The dermis of cetaceans is in constant contact with microbial species. Although the skin of the bottlenose dolphin provides adequate defense against most disease-causing microbes, it also provides an environment for microbial community development. Microbial community uniqueness and richness associated with bottlenose dolphin skin is a function of varying habitats and changing environmental conditions. The current study uses ribosomal DNA as a marker to identify bacteria found on the skin of coastal and offshore bottlenose dolphins off of Southern California. The unique microbial communities recovered from these dolphins suggest a greater microbial diversity on the skin of offshore ecotype bottlenose dolphins, while microbial populations associated with the coastal ecotype include species that are more closely related to each other and that suggest exposure to communities that are likely to be associated with terrestrial runoff.

Week of 23 October 2017

**Abstract – Rationale:** The ecological application of stable isotope analysis (SIA) relies on taxa- and tissue-specific stable carbon (Δ13C) and nitrogen (Δ15N) isotope discrimination factors, determined with captive animals reared on known diets for sufficient time to reflect dietary isotope ratios. However, captive studies often prohibit lethal sampling, are difficult with endangered species, and reflect conditions not experienced in the wild.

**Methods:** We overcame these constraints and determined the Δ13C and Δ15N values for skin and cortical bone from green sea turtles (*Chelonia mydas*) that died in captivity and evaluated the utility of a mathematical approach to predict discrimination factors. Using stable carbon (δ13C values) and nitrogen (δ15N values) isotope ratios from captive and wild turtles, we established relationships between bone stable isotope (SI) ratios and those from skin, a non-lethally sampled tissue, to facilitate comparisons of SI ratios among studies using multiple tissues.

**Results:** The mean (±SD) Δ13C and Δ15N values (‰) between skin and bone from captive turtles and their diet (non-lipid-extracted) were 2.3 ± 0.3 and 4.1 ± 0.4 and 2.1 ± 0.6 and 5.1 ± 1.1, respectively. The mathematically predicted Δ13C and Δ15N values were similar (to within 1‰) to the experimentally derived values. The mean δ15N values from bone were higher than those from skin for captive (+1.0 ± 0.9‰) and wild (+0.8 ± 1.0‰) turtles; the mean δ13C values from bone were lower than those from skin for wild turtles (−0.6 ± 0.9‰), but the same as for captive turtles. We used linear regression equations to describe bone vs skin relationships and create bone-to-skin isotope conversion equations.

**Conclusions:** For sea turtles, we provide the first (a) bone-diet SI discrimination factors, (b) comparison of SI ratios from individual-specific bone and skin, and (c) evaluation of the application of a mathematical approach to predict stable isotope discrimination factors. Our approach opens the door for future studies comparing different tissues, and relating SI ratios of captive to wild animals.


**Abstract**—Climate variability alters nitrogen cycling, primary productivity, and dissolved oxygen concentration in marine eco-systems. We examined the role of this variability (as measured by six variables) on food chain length (FCL) in the California Current (CC) by reconstructing a time series of amino acid–specific δ15N values derived from common dolphins, an apex pelagic predator, and using two FCL proxies. Strong declines in FCL were observed after the 1997–1999 El Niño Southern Oscillation (ENSO) event. Bayesian models revealed longer FCLs under intermediate conditions for surface temperature, chlorophyll concentration, multivariate ENSO index, and total plankton volume but not for hypoxic depth and nitrate concentration. Our results challenge the prevalent paradigm that suggested long-term stability in the food web structure in the CC and, instead, reveal that pelagic food webs respond strongly to disturbances associated with ENSO events, local oceanography, and ongoing changes in climate.

**Week of 16 October 2017**

Connie Ka Yan Ng, Peter H. Dutton, He Xiang Gu, Tsung Hsien Li, Ming Bin Ye, Zhong Ron Xia, Fei Yan Zhang, Jin Xia Duan, Chung Kang Hsu, George H. Balazs and Margaret B. Murphy. 2017. Regional conservation implications of green turtle (*Chelonia mydas*) genetic stock composition in China. Chelonia Conservation and Biology 16(2) doi:10.2744/CCB-1253

**Abstract**—Sea turtles are globally endangered and face anthropogenic threats, such as direct harvest, bycatch, and habitat degradation. Genetic studies help identify connectivity between nesting and foraging grounds for conservation and management. However, information on genetic stock composition of green turtles (*Chelonia mydas*) in the South China Region (including Hong Kong, Guangdong Province, and Taiwan) is severely limited. In this study, mixed stock analysis based on the 760-bp mitochondrial DNA (mtDNA) control region of green turtles (n = 110) revealed that the primary source rookeries in the Pacific contributing to foraging green turtle aggregations in the South China Region were Peninsular Malaysia, Yap in the Federated States of Micronesia, Aru of Indonesia, Sulu Sea, northeastern Borneo, Republic of Marshall Islands, Wanan of Taiwan, and the central Ryukyu and Yaeyama of Japan. This study is the first to investigate and report the source nesting populations of a relatively large number of foraging green turtles in the region. The genetic results also indicate possible use of coastal Guangdong, the Taiwan Strait, and the East China Sea as habitat by pelagic-
phase green turtles hatched from nesting beaches in Taiwan and mainland China. As a precautionary approach for effective sea turtle conservation, conservation and management of each distinct green turtle source rookery as well as foraging aggregations sourced from multiple natal origins in the South China Region is needed to preserve genetic diversity for the species. Anthropogenic threats to nesting and foraging habitats and migratory pathways, such as direct take for trade and fishery impacts, should be thoroughly assessed and effectively mitigated by regional collaboration to sustain these populations.

**Week of 10 October 2017**


Abstract – A seasonally predictable, strong, and shallow thermocline makes the Costa Rica Dome a distinct biological habitat where phytoplankton and zooplankton biomass are higher than in surrounding waters in the eastern tropical North Pacific. We constructed seasonal climatologies of oceanographic variables (sea surface temperature and salinity, mixed layer depth, thermocline depth and strength, a stratification index, surface winds and currents, and upwelling) from a composite of ocean reanalysis data sets, plus two primary production variables (surface chlorophyll and net primary productivity). The results confirm a previous study of the annual cycle based on shipboard oceanographic observations. Based on ten SWFSC cetacean and ecosystem surveys of the eastern tropical Pacific during 1986-2006, we estimated spatial distributions of the encounter rate of commonly encountered cetaceans with generalized additive models that relate observed sightings to environmental variables. Among the 21 cetacean species and subspecies present in the Costa Rica Dome region, three show a clear association with the Dome and 14 have distributions that extend into the Dome. The Costa Rica Dome is a regional center of high productivity and likely supports high prey availability for cetacean predators both within the Dome and in surrounding waters. The coastal warm pool to the northwest of the Dome and the productive equatorial waters to the south are also important regional habitats for cetaceans.

**Week of 2 October 2017**


Abstract – During dedicated surveys for the Critically Endangered eastern stock of North Pacific right whales *Eubalaena japonica* (NPRW) in the Bering Sea, focal follows (FFs) were combined with passive acoustic monitoring to correlate vocal activity with dive behavior. During FFs, impulsive gunshot calls (hereafter ‘gunshots’), similar to those produced by other right whale populations, were localized to male and female NPRWs. The timing of gunshots correlated strongly with diving behavior observed during the FFs. Log survivorship analysis of inter-blow intervals showed a bout criterion interval of 40 s, separating the data into shorter surfacings and longer dives. For both, gunshots were skewed closer to the end of the sequence (modal gunshot to blow times: 5 s for dives, 7 s for surfacings) than the beginning (modal blow to gunshot times: 22 s for dives, 13 s for surfacings). Gunshots were more commonly produced during dives than surfacings. Mean gunshot calling rate during FFs was 133.0 calls h⁻¹ (range: 38.9–425.0). Other NPRW calls, including upcalls, the predominant call used to identify right whales acoustically, were not detected during the FFs. To determine comparative call detection rates, an additional 180 h of non-FF recordings were analyzed. Gunshots were detected ~50 times more frequently than upcalls (mean: 228.3 vs. 4.3 calls h⁻¹, respectively), with a maximum gunshot calling rate of 835.7 calls h⁻¹. This is the first study to definitively attribute gunshots to NPRW, and demonstrates the importance of including gunshots in passive acoustic studies, which will greatly increase NPRW detectability while supporting more accurate determinations of their spatio-temporal distribution.

**Week of 18 September 2017**

Abstract — While ecologists have long recognized the influence of spatial resolution on species distribution models (SDMs), they have given relatively little attention to the influence of temporal resolution. Considering temporal resolutions is critical in distribution modelling of highly mobile marine animals, as they interact with dynamic oceanographic processes that vary at time-scales from seconds to decades. We guide ecologists in selecting temporal resolutions that best match ecological questions and ecosystems, and managers in applying these models. We group the temporal resolutions of environmental variables used in SDMs into three classes: instantaneous, contemporaneous and climatological. We posit that animal associations with fine-scale and ephemeral features are best modelled with instantaneous covariates. Associations with large scale and persistent oceanographic features are best modelled with climatological covariates. Associations with mesoscale features are best modelled with instantaneous or contemporaneous covariates if ephemeral processes are present or interannual variability occurs, and climatological covariates if seasonal processes dominate and interannual variability is weak.

Week of 5 September 2017


Abstract — In 2015, NOAA Fisheries Southwest Fisheries Science Center (SWFSC) undertook a Collaborative Large Whale Survey (CLaWS) from 9 July through 9 November aboard NOAA Ship Reuben Lasker. The survey was a collaborative effort among SWFSC, NOAA Fisheries Alaska Fisheries Science Center and Fisheries and Oceans Canada. The study was conducted in U.S. and Canadian waters of the eastern North Pacific between Kodiak Island, Alaska, and San Diego, California. This catalog provides identification photographs of 131 gray whales (Eschrichtius robustus) photographed during the survey between central California and Kodiak, Alaska. The overarching objective of this catalog is to facilitate regional and international cooperation and collaboration between research groups collecting data on gray whales in the North Pacific.

Week of 28 August 2017


Abstract – The complex processes involved with animal migration have long been a subject of biological interest and broad-scale movement patterns of many marine turtle populations still remain unresolved. While it is widely accepted that once marine turtles reach sexual maturity they home to natal areas for nesting or reproduction, the role of philopatry to natal areas during other life stages has received less scrutiny, despite widespread evidence across the taxa. Here we report on genetic research that indicates that juvenile hawksbill turtles (Eretmochelys imbricata) in the eastern Pacific Ocean use foraging grounds in the region of their natal beaches, a pattern we term natal foraging philopatry (NFP). Our findings confirm that traditional views of natal homing solely for reproduction are incomplete and that many marine turtle species exhibit philopatry to natal areas to forage. Our results have important implications for life-history research and conservation of marine turtles and may extend to other wide-ranging marine vertebrates that demonstrate natal philopatry.

Abstract – Understanding population dynamics in broadly distributed marine species with cryptic life history stages is challenging. Information on the population dynamics of sea turtles tends to be biased toward females due to their accessibility for study on nesting beaches. Males are encountered only at sea; there is little information about their migratory routes, residence areas, foraging zones, and population boundaries. In particular, male leatherbacks (*Dermochelys coriacea*) are quite elusive; little is known about adult and juvenile male distribution or behavior. The at-sea distribution of male turtles from different breeding populations is not known. Here, 122 captured or stranded male leatherback turtles from the USA, Turkey, France, and Canada (collected 1997-2012) were assigned to one of nine Atlantic-basin populations using genetic analysis with microsatellite DNA markers. We found that all turtles originated from western Atlantic nesting beaches (Trinidad 55%, French Guiana 31%, and Costa Rica 14%). Although genetic data for other Atlantic nesting populations were represented in the assignment analysis (St. Croix, Brazil, Florida, and Africa (west and south), none of the male leatherbacks included in this study were shown to originate from these populations. This was an unexpected result based on estimated source population sizes. One stranded turtle from Turkey was assigned to French Guiana, while others that stranded in France were from Trinidad or French Guiana breeding populations. For 12 male leatherbacks in our dataset, natal origins determined from the genetic assignment tests were compared to published satellite and flipper tag information to provide evidence of natal homing for male leatherbacks, which corroborated our genetic findings. Our focused study on male leatherback natal origins provides information not previously known for this cryptic but essential component of the breeding population. This method should provide a guideline for future studies, with the ultimate goal of improving management and conservation strategies for threatened and endangered species by taking the male component of the breeding population into account.

Week of 21 August 2017


Abstract – For several species – fin whale, sperm whale, and beaked whales – Bayesian trend models were previously fit to data from six visual line-transect surveys conducted in the California Current between 1991 – 2008. In 2014, the NOAA Southwest Fisheries Science Center conducted another, seventh, comparable line-transect survey: the California Current Cetacean and Ecosystem Assessment Survey (CalCurCEAS). Updated trend estimates incorporating the new survey data have been published for fin whales but not yet for beaked whales or sperm whales. Here, new trend model estimates (of population trend and abundance) are presented for beaked whales and sperm whales. There is little evidence of trends in overall sperm whale abundance, but the new analysis supports prior evidence for an increasing number of sperm whales that occur in small groups (presumed to be adult or near-adult males). Cuvier’s beaked whales appear to have decreased in abundance from high values in 1991-93, but that decline now appears to have leveled off. There is some weak evidence of an increasing trend in Baird’s beaked whales. *Mesoplodon* beaked whales showed markedly higher abundance in 2014, reversing a declining trend from 1991-2008 that had been noted in a previous analysis. The increase may have be driven by an influx of tropical species of *Mesoplodon* during the unusually warm ocean conditions in 2014.


Abstract – Small cetaceans (dolphins and porpoises) face serious anthropogenic threats in coastal habitats. These include bycatch in fisheries; exposure to noise, plastic and chemical pollution; disturbance from boaters; and climate change. Generating reliable abundance estimates is essential to assess sustainability of bycatch in fishing gear or any other form of anthropogenic removals and to design conservation and recovery plans for endangered species. Cetacean abundance estimates are lacking from many coastal waters of many developing countries. Lack of funding and training opportunities makes it difficult to fill in data gaps. Even if international funding were found for surveys in developing countries, building local capacity would be necessary to sustain efforts over time to detect trends and monitor biodiversity loss. Large-scale, shipboard surveys can cost tens of thousands of US dollars each day. We focus on methods to generate preliminary abundance estimates from low-cost, small-boat surveys that embrace a ‘training-while-doing’ approach to fill in data gaps while
simultaneously building regional capacity for data collection. Our toolkit offers practical guidance on simple design and field data collection protocols that work with small boats and small budgets, but expect analysis to involve collaboration with a quantitative ecologist or statistician. Our audience includes independent scientists, government conservation agencies, NGOs and indigenous coastal communities, with a primary focus on fisheries bycatch. We apply our Animal Counting Toolkit to a small-boat survey in Canada’s Pacific coastal waters to illustrate the key steps in collecting line transect survey data used to estimate and monitor marine mammal abundance.


Abstract – Green sea turtles, Chelonia mydas, are known to inhabit populated and often urbanized areas. To understand turtle habitat use and behavior within these unique habitats, seven juvenile green turtles were fitted with acoustic transmitters (September 2012 – August 2014), of which two transmitters included an accelerometer (AP transmitter). One individual fitted with an AP transmitter was tracked using a passive acoustic array in an urbanized river, the San Gabriel River, Long Beach, CA (33°45’ N, 118°05’ W). Three additional turtles in this river and three turtles (one with AP transmitter) in a restored estuary (33°44’ N, 118°03’ W) in southern California were actively tracked for two non-consecutive 24-h periods. Those fitted with AP transmitters indicated that turtles were less active at night (0.58 ± 0.56 m/s² and 0.50 ± 0.63 m/s²) than during the day (0.86 ± 0.63 m/s² and 0.78 ± 0.60 m/s²) at both sites. Activity data and corresponding movements of the actively tracked turtle fitted with the AP transmitter were used to infer resting periods for other tracked individuals. Turtles rested near bridge pilings and runoff outflows in the river to potentially shelter from tidal flow. Turtles used significantly larger daily areas in the urbanized river (0.046 ± 0.023 km²) where resources may be patchier and less abundant, compared to turtles in the estuary (0.024 ± 0.012 km²) where large, dense eelgrass beds are present. Based on the habitat use and behaviors of green sea turtles, it appears that some green sea turtles are able to make use of both highly developed and restored habitats and likely benefit from certain aspects of development.


Abstract – The first documented long-term sea turtle research and conservation project in the world was officially launched in Latin America (Tortuguero, Costa Rica) in 1955. Despite the enormous advances in research and conservation in the nearly seven decades since, many questions still remain unanswered about fundamental aspects of ecology and population dynamics that hinder the conservation of sea turtles in the region. To catalyze further dissemination of information and improvement of sea turtle conservation, this Special Issue presents 10 papers solely focused on studies conducted in Latin America. This Special Issue resulted from an initiative launched to celebrate the 36th Annual Symposium on Sea Turtle Biology and Conservation, held in Peru in March 2016 - the first time this event was held in South America. The articles featured present novel results for four of the five species of sea turtles present in this region, with data collected as far back as 1971 and as recent as 2016. The studies cover diverse subjects including the nesting ecology for the most endangered populations of sea turtles in the world - the Eastern Pacific hawksbill turtle (Eretmochelys imbricata) and leatherback turtle (Dermochelys coriacea); the origins and connectivity of nesting and foraging populations of hawksbills and green turtles (Chelonia mydas); the detection of a new foraging ground for hawksbills in the Eastern Pacific; and the pervasive occurrence of incidental capture as well as illegal retention of sea turtles. The recovery of these imperiled marine reptiles relies on information to design and implement sound conservation actions; in this regard, the papers in this Special Issue are making a vital contribution, following the initial efforts launched nearly 70 years ago.


Abstract – Small-scale coastal fisheries can cause detrimental impacts to non-target megafauna through bycatch. This can be particularly true when high-use areas for such species overlap with fishing grounds, as is
the case with hawksbill turtle (*Eretmochelys imbricata*) aggregations at lobster gillnet fishing sites in El Salvador and Nicaragua. We quantified hawksbill bycatch by partnering with local fishers to record data for 690 gillnet sets on rocky reefs at Los Cóbanos Reef Marine Protected Area (2008-2009) and Punta Amapala (2012-2014) in El Salvador, and La Salvia (2012-2014) in Nicaragua. Based on 31 observed hawksbill captures, the mean bycatch-per-unit-effort (0.0022; individuals per set = 0.0450) and mortality (0.74) are among the highest reported for the species across fishing gear types and oceanic regions worldwide, and we conservatively estimate that at least 227 juvenile hawksbill captures occurred in lobster gillnet fishing fleets at our sites during the study. Estimated mortality for the 227 hawksbills -which could approach the 74% observed mortality of total captures- from interactions with lobster gillnet fisheries at these sites during the study period may constitute the greatest single source of human-induced in-water mortality for juvenile, sub-adult, and adult hawksbills in the eastern Pacific, and is of grave concern to the population. Based on our findings, we discuss neritic habitat use by hawksbills during their ‘lost years’ and offer recommendations for bycatch reduction strategies, including community-based efforts to enhance sustainable self-governance via the establishment of locally crafted conservationist norms and marine protected areas at important developmental habitat.


Abstract – Prior to 2007, efforts to monitor and conserve hawksbill turtles (*Eretmochelys imbricata*) in the eastern Pacific Ocean were opportunistic and records were virtually non-existent. The first abundance estimates were published in 2010, but contained limited data on the species. Ongoing research since that time has led to the identification of several rookeries, including sites containing large proportions of the overall hawksbill nesting currently known to occur in the region. Monitoring projects were established at several sites and have since provided substantial nesting data on the species. Here we summarize data collected between 1983 and March 2016 from all sites (n = 9) confirmed to host >10 nests in any given season to provide an update on hawksbill nesting in the eastern Pacific. We documented a total of 3,508 hawksbill nests, 265,024 hatchlings and 528 individual nesting females in the region. The vast majority of these records (99.4%, 99.9% and 99.6%, respectively) were generated subsequent to 2007, coinciding with the discovery of eight of the nine rookeries included in this study and the organization of monitoring efforts at those sites, which led to the increased documentation conferred here. Our findings should not be misconstrued as increases in actual nesting or signs of recovery, which could diminish the ongoing need for conservation actions, but rather as optimism, that there is still an opportunity to restore the species in the eastern Pacific. The top three sites in terms of average annual number of nests were Estero Padre Ramos (Nicaragua; 213.2 ± 47.6 nests), Bahia de Jiquilisco (El Salvador; 168.5 ± 46.7 nests) and Aserradores (Nicaragua; 100.0 ± 24.0 nests), and all three sites are located in mangrove estuaries in Central America, highlighting the importance of these rookeries/habitats for the survival and recovery of hawksbills in the region. The remaining six sites received between 6.9 ± 7.3 nests (Costa Careyes, Mexico) and 59.3 ± 17.7 nests (Los Cobanos, El Salvador) annually. By integrating data collected on nesting hawksbills with local conservation realities at the most important known hawksbill rookeries in the eastern Pacific, we provide a more holistic view of the conservation status and management needs of the species in this ocean region.


Abstract – Hawksbill sea turtles (*Eretmochelys imbricata*) inhabiting the eastern Pacific Ocean are one of the world’s most threatened marine turtle management units. Despite the fact that knowledge about the status of sea turtles at foraging grounds is a key element for developing the effective conservation strategies, comprehensive studies of hawksbills at foraging habitats in the eastern Pacific remain lacking. For many years anecdotal information indicated Coiba Island National Park in Panama as a potentially important hawksbill foraging ground, which led to the initiation of monitoring surveys in September 2014. Ongoing mark-recapture surveys to assess population status, generate demographic data and identify key foraging sites have been conducted every six months in the park since that time. To date, a total of six monitoring campaigns consisting of four days each have been conducted, leading to the capture and tagging of 186 hawksbills, 51 of which were recaptured at least once. The size range of captured individuals was 30.0 to 75.5 cm and largely comprised of
juveniles. Somatic growth rates of individual hawksbills were highly variable, ranging from -0.78 to 7.1 cm year^-1. To our knowledge, these are the first published growth rates for juvenile hawksbill turtles in the eastern Pacific Ocean. When these growth data are combined with information on hawksbill demography and distribution, our findings indicate Coiba Island National Park is one of the most important known foraging sites for hawksbill sea turtles in the eastern Pacific Ocean.

**Week of 7 August 2017**

**Nicole E. Beaulieu-McCoy, Kathryn K. Sherman, Marisa N. Trego, Daniel E. Crocker and Nicholas M. Kellar.** 2017. Initial validation of blubber cortisol and progesterone as indicators of stress response and maturity in an otariid; the California sea lion (*Zalophus californianus*). General and Comparative Endocrinology.

Abstract – Chronic stress can have detrimental effects on an individual’s health and reproductive success. The use of cortisol quantification as an indicator of stress in free-ranging cetaceans and phocids is increasing but no studies have applied this technique on blubber in otariids. We measured cortisol concentrations in blubber samples obtained from California sea lions, *Zalophus californianus*, stranded in San Diego County and those incidentally killed in the California drift gillnet fishery. We also measured progesterone concentrations to assess female reproductive status and, in males, as a potential secondary measure of adrenal steroid production. Blubber cortisol and progesterone values were compared across demographic groups (sex and maturity), season and proportion blubber lipid extracted. Stranded animals (247.3 ± 70.767SE ng/g blubber) had significantly higher cortisol concentrations compared to fishery bycaught (8.1 ± 2.108SE ng/g blubber) animals. These findings are likely driven by inherent differences in the cause of death and associated nutritional state coupled with the mean duration of expiration for these two groups of animals (i.e. the duration from an animal’s initial perception of the threat-to-self until death). The duration of transition from healthy state to death in stranded animals is on the order of many hours to weeks while in fishery bycaught animals, this transition occurs much more rapidly (i.e., seconds to tens of minutes). The presumed longer duration of the mortality event in stranded animals gives sufficient time for elevated cortisol to diffuse into the blubber. No significant differences between demographic groups, or season were found. However, blubber cortisol declined inversely with proportion blubber lipid extracted, suggesting utility in assessing long-term nutritional status. Blubber progesterone was significantly higher in mature females than immature females (153.8 ± 54.546SE ng/g blubber and 9.7 ± 3.60SE ng/g blubber respectively), containing on average 15 times more progesterone, irrespective of pregnancy state. Additionally, a significant relationship between mean cortisol and progesterone was found in males with >35% blubber lipid (p < 0.0001). This study is an initial step in validating blubber cortisol and progesterone concentrations as a potential marker of stress response and reproductive state, respectively, in otariids. Especially when paired with dart biopsying, this approach could represent a relatively rapid way to assess baseline stress, nutritional status and reproductive states in otariids while minimizing the effects of sampling.

**Week of 31 July 2017**


Abstract – Passive acoustic surveys are a useful tool for long-term assessment of cetacean populations. However, the application of these methods requires that species of interest produce distinctive, well-characterized vocalizations. Several sympatric species of cetaceans produce narrow-band, high-frequency (NBHF) echolocation clicks which are difficult to distinguish. On the U.S. West Coast, Dall's porpoise (*Phocoenoides dalli*) and harbor porpoise (*Phocoena phocoena*) emit NBHF echolocation clicks and overlap in distribution. To determine whether different passive acoustic instruments could be used to monitor harbor porpoise, we recorded harbor porpoise echolocation clicks simultaneously on an autonomous hydrophone recording system (SoundTrap, Ocean Instruments New Zealand) and on a commonly used passive acoustic monitoring device (C-POD, Chelonia Ltd., UK) and investigated whether the number and peak frequency of recorded echolocation clicks were consistent between the two instruments. We found that the number of echolocation clicks recorded by the two instruments was highly correlated. However, the C-POD and SoundTrap measurements of the peak frequency of echolocation signals were not well-correlated. This
suggests that while both instruments are capable of detecting harbor porpoise echolocation clicks, it may not be feasible to use C-PODs to discriminate harbor porpoise echolocation clicks in regions where multiple species with NBHF echolocation clicks are present. The use of calibrated hydrophones with full-bandwidth recording instruments may be required for this task.


Summary – This science guide describes North Pacific gray whales as they migrate from their summer feeding areas in frigid Arctic waters to wintering areas in warm lagoons off Baja California. Nature Unfolding © Science Guide series coalesce science, literature and imagery to inspire a deeper connection with nature. A compilation of natural science illustrations, a migration map, photos, and other diagrams provide current information written by Dave Weller. Designed and illustrated by Dawn N. Ericson, edited and illustrations by Dominique Navarro. This guide aligns with the California State Board of Education science content standards for earth science - grades K-12. For details, contact dave.weller@noaa.gov and see https://www.amazon.com/s/ref=dp_byline_sr_book_2?ie=UTF8&field-author=Ph.D.+David+W.+Weller&search-alias=books&text=Ph.D.+David+W.+Weller&sort=relevancerank

Week of 24 July 2017


Abstract – The 2011 release of Fukushima-derived radionuclides into the Pacific Ocean made migratory sharks, teleosts, and marine mammals a source of speculation and anxiety regarding radiocesium (134+137Cs) contamination, despite a lack of actual radiocesium measurements for these taxa. We measured radiocesium in a diverse suite of large predators from the North Pacific Ocean and report no detectable (i.e., ≥ 0.1 Bq kg-1 dry wt) of Fukushima-derived 134Cs in all samples, except in one olive ridley sea turtle (Lepidochelys olivacea) with trace levels (0.1 Bq kg-1). Levels of 137Cs varied within and across taxa, but were generally consistent with pre-Fukushima levels and were lower than naturally-occurring 40K by one to two orders of magnitude. Predator size had a weaker effect on 137Cs and 40K levels than tissue lipid content. Predator stable isotope values (δ13C and δ15N) were used to infer recent migration patterns, and showed that predators in the central, eastern, and western Pacific should not be assumed to accumulate detectable levels of radiocesium a priori. Non-detection of 134Cs and low levels of 137Cs in diverse marine megafauna far from Fukushima confirms negligible increases in radiocesium, with levels comparable to those prior to the release from Fukushima. Reported levels can inform recently developed models of cesium transport and bioaccumulation in marine species.

Week of 3 July 2017


Week of 26 June 2017


Casale Paola, Gaspard Abitsi, Marie Pierre Aboro, Pierre Didier Agamboue, Laureen Agbode, Nontse’ Lois Allela, Davy Angueko, Jean Noel Bibang Bi Nguema, Francois Boussamba, Floriane Cardiec, Emmanuel Chartrain, Claudio

Abstract – Obtaining the representative morphological data required for traditional taxonomy is difficult, and sometimes impossible, for cetaceans, especially large ones. As a result, three quarters of the 88 currently recognized extant species have no subspecies and 40 taxa likely have additional unnamed taxa. Conservation needs give urgency to improving taxonomy because unnamed taxa are unlikely to receive protection equivalent to that received by named taxa. Genetic data can improve efforts to delimit subspecies, but the markers and methods used have varied and the magnitude of genetic difference used to justify subspecies distinctions across studies has also varied. Here, we define the concepts of populations, subspecies, and species to establish a foundation for developing guidelines (data to include and analyses to conduct) and quantitative standards (the magnitude of differentiation expected at different taxonomic levels) for using genetic data to support taxonomic recognition. Our definition is particularly applicable to data-poor groups because it allows for naming a subspecies when there is uncertainty about whether lineages have diverged sufficiently for species-level recognition. This allows a species that lacks convincing data for lineage divergence to be recognized as a subspecies while sufficient data are accrued, which could take decades for some cetaceans.


Abstract – The vast and remote distributions and large body size of most cetaceans make it difficult to obtain and maintain morphological collections adequate for advancing sound taxonomic arguments. Consequently, genetic data are playing an increasingly important role in cetacean species and subspecies delimitation. We review seven categories of analytical methods useful in delimiting subspecies based on genetic data. For each category, we summarize its utility in evaluating putative subspecies, the types of markers to which it can be applied, and potential challenges in interpreting results in a taxonomic context. We focus on the utility of each type of method to evaluate the critical features distinguishing subspecies from populations and species: the degree of diagnosability between putative taxa and the extent to which the putative taxa have diverged along separate evolutionary pathways. We conclude that diagnosability is best estimated with either assignment tests or multivariate methods, while evaluating the degree of divergence requires a synthesis of multiple lines of evidence derived from different analytical methods and different data types, including nongenetic data.

Abstract – Uncertainty in marine mammal taxonomy is increasingly being addressed using molecular genetic data. We examined 32 peer-reviewed articles published between 1994 and 2011 to review methodological practices, consistency of markers and analytical methods, and overall quality of arguments used when genetic data have been employed to delimit new species and subspecies of marine mammals. The mitochondrial DNA (mtDNA) control region was the primary genetic marker used in these studies, but analytical methods varied greatly across studies. Diagnosability, a common metric for delimiting subspecies with morphological data, was only used through citing of fixed differences in mtDNA sequences. Assignment tests based on microsatellite data were less common but were applied at both taxonomic levels. Nuclear DNA sequence data were rarely used. Basic background material needed to evaluate the strength of arguments, such as distribution and sampling maps, were often missing. For most studies, sample sizes were good, but adequate geographic sampling for broadly distributed taxa was often lacking, diminishing the strength of evidence for taxonomic distinctness. Examining these empirical cases revealed a mixture of sound and inadequate practices for genetic studies of cetacean taxonomy and suggested that improvements could be made to the field by developing standard guidelines.


Abstract – Cetacean taxonomy continues to be in flux and molecular genetic analyses examining alpha taxonomy in cetaceans have relied heavily on the mitochondrial DNA control region. However, there has been little consistency across studies; a variety of metrics and levels of divergence have been invoked when delimiting new cetacean species and subspecies. Using control region sequences, we explored, across pairs of well-recognized cetacean populations, subspecies, and species, a suite of metrics measuring molecular genetic differentiation to examine which metrics best categorize these taxonomic units. Net's estimate of net divergence (dA) and percent diagnosability performed best. All but a single, recently diverged species were unambiguously identified using these metrics. Many subspecies were found at intermediate values as expected, allowing separation from both populations and species, but several had levels of divergence equivalent to populations, resulting in underclassification errors using this single marker. Coupling dA with additional measures, such as percent diagnosability, examining appropriate nuclear genetic markers, and interpreting results in a broader biological context will improve taxonomic investigations in cetaceans.


Abstract – We examine the use of an ensemble method, Random Forests, to delimit subspecies using mitochondrial DNA (mtDNA) sequences. Diagnosability, a measure of the ability to correctly determine the taxon of a specimen of unknown origin, has historically been used to delimit subspecies, but few studies have explored how to estimate it from DNA sequences. Using simulated and empirical data sets, we demonstrate that Random Forests produces classification models that perform well for diagnosing subspecies and species. Populations with strong social structure and relatively low abundances (e.g., killer whales, Orcinus Orca) were found to be as diagnosable as species. Conversely, comparisons involving subspecies that are abundant (e.g., spinner and spotted dolphins, Stenella longirostris and S. attenuata), are only as diagnosable as many population comparisons. Estimates of diagnosability reported in subspecies and species descriptions should include confidence intervals, which are influenced by the sample sizes of the training data. We also stress the importance of reporting the certainty with which individuals in the training data are classified in order to communicate the strength of the classification model and diagnosability estimate. Guidance as to ideal minimum diagnosability thresholds for subspecies will improve with more comprehensive analyses; however, values in the range of 80%-90% are considered appropriate.
Abstract – Taxonomy is an imprecise science that delimits the evolutionary continuum into discrete categories. For marine mammals, this science is complicated by the relative lack of morphological data for taxa that inhabit remote and often vast ranges. We provide guidelines to promote consistency in studies relying primarily on molecular genetic data to delimit cetacean subspecies from both populations and species. These guidelines identify informational needs: basis for the taxonomic hypothesis being tested, description of current taxonomy, description of relevant life history, sample distribution, sample size, number and sequence length of genetic markers, description of measures taken to ensure data quality, summary statistics for the genetic markers, and analytical methods used to evaluate the genetic data. We propose an initial set of quantitative and qualitative standards based on the types of data and analytical methods most readily available at present. These standards are not expected to be rigidly applied. Rather, they are meant to encourage taxonomic arguments that are consistent and transparent. We hope professional societies, such as the Society for Marine Mammalogy, will adopt quantitative standards that evolve as new data types and analytical methods become widely available.

Week of 19 June 2017


Abstract – Detection distances are critical for cetacean density and abundance estimation using distance sampling methods. Data from a drifting buoy system consisting of an autonomous recorder and a two-element vertical hydrophone array at ~100-m depth are used to evaluate three methods for estimating the horizontal distance (range) to beaked whales making echolocation clicks. The precision in estimating time-differences-of-arrival (TDOA) for direct- and surface-reflected-path clicks is estimated empirically using repeated measures over short time periods. A Teager-Kaiser energy detector is used to improve estimates of TDOA for surface-reflected signals. Simulations show that array tilt in the direction of the source cannot be reliably estimated given this array geometry and these measurements of TDOA error, which means that range cannot be reliably estimated. If array tilt can be reduced to less than 0.5°, range can be reliably estimated up to ~3000 m. If array depth is increased to 200 m and array tilt is less than 1°, range can be reliably estimated up to ~5000 m. Prior information on the depth of vocalizing beaked whales and estimates of declination angle can be used to precisely estimate range, but different analytical methods are required to avoid bias and to treat distributions of depth probabilistically.


Abstract – Geographic variation in external morphology is thought to reflect an interplay between genotype and the environment. Morphological variation has been well-described for a number of cetacean species, including the bottlenose dolphin (Tursiops truncatus). In this study we analyzed dorsal fin morphometric variation in coastal bottlenose dolphins to search for geographic patterns at different spatial scales. A total of 533 dorsal fin images from 19 available photo-identification catalogs across the three Mexican oceanic regions (Pacific Ocean n = 6, Gulf of California n = 6, and Gulf of Mexico n = 7) were used in the analysis. Eleven fin shape measurements were analyzed to evaluate fin polymorphism through multivariate tests. Principal Component Analysis on log-transformed standardized ratios explained 94% of the variance. Canonical Discriminant Function Analysis on factor scores showed separation among most study areas (p < 0.05) with exception of the Gulf of Mexico where a strong morphometric cline was found. Possible explanations for the observed differences are related to environmental, biological and evolutionary processes. Shape distinction between dorsal fins from the Pacific and those from the Gulf of California were consistent with previously reported differences in skull morphometrics and genetics. Although the functional advantages of dorsal fin shape remains to be assessed, it is not unlikely that over a wide range of environments, fin shape may represent a trade-off among thermoregulatory capacity, hydrodynamic performance and the swimming/hunting behavior of the species.

*Abstract* – Marine turtles migrate across long distances, exhibit complex life histories, and occupy habitats that are difficult to observe. These factors present substantial challenges to understanding fundamental aspects of their biology or assessing human impacts, many of which are important for the effective conservation of these threatened and endangered species. The early development and application of genetic tools made important contributions to understanding marine turtle population and evolutionary biology, such as providing evidence of regional natal homing by breeding adults, establishing connectivity between rookeries and foraging habitats, and determining phylogeography and broad scale stock structure for most marine turtle species. Recent innovations in molecular technologies, statistical methods, and creative application of genetic tools have significantly built upon this knowledge to address key questions in marine turtle biology and conservation management. Here, we evaluate the latest major advances and potential of marine turtle genetic applications, including improved resolution and large-scale syntheses of population structure, connectivity and phylogeography, estimation of key demographic rates such as age to maturity and operational or breeding sex ratios, insight into reproductive strategies and behavior, and assessment of differential human impacts among populations. We then discuss remaining challenges and emerging capabilities, such as rapid, multiplexed genotyping, and investigation of the genomic underpinnings of adaptive variation afforded by high-throughput sequencing technologies.


*Abstract* – Marine mammal interactions (i.e., hookings and entanglements) with the Hawaii and American Samoa longline fisheries observed during 2010–2014 were compiled, and the number of marine mammal deaths, serious injuries, and non-serious injuries by fishery, species, and management area were assessed. These values form the basis of the mortality and serious injury estimates included in the stock assessment reports of stocks impacted by these fisheries. Injury determinations were made using a nationally standardized process and established criteria for distinguishing serious from non-serious injuries (National Marine Fisheries Service, 2012). In the Hawaii deep-set fishery, 46 marine mammal interactions were observed from 2010 to 2014; most involved false killer whales (54.3%), resulted in death or serious injury (78.3%), and occurred outside the U.S. exclusive economic zone (EEZ) (54.3%). In the Hawaii shallow-set fishery, 54 marine mammal interactions were observed from 2010 to 2014; most involved Risso’s dolphins (37.0%), resulted in death or serious injury (72.2%), and occurred outside the U.S. EEZ (92.6%). In the American Samoa deep-set fishery, 14 marine mammal interactions were observed from 2010 to 2014; most involved rough-toothed dolphins (42.9%), resulted in death or serious injury (92.9%), and occurred within the U.S. EEZ (78.6%).


*Abstract* – There are two commonly utilised, but distinct, methods for measuring carapace length of leatherback turtles (*Dermochelys coriacea*). Either the carapace is measured along the central ridge or to the side of the central ridge. Here, we demonstrate that these two measurements produce differing results. Moreover, we formulate a globally-applicable correction factor to standardise between these two measurements. Standardised curved carapace length measurements from leatherback turtles at nesting sites worldwide generally fit into 3 size categories: small (<150 cm; Atlantic: Southeast and Pacific: East), mid-sized (150-157.5 cm; Atlantic: Northwest), and large (>157.5 cm; Indian: Southwest, Indian: Northeast, and Pacific: West).

Abstract – Breeding-season distribution and population growth rate of California sea lions (*Zalophus californianus*) in the U.S. population are estimated from counts of pups and non-pups collected during 1964 to 2014. Pup and non-pup count data were compiled from published and unpublished sources. These data showed that during this period the U.S. count of live-pups increased at an average annual rate of 4.7% per year (L95% CI=4.2%, U95% CI=5.2%). Average annual growth rates of live-pup counts at the four main island- rookeries in southern California (Santa Barbara Island, San Clemente Island, San Nicolas Island, and San Miguel Island; hence fore referred to as the Main Channel Islands) ranged from 4.2% to 5.5% from 1964 to 2014. The Channel Islands count of non-pups (non-pup counts were unavailable for the entire U.S. population prior to 2003) increased at an average annual growth rate of 2.8% per year (L95% CI=2.4%, U95% CI=3.4%). San Nicolas Island and San Miguel Island were the largest rookeries in the U.S. population, both having the most pups and non-pups. Prior to 1990, 59.2% of live pups counted in the Channel Islands were on San Miguel Island, and 32.4% were on San Nicolas Island. After 1990, these islands constituted 44.9% and 45.6% of Channel Island pups, respectively. California-wide surveys conducted during 2003-2005, 2007, and 2011-2013 indicated that the Main Channel Islands rookeries accounted for 99.71% of live pups counted in California and 77.35% of hauled-out non-pups in California during the breeding season. Sea lion counts were modeled (using generalized linear modeling) as a function of sea level height at Los Angeles, California (SLH-LA), Pacific Decadal Oscillation (PDO), North Pacific Gyre Oscillation (NPGO), and Multivariate El Niño Index (MEI). This model indicated that more pups were produced during cold-water conditions and fewer pups were produced during warm-water conditions, and that fewer non-pups were present at southern California rookeries during warm-water conditions and more were present during cold-water conditions.


Abstract – Aerial photographic surveys targeting California sea lions conducted during July 2011-2015 were used to describe inter-island and intra-island distributions of California sea lions, northern elephant seals, Pacific harbor seals, and Steller sea lions within the Channel Islands. Age/sex class counts were made for California sea lions, Steller sea lions, and northern elephant seals, but not for Pacific harbor seals. Each island was subdivided into areas to document intra-island distribution of each species. California sea lions were found at all of the Channel Islands. However, San Miguel Island, San Nicolas Island, Santa Barbara Island, and San Clemente Island accounted for 99.8% to 99.9% of California sea lion pups counted, with San Miguel Island and San Nicolas Island having the most pups and non-pups of those four islands. In July 2015, when all islands were surveyed for elephant seals, 2790 elephant seals (61.3% of Channel Islands total) were at San Miguel Island, 932 (20.5% of total) at San Nicolas Island, and 816 (17.9% of total) at Santa Rosa Island. There were 1367 Pacific harbor seals counted at the Channel Islands in July 2015, and a single Steller sea lion was counted at San Nicolas Island in 2013.

Week of 15 May 2017


Abstract – Managing marine species effectively requires spatially and temporally explicit knowledge of their density and distribution. Habitat-based density models, a type of species distribution model (SDM) that uses habitat covariates to estimate species density and distribution patterns, are increasingly used for marine management and conservation because they provide a tool for assessing potential impacts (e.g., from fishery bycatch, ship strikes, anthropogenic sound) over a variety of spatial and temporal scales. The abundance and distribution of many pelagic species exhibit substantial seasonal variability, highlighting the importance of predicting density specific to the season of interest. This is particularly true in dynamic regions like the California Current, where significant seasonal shifts in cetacean distribution have been documented at coarse scales. Finer scale (10 km) habitat-based density models were previously developed for many cetacean species.
occurs in this region, but most models were limited to summer/fall. The objectives of our study were two-fold: 1) develop spatially-explicit density estimates for winter/spring to support management applications, and 2) compare model-predicted density and distribution patterns to previously developed summer/fall model results in the context of species ecology. We used a well-established Generalized Additive Modeling framework to develop cetacean SDMs based on 20 California Cooperative Oceanic Fisheries Investigations (CalCOFI) shipboard surveys conducted during winter and spring between 2005 and 2015. Models were fit for short-beaked common dolphin (Delphinus delphis delphis), Dall’s porpoise (Phocoenoides dalli), and humpback whale (Megaptera novaeangliae). Model performance was evaluated based on a variety of established metrics, including the percentage of explained deviance, ratios of observed to predicted density, and visual inspection of predicted and observed distributions. Final models were used to produce spatial grids of average species density and spatially-explicit measures of uncertainty. Results provide the first fine scale (10 km) density predictions for these species during the cool seasons and reveal distribution patterns that are markedly different from summer/fall, thus providing novel insights into species ecology and quantitative data for the seasonal assessment of potential anthropogenic impacts.

**Week of 8 May 2017**


**Abstract –** As awareness of the effects of anthropogenic noise on marine mammals has grown, research has broadened from evaluating physiological responses, including injury and mortality, to considering effects on behavior and acoustic communication. Most mitigation efforts attempt to minimize injury by enabling animals to move away as noise levels are increased gradually. Recent experiences demonstrate that this approach is inadequate or even counterproductive for small, localized marine mammal populations, for which displacement of animals may itself cause harm. Seismic surveys within the ranges of harbor porpoise Phocoena phocoena in California and Māui dolphin Cephalorhynchus hectori māui in New Zealand highlight the need to explicitly consider biological risks posed by displacement during survey planning, monitoring, and mitigation. Consequences of displacement are poorly understood, but likely include increased stress and reduced foraging success, with associated effects on survival and reproduction. In some cases, such as the Critically Endangered Māui dolphin, displacement by seismic activities risks exposing the remaining 55 dolphins to bycatch in nearby fisheries. Similar concerns about military and industrial activities exist for island-associated species such as melon-headed whales Peponocephala electra in Hawai‘i; shelf-break associated species such as Cuvier’s beaked whales Ziphius cavirostris off the US Atlantic coast, and whales foraging in coastal habitats, such as the Critically Endangered western gray whale Eschrichtius robustus. We present an expanded framework for considering disturbance effects that acknowledges scientific uncertainty, providing managers and operators a more robust means of assessing and avoiding potential harm associated with both displacement and direct effects of intense anthropogenic noise exposure.


**Abstract –** Existing molecular techniques to determine sex of pinnipeds rely on multiplex PCR amplification and gel electrophoresis, and are consequently expensive, time consuming, insensitive and involve handling hazardous DNA-binding dyes. We developed a qPCR high resolution melt (HRM) assay that involves a single multiplex PCR with dissociation/melting-curve analysis to determine the melting point temperatures (Tm) of two PCR products. Two sets of primers were selected to amplify short regions of the SRY and ZFX/ZFY loci for molecular sex identification. Primers were designed based on alignment of a broad range of pinniped species to maximize applicability for most or all of the 33 species representing 2 complete superfamilies in the sub-order Caniformia. The assay was validated using 15 pinniped species totaling 122 animals of known sex. The co-amplification of short products also demonstrated improved results for sex determination of degraded samples. The use of a single step qPCR saves time and reduces the cost of running sex determination tests through reduction of labor and supply costs. This new technique will generate results more quickly and reliably, aiding in the study of population health and sex-specific dispersal and behavior patterns.

No Abstract


Abstract - Complex foldings of the vaginal wall are unique to some cetaceans and artiodactyls and are of unknown function(s). The patterns of vaginal length and cumulative vaginal fold length were assessed in relation to body length and to each other in a phylogenetic context to derive insights into functionality. The reproductive tracts of 59 female cetaceans (20 species, 6 families) were dissected. Phylogenetically-controlled reduced major axis regressions were used to establish a scaling trend for the female genitalia of cetaceans. An unparalleled level of vaginal diversity within a mammalian order was found. Vaginal folds varied in number and size across species, and vaginal fold length was positively allometric with body length. Vaginal length was not a significant predictor of vaginal fold length. Functional hypotheses regarding the role of vaginal folds and the potential selection pressures that could lead to evolution of these structures are discussed. Vaginal folds may present physical barriers, which obscure the pathway of seawater and/or sperm travelling through the vagina. This study contributes broad insights to the evolution of reproductive morphology and aquatic adaptations and lays the foundation for future functional morphology analyses.


Abstract- Breeding habitats are not well defined for many marine species. We used satellite telemetry and switching state-space modeling (SSM) to define inter-nesting habitat used by Kemp’s ridley turtles (Lepidochelys kempii) in the Gulf of Mexico. Turtles were tagged after nesting at Padre Island National Seashore, Texas, USA from 1998 through 2013 (PAIS; n = 60); Rancho Nuevo, Tamaulipas, Mexico during 2010 and 2011 (RN; n = 11); and Tecolutla, Veracruz, Mexico during 2012 and 2013 (VC; n = 11). Inter-nesting habitat lies in nearshore western Gulf of Mexico waters in the USA and Mexico with mean water depth of 14 to 19 m within a mean distance to shore of 6 to 11 km as estimated by 50% kernel density estimate, α-Hull, and minimum convex polygon methodologies. Turtles tracked during the inter-nesting period moved on average 18 km/day and a mean total distance of 399 km; mean home ranges occupied were 727 to 2984 km². Our results indicate that these nearshore Gulf waters represent a critical inter-nesting habitat for this species, where threats such as shrimp trawling and oil and gas platforms also occur. A large portion of adult females occupies this habitat for months during each nesting season. However, there is a gap in our understanding of dates when these turtles depart from foraging grounds and arrive in waters off the nesting beach, and thus of the total duration of time spent in these waters, which highlights the need for tracking adult females from foraging grounds to nesting beaches. Furthermore, the concentration of inter-nesting habitat for this species in nearshore waters of the western Gulf of Mexico in both the USA and Mexico demonstrates that international cooperation is necessary to protect essential inter-nesting habitat for this imperiled species.
https://doi.org/10.3354/meps12012

Abstract – A decade of visual surveys (2005-2014) revealed that humpbacks Megaptera novaeangliae occupy a temperate fjord system in British Columbia, Canada, in a wave pattern that propagates from outer channels in the summer to deep inland channels in late fall. Monte Carlo randomization confirmed this apparent pattern statistically. ‘Before’ and ‘after’ shift phases were most evident in July and October, respectively. We hypothesized that the ‘whale wave’ was being driven by (1) prey following, (2) the tracking of environmental proxies, (3) fine-scale philopatry, or some combination of these three factors. To evaluate these hypotheses, we collected new data in 2015, including visual and hydroacoustic surveys and oceanographic sampling. To both full-season and monthly datasets, we fit generalized additive models (GAMs) in a stepwise procedure, using variable sets that represent our hypotheses. Prey models were generally the worst predictors of humpback distribution, while the most complex habitat models were the best. The Prey model performed best in June but increasingly poorly in remaining months. The performance of all models declined throughout the season, suggesting not only that this whale wave is being driven by needs other than food, but also that untested variable(s) inform late-season distribution. Alternative explanations of the wave include physiological maintenance and social habitat partitioning. Our findings demonstrate that marine predators can use complex spatial strategies not only to navigate vast areas of ocean but also to exploit specific habitats thoroughly. Though annually persistent and specific in structure, the whale wave would go (and has gone) unnoticed in typical marine mammal surveys.


Abstract – Rorqual whales (f. Balaenopteridae) supposedly respond to increases in prey supply according to both aggregative and feeding thresholds. With the former, they gather in areas above a minimum prey density set by their basal metabolic needs. With the latter, feeding occurs only above a prey density set by the energetic cost of lunge feeding. To compare prey preferences and the two threshold types in sympatric rorquals, I conducted systematic transect surveys and behavioral observations of humpback whales (Megaptera novaeangliae) and fin whales (Balaenoptera physalus) in a British Columbia fjord system. While multiple prey features were found to influence whale aggregation and feeding, both threshold types were observed in each species’ response to krill volume. Humpback response to prey features was less predictable and influenced by more factors than that of fin whales, which appeared to be exclusively euphausivorous and interested in the deepest high-volume krill patches within the deepest channels. Compared with fin whales, humpbacks found higher-volume krill patches and had higher aggregative thresholds, but had lower feeding thresholds. Findings aligned overall with the expectations that aggregative behavior is responsive to local prey supply, while feeding thresholds are governed by less mutable energetic constraints imposed by body size and feeding mode. Both aggregative and feeding threshold responses appeared to be a function of local conditions: As total krill-like backscatter increased, feeding thresholds stabilized (became more nonlinear and more nonrandom), while aggregative thresholds destabilized. All results emphasized the importance of incorporating observations of feeding effort in studies of prey preference and habitat use.

Week of 6 March 2017


Abstract: – Ontogenetic niche theory predicts that individuals may undergo one or more changes in habitat or diet throughout their lifetime to maintain optimal growth rates, or to optimize trade-offs between mortality risk and growth. We combine skeletochronological and stable nitrogen isotope (δ15N) analyses of sea turtle humeri (n = 61) to characterize the growth dynamics of juvenile loggerhead sea turtles (Caretta caretta) during an oceanic-to-neritic ontogenetic shift. The primary objective of this study was to determine how ontogenetic niche theory extends to sea turtles, and to individuals with different patterns of resource use (discrete shifters, n = 23; facultative shifters n = 14; non-shifters, n = 24). Mean growth rates peaked at the start of the ontogenetic shift (based on change in δ15N values), but returned to pre-shift levels within 2 years. Turtles generally only experienced 1 year of relatively high growth, but the timing of peak growth relative to the start of an ontogenetic shift varied among individuals (before, n = 14; during, n = 12; after, n = 8). Furthermore, no
reduction in growth preceded the transition, as is predicted by ontogenetic niche theory. Annual growth rates were similar between non-transitioning turtles resident in oceanic and neritic habitats and turtles displaying alternative patterns of resource use. These results suggest that factors other than maximization of size-specific growth may more strongly influence the timing of ontogenetic shifts in loggerhead sea turtles, and that alternative patterns of resource use may have limited influence on somatic growth and age at maturation in this species.

*Week of 27 February 2017*

(No abstract)

(No abstract)

*Week of 13 February 2017*


*Abstract* – Divergence in acoustic signals used by different populations of marine mammals can be caused by a variety of environmental, hereditary, or social factors, and can indicate isolation between those populations. Two types of genetically and morphologically distinct short-finned pilot whales, called the Naisa- and Shiho-types when first described off Japan, have been identified in the Pacific Ocean. Acoustic differentiation between these types would support their designation as sub-species or species, and improve the understanding of their distribution in areas where genetic samples are difficult to obtain. Calls from two regions representing the two types were analyzed using 24 recordings from Hawai‘i (Naisa-type) and 12 recordings from the eastern Pacific Ocean (Shiho-type). Calls from the two types were significantly differentiated in median start frequency, frequency range, and duration, and were significantly differentiated in the cumulative distribution of start frequency, frequency range, and duration. Gaussian mixture models were used to classify calls from the two different regions with 74% accuracy, which was significantly greater than chance. The results of these analyses indicate that the two types are acoustically distinct, which supports the hypothesis that the two types may be separate sub-species.


*Abstract* – Nicaragua’s Bosawás Biosphere Reserve is a vast forested area inhabited largely by indigenous Mayangna and Miskitu people. Most Bosawás residents rely on subsistence hunting and swidden agriculture, and hunting dogs are important for finding and securing wild game. We investigated the health of hunting dogs in three communities differing in location, size, and economy. Dogs in all communities were nutritionally compromised and experienced a heavy burden of disease. Seroprevalence of canine distemper, canine parvovirus, *Rickettsia rickettsii*, and *Leptospira* spp. exceeded 50% of dogs. At least one dog was actively shedding leptospires in urine, and many dogs were anemic and/or dehydrated. These dogs interact with wildlife in the forest and humans and domestic livestock in the communities, and may therefore serve as sources of zoonotic and wildlife diseases. Bosawás represents one of the largest intact tracts of habitat for jaguars (*Panthera onca*) in Central America, and given that these communities are located within the forest, jaguars may be at risk from disease spillover from hunting dogs. Dog owners reported that four of 49 dogs had been attacked and killed by jaguars in the past year, and that retaliatory killing of jaguars was sometimes practiced. Disease spillover from dogs to wildlife could occur both in the course of dogs’ hunting activities as well as during jaguar attacks. A better understanding of dog depredation by jaguars, pathogen exposure in jaguars, and
a management strategy for the hunting dog population, are urgently needed to mitigate these dual threats to jaguars, improve the lives of hunting dogs, and safeguard the health of their owners.

**Week of 6 February 2017**


**Abstract** – Following the Deepwater Horizon oil spill, reproductive success rates in two northern Gulf of Mexico (GOMx) bottlenose dolphin (Tursiops truncatus) stocks exposed to oil were evaluated for four years during and after the spill (2010-2015). Pregnancy was determined from either 1) ultrasound examinations of the reproductive tract during capture-release health assessments, or 2) endocrine evaluations of blubber collected from dart biopsies of free-ranging dolphins. Follow-up photo-identification was used to track the status of pregnant females and any associated calves for at minimum of one year after the initial pregnancy detection (IPD). For pregnant females observed following IPD, individuals seen with a calf (reproductive success) and without one (reproductive failure) were recorded. The resulting reproductive success rates for both GOMx stocks (19.4%; 7/36) were less than a third of those reported in other areas not impacted by the spill (i.e., Sarasota Bay, FL; Indian River Lagoon, FL; and Charleston Harbor, SC) using similar techniques (64.7%; 22/34). We evaluated the relationships between reproductive success and 13 potential covariates, including stock, sighting frequency, ordinal date, progesterone, cortisol, thyroid hormones, leukocyte count, and lung health score, with a Bayesian generalized linear selection model. A strong inverse relationship (Bayes factor > 20) between reproductive success and total leukocyte count was found; there were no successes associated with maternal leukocyte counts higher than 11 cells/nL (n=18/32). The high reproductive failure rates measured in both GOMx stocks following the oil spill are consistent with mammalian literature that shows a link between petroleum exposure and reproductive impairments.

---This paper is part of a special issue of Endangered Species Research, entitled: Effects of the Deepwater Horizon oil spill on protected marine species. http://www.int-res.com/abstracts/esr/v33/... The Deepwater Horizon oil spill (DWH) covered over 110,000 square kilometers of the ocean surface and reached over 2000 kilometers of shoreline in the northern Gulf of Mexico in 2010. This extensive oiling contaminated vital foraging, migratory, and breeding habitats at the surface, in the water column, and on the ocean bottom throughout the northern Gulf of Mexico. Multiple protected marine species, including marine turtles and marine mammals were affected. The pervasive and prolonged nature of the DWH spill made exposure to oil inescapable for many animals, and caused significant injuries to marine turtle and marine mammal populations in the northern Gulf of Mexico. The unprecedented size and duration of the DWH spill required different assessment and response approaches than those used in previous spills that occurred closer to shore and in smaller, more confined areas. The papers in this Theme Section of Endangered Species Research highlight the interdisciplinary approaches needed to evaluate and quantify the nature and magnitude of exposures to oil and the resulting mortality of protected species. Deepwater Horizon was unprecedented in terms of its size and duration, and the incredible science that came in its aftermath greatly influenced the $4.5 billion settlement that was reached, the largest of its kind in US history. In this issue an impressive twenty papers were published on the effects of the spill on cetacean and sea turtle populations in the Gulf. Findings showed significant long-term effects on sea turtle and cetacean health and reproduction, which will likely continue to impact these populations for years to come.


**Abstract** – **Aim:** Human activities are creating conservation challenges for cetaceans. Spatially explicit risk assessments can be used to address these challenges, but require species distribution data, which are limited for many cetacean species. This study explores methods to overcome this limitation. Blue whales (Balaenoptera musculus) are used as a case study because they are an example of a species that have well-defined habitat and are subject to anthropogenic threats.
**Location:** Eastern Pacific Ocean, including the California Current (CC) and eastern tropical Pacific (ETP), and northern Indian Ocean (NIO).

**Methods:** We used 12 years of survey data (377 blue whale sightings and approximately 225,400 km of effort) collected in the CC and ETP to assess the transferability of blue whale habitat models. We used the models built with CC and ETP data to create predictions of blue whale distributions in the data-poor NIO because key aspects of blue whale ecology are expected to be similar in these ecosystems.

**Results:** We found that the ecosystem-specific blue whale models performed well in their respective ecosystems, but were not transferable. For example, models built with CC data could accurately predict distributions in the CC, but could not accurately predict distributions in the ETP. However, the accuracy of models built with combined CC and ETP data was similar to the accuracy of the ecosystem-specific models in both ecosystems. Our predictions of blue whale habitat in the NIO from the models built with combined CC and ETP data compare favourably to hypotheses about NIO blue whale distributions, provide new insights into blue whale habitat, and can be used to prioritize research and monitoring efforts.

**Main Conclusions:** Predicting cetacean distributions in data-poor ecosystems using habitat models built with data from multiple ecosystems is potentially a powerful marine conservation tool and should be examined for other species and regions.

Week of 23 January 2017


*Abstract* – There are two recognized species in the genus *Berardius*, Baird’s and Arnoux’s beaked whales. In Japan, whales have traditionally recognized two forms of Baird’s beaked whales, the common “slate-gray” form and a smaller, rare “black” form. Previous comparison of mtDNA control region sequences from three black specimens to gray specimens around Japan indicated that the two forms comprise different stocks and potentially different species. We have expanded sampling to include control region haplotypes of 178 Baird’s beaked whales from across their range in the North Pacific. We identified five additional specimens of the black form from the Aleutian Islands and Bering Sea, for a total of eight “black” specimens. The divergence between mtDNA haplotypes of the black and gray forms of Baird’s beaked whale was greater than their divergence from the congeneric Arnoux’s beaked whale found in the Southern Ocean, and similar to that observed among other congeneric beaked whale species. Taken together, genetic evidence from specimens in Japan and across the North Pacific, combined with evidence of smaller adult body size, indicate presence of an unnamed species of *Berardius* in the North Pacific.


*Abstract* – Marine mammal, sea turtle, and seabird bycatch was estimated for the California swordfish drift gillnet fishery during a 26-year period (1990-2015), using random forest regression trees. Tree estimates were compared with traditional annual ratio estimates generated from the same observer data. Ratio estimates suffer from systematic bias (under- and overestimation of bycatch) when observed bycatch is rare, bycatch rates are inferred only from same-year data, and observer coverage is low. Model-based approaches result in more stable annual bycatch estimates with better precision, because estimates are informed by all available data. Even in years with zero observed bycatch, expected values from regression trees are usually positive (sometimes fractions of animals) and have error estimates (thus acknowledging the possibility that animals may be caught even when none are observed), whereas corresponding ratio estimates would be zero and have no error estimates. Regression tree bycatch models include a suite of oceanographic, location, and gear variables used as predictors to estimate bycatch at the fishing-set level. Variables that significantly influenced bycatch rates were identified with a variable selection approach using the R-package rFPermute and validated with a simulated bycatch dataset. Results indicate that rFPermute can succeed in identifying significant predictor variables for rare bycatch events, even when these events represent <1% of all data.

Abstract – Network modeling techniques provide a means for quantifying social structure in populations of individuals. Data used to define social connectivity are often expensive to collect and based on case-specific and ad hoc criteria. Moreover, in applications involving animal social networks, collection of these data is often opportunistic and can be invasive. Frequently, the social network of interest for a given population is closely related to the way individuals move. Thus telemetry data, which are minimally-invasive and relatively inexpensive to collect, present an alternative source of information. We develop a framework for using telemetry data to infer social relationships among animals. To achieve this, we propose a Bayesian hierarchical model with an underlying dynamic social network controlling movement of individuals via two mechanisms: an attractive effect, and an aligning effect. We demonstrate the model and its ability to accurately identify complex social behavior in simulation, and apply our model to telemetry data arising from killer whales. Using auxiliary information about the study population, we investigate model validity and find the inferred dynamic social network is consistent with killer whale ecology and expert knowledge.


Abstract – The effective evaluation of trophic interactions in pelagic food webs is essential for understanding food web ecology, conservation biology, and management. We tested the applicability of compound-specific isotope analysis of amino acids (CSIA-AA) for (1) characterizing trophic positions (TPs) of nine species from four trophic groups (tunas, squids, myctophids, and euphausiids) within a pelagic food web in the eastern tropical Pacific (ETP) Ocean, (2) evaluating trophic discrimination factors (TDFs) of each trophic group, and (3) detecting spatial changes in TPs and food chain length across a region with heterogeneous productivity. Although d15N values of bulk tissues generally increased from south-to-north, CSIA-AA revealed that trophic positions were uniform throughout our study area. These results suggest that variability in d15N values were largely driven by nitrogen cycling dynamics in the ETP, which highlights the importance of these processes for the interpretation of d15N values in food web studies. Absolute TP estimates were unrealistic for higher-level species, and TDFs (tunas: 4.0ppt, squids: 4.6ppt, myctophids: 5.0ppt, and euphausiids: 7.0ppt) were lower than a widely used ecosystem TDF. We used remotely sensed oceanographic data to evaluate the physical oceanography and biological productivity throughout our study area and found significant relationships between d15N values, nitrate concentrations, and SST across our study area. We did not find a gradient in phytoplankton cell size co-occurring with an expected productivity gradient across our sampling region, which substantiated our isotope results indicating non-significant spatial changes in TP and food chain length across the ETP.


Abstract - Many aspects of blue whale biology are poorly understood. Some of the gaps in our knowledge, such as those regarding their basic taxonomy and seasonal movements, directly affect our ability to monitor and manage blue whale populations. As a step towards filling in some of these gaps, microsatellite and mtDNA sequence analyses were conducted on blue whale samples from the Southern Hemisphere, the eastern tropical Pacific (ETP) and the northeast Pacific. The results indicate that the ETP is differentially used by blue whales from the northern and southern eastern Pacific, with the former showing stronger affinity to the region off Central America known as the Costa Rican Dome, and the latter favouring the waters of Peru and Ecuador. Although the pattern of genetic variation throughout the Southern Hemisphere is compatible with the recently proposed subspecies status of Chilean blue whales, some discrepancies remain between catch lengths and lengths from aerial photography, and not all blue whales in Chilean waters can be assumed to be of this type.
Also, the range of the proposed Chilean subspecies, which extends to the Galapagos region of the ETP, at least seasonally, perhaps should include the Costa Rican Dome and the eastern North Pacific as well.


Abstract – Millions of spinner (Stenella longirostris) and pantropical spotted dolphins (Stenella attenuata) died as bycatch in tuna nets in the eastern tropical Pacific Ocean. Despite three decades of protection, they show little-to-no sign of recovery. In efforts to establish biologically meaningful management boundaries for recovery, endemic subspecies and multiple stocks have been proposed. However, genetic differentiation among most of these units has been difficult to identify, possibly due to low statistical power stemming from large historical abundances, ongoing gene flow, and recent divergence. We tested for genetic structure at multiple hierarchical levels by analyzing the largest dataset to date brought to bear on these questions. Single nucleotide polymorphisms (SNPs) were collected from nuclear DNA regions associated with the restriction enzyme site PstI from 72 spinner dolphins and 58 pantropical spotted dolphins using genotype-by-sequencing (GBS). Our results support the current subspecies for both species and indicate stock-level separation for Tres Marias spinner dolphins and the two offshore pantropical spotted dolphin stocks in this area. These results are critically important for the ongoing management and recovery of these highly-impacted pelagic dolphins in the eastern tropical Pacific Ocean.


Abstract - To effectively protect and manage marine mammals, contemporary information on their abundance and distribution is essential. Several factors influence present-day insight including the accessibility of the study area and the degree of difficulty in locating and studying target species. The offshore waters of the Gulf of Alaska are important habitat to a variety of cetaceans yet have remained largely unsurveyed due to its remote location, vast geographic area, and challenging environmental conditions. Between 2009 and 2015, three vessel surveys were conducted using line-transect sampling methods to estimate cetacean abundance and density. Here, we present results on the distribution for all species encountered and density and abundance for six species, including humpback whales (Megaptera novaeangliae), fin whales (Balaenoptera physalus), sperm whales (Physeter macrocephalus), blue whales (B. musculus), killer whales (Orcinus Orca), and Dall’s porpoise (Phocoenoides dallii). Fin whales, humpback whales, and Dall’s porpoise were the most abundant species. Beaked whales were documented only in 2015. Prior to this study, recent sightings of blue whales were rare, likely related to the lack of offshore survey coverage. No North Pacific right whales (Eubalaena japonica) were sighted, underscoring the critically endangered status of this species in a formerly populous habitat. Although these results provide the first estimates from offshore waters, additional effort is necessary to assess trends and to obtain baseline data for the rare and cryptic species in order to better inform conservation and management actions.

Week of 19 December 2016


Abstract – Passive acoustic monitoring of dolphins is limited by our ability to classify calls to species. Significant overlap in call characteristics among many species, combined with a wide range of call types and acoustic behavior, makes classification of calls to species challenging. Here, we introduce BANTER, a compound acoustic classification method for dolphins that utilizes information from all call types produced by dolphins rather than a single call type, as has been typical for acoustic classifiers. Output from the passive acoustic monitoring software, PAMGuard, was used to create independent classifiers for whistles, echolocation clicks, and burst pulses, which were then merged into a final, compound classifier for each species. Classifiers for five species found in the California Current ecosystem were trained and tested using 153 single-species acoustic events recorded during a 4.5 mo combined visual and acoustic shipboard cetacean survey off the west coast of the United States. Correct classification scores for individual species ranged from 71% to 92%, with an
overall correct classification score of 84% for all five species. The conceptual framework of this approach easily lends itself to other species and study areas as well as to noncetacean taxa.

**Week of 12 December 2016**


No abstract


Abstract – The vaquita (Phocoena sinus) is the world's most endangered marine mammal with approximately 245 individuals remaining in 2008. This species of porpoise is endemic to the northern Gulf of California, Mexico, and historically the population has declined because of unsustainable bycatch in gillnets. An illegal gillnet fishery for an endangered fish, the totoaba (Totoaba macdonaldi), has recently resurfaced throughout the vaquita's range. The secretive but lucrative wildlife trade with China for totoaba swim bladders has probably increased vaquita bycatch mortality by an unknown amount. Precise population monitoring by visual surveys is difficult because vaquitas are inherently hard to see and have now become so rare that sighting rates are very low. However, their echolocation clicks can be identified readily on specialized acoustic detectors. Acoustic detections on an array of 46 moored detectors indicated vaquita acoustic activity declined by 80% between 2011 and 2015 in the central part of the species’ range. Statistical models estimated an annual rate of decline of 34% (95% Bayesian credible interval –48% to –21%). Based on results from 2011 to 2014, the government of Mexico enacted and is enforcing an emergency 2-year ban on gillnets throughout the species’ range to prevent extinction, at a cost of US$74 million to compensate fishers. Developing precise acoustic monitoring methods proved critical to exposing the severity of vaquitas’ decline and emphasizes the need for continual monitoring to effectively manage critically endangered species.


Abstract - Delineating populations of pantropical marine fish is a difficult process, due to widespread geographic ranges and complex life history traits in most species. Exocoetus volitans, a species of two-winged flyingfish, is a good model for understanding large-scale patterns of epipelagic fish population structure because it has a circumtropical geographic range and completes its entire life cycle in the epipelagic zone. Buoyant pelagic eggs should dictate high local dispersal capacity in this species, although a brief larval phase, small body size, and short lifespan may limit the dispersal of individuals over large spatial scales. Based on these biological features, we hypothesized that E. volitans would exhibit statistically and biologically significant population structure defined by recognized oceanographic barriers. We tested this hypothesis by analyzing cytochrome b mtDNA sequence data (1106 bps) from specimens collected in the Pacific, Atlantic and Indian oceans (n = 266). AMOVA, Bayesian, and coalescent analytical approaches were used to assess and interpret population-level genetic variability. A parsimony-based haplotype network did not reveal population subdivision among ocean basins, but AMOVA revealed limited, statistically significant population structure between the Pacific and Atlantic Oceans (φST = 0.035, p<0.001). A spatially-unbiased Bayesian approach identified two circumtropical population clusters north and south of the Equator (φST = 0.026, p<0.001), a previously unknown dispersal barrier for an epipelagic fish. Bayesian demographic modeling suggested the effective population size of this species increased by at least an order of magnitude ~150,000 years ago, to more than 1 billion individuals currently. Thus, high levels of genetic similarity observed in E. volitans can be explained by high rates of gene flow, a dramatic and recent population expansion, as well as extensive and consistent dispersal throughout the geographic range of the species.


Abstract – The number of Mexico's endemic porpoise, the vaquita (Phocoena sinus), is collapsing primarily due to bycatch in illegal gillnets set for totoaba (Totoaba macdonaldi), an endangered fish whose swim bladders are exported to China. Previous research estimated that vaquitas declined from about 567 to 245 individuals
between 1997 and 2008. Acoustic monitoring between 2011 and 2015 showed a decline of 34%/year. Here, we combine visual line transect and passive acoustic data collected simultaneously in a robust spatial analysis to estimate that only 59 (95% Bayesian Credible Interval [CRI] 22–145) vaquita remained as of autumn 2015, a decrease since 1997 of 92% (95% CRI 80–97%). Risk analysis suggests that if the current, temporary gillnet ban is maintained and effectively enforced, vaquitas could recover to 2008 population levels by 2050. Otherwise, the species is likely to be extinct within a decade.

**Week of 5 December 2016**


**Abstract** - The green turtle (*Chelonia mydas*) foraging aggregation along the Texas coast has increased dramatically in recent years, but the source populations for these turtles have not been adequately resolved. Previous mixed stock analysis (MSA) based on 490 base pair (bp) mitochondrial control region haplotypes suggested a large Florida contribution, but widespread sharing of common haplotypes among potential source populations and incomplete source population baseline data precluded precise assessment. To test the hypothesis that Texas turtles may represent proximal western Gulf of Mexico (GoM) nesting populations, we analyzed novel rookery samples from Rancho Nuevo, Tamaulipas, Mexico (RNMX) and conducted oceanic connectivity simulations. The RNMX samples yielded haplotypes CM-A1.1 and CM-A3.1 in frequencies not significantly different from those of the central eastern Florida nesting population. However, mitogenomic sequencing identified a diagnostic mitochondrial SNP (mtSNP) variant that is fixed in RNMX relative to the Florida CM-A1.1 lineage. Pairwise comparisons indicate that the Tamaulipas rookery represents a discrete population relative to those previously described in the northern Greater Caribbean, warranting recognition of a western GoM management unit (MU). Contrary to previous findings, the Florida populations were ruled out as major contributors to the Texas aggregation through screening of the mtSNP. Mixed stock analysis incorporating the mtSNP data suggested a western GoM origin for approximately 70% of the Texas foraging aggregation, with Quintana Roo contributing the majority of the remainder. Backtracking simulations within an ocean circulation model were broadly congruent with genetic results in indicating substantial probability of oceanic transport from Mexican rookeries to the Texas coast (68%) while also dismissing the possibility of transport from the eastern Florida rookeries (0%). The mixed stock analyses and backtracking simulations are consistent with previous hypotheses implicating oceanic dispersal followed by natal homing by neritic juveniles to explain juvenile green turtle distributions. In contrast to a pattern of stepping stone connectivity across the remaining northern Greater Caribbean, the Texas foraging aggregation was distinct from all others analyzed in the region, including one in the eastern GoM. This isolation highlights the significance of Texas as developmental habitat for the proposed western GoM MU and reiterates the importance of continued international cooperation to facilitate recovery of this stock. This study also underscores the importance of satisfying underlying assumptions of mixed stock analysis in order to make robust inferences of connectivity.

**Week of 7 November 2016**


**Abstract** – An understanding of population dynamics is needed to assess the viability of migratory species. Monitoring of marine turtles at foraging grounds may detect changes in population trends that would take decades to be seen at nesting beaches. Mixed Stock Analysis using molecular markers provides a tool for estimating the origin of turtles sampled at foraging grounds. Here, we analysed mitochondrial DNA sequences of 90 immature green turtles at 2 foraging grounds in northwestern Sabah, Malaysia. We used data from 30 Indo-Pacific green turtle rookeries as the baseline for tracing the origin of turtles at the 2 foraging grounds. The inferred origins of turtles at the 2 locations were not different and indicated that the majority originated from 3 major populations in Southeast Asia, the Turtle Islands of Sarawak in northwestern Borneo (29%), the Turtle Islands Heritage Protected Area (TIHPA) (28%) and Peninsular Malaysia (25%). Previous analyses indicated a
1:4 female-biased sex ratio at the foraging grounds, and based on our results, this largely reflects the use of unshaded beach hatcheries at some of the source rookeries for decades, which resulted in mostly female hatchlings. This result is supported by differences in the origins of male and female turtles. The result suggests a greater proportion of males originating from Peninsular Malaysia and fewer males originating from Sarawak and possibly the TIHPA compared to females. We discuss the implications of hatchery practices that influence sex ratios of hatchlings and recommend future research to improve the management of marine turtles in the region.


Abstract – Nontargeted GC×GC-TOF/MS analysis of blubber from 8 common bottlenose dolphins (Tursiops truncatus) inhabiting the Southern California Bight was performed to identify novel, bioaccumulative DDT-related compounds and to determine their abundance relative to the commonly studied DDT-related compounds. We identified 45 bioaccumulative DDT-related compounds of which the majority (80%) is not typically monitored in environmental media. Identified compounds include transformation products, technical mixture impurities such as tris(chlorophenyl)methane (TCPM), the presumed TCPM metabolite tris(chlorophenyl)methanol (TCPMOH), and structurally related compounds with unknown sources, such as hexa- to octachlorinated diphenylethane. To investigate impurities in pesticide mixtures as possible sources of these compounds, we analyzed technical DDT, the primary source of historical contamination in the region, and technical Dicofol, a current use pesticide that contains DDT-related compounds. The technical mixtures contained only 33% of the compounds identified in the blubber, suggesting that transformation products contribute to the majority of the load of DDT-related contaminants in these sentinels of ocean health. Quantitative analysis revealed that TCPM was the second most abundant compound class detected in the blubber, following DDE, and TCPMOH loads were greater than DDT. QSPr estimates verified 4,4′,4″-TCPM and 4,4′,4″-TCPMOH are persistent and bioaccumulative.

Week of 24 October 2016


Abstract – Sea turtle nests usually suffer a high mortality on important nesting grounds. Understanding the main factors that influence hatching success and productivity on important rookeries of endangered populations is essential to properly manage and protect them. The amount of clay can be high on some nesting beaches and could affect egg incubation. In the main loggerhead rookery in the Eastern Atlantic (Boa Vista, Cape Verde), clays and silts are very common on nearly 10% of the main nesting beaches, and turtles do not avoid clay substrates when they lay their eggs. Nests incubated on sandy substrates rich on clay and silt had a very high mortality. The same occurs on nests with the eggs stained with clay and incubated in sand free of clay. The eggs experimentally incubated with a covering layer of clay (30%, 50% and 80% of the eggshell) suffered an important loss of water, which in the extreme cases was irreversible, causing the death of the embryos. 75% of the eggs with 80% of their eggshells covered with clay died, while the mortality rate of the control eggs was only 25%. The salt content of the clay/silt seems not to be responsible for the egg dehydration and death. The hatchlings born from eggs with only 30% of the eggshell covered by clay were slower that those born from control eggs. Substrates with a significant presence of clay/silt can seriously disrupt embryonic development, reducing the emergence success of nests and should be avoided on nest relocation programs.


No abstract

Week of 17 October 2016

Abstract — 1. Climate change is predicted to intensify the impacts of invasive species by enhancing their performance relative to their native counterparts. However, few studies have compared the performance of invasive predators and native prey, despite the fact that non-native predators are well known to disrupt native communities.

2. The ‘trophic sensitivity hypothesis’ suggests that predators are less tolerant of increasing environmental stress than their prey, whereas the ‘tolerant invaders hypothesis’ suggests that invaders are more tolerant than native species due to selection during the introduction process. It is therefore unclear how invasive predators will respond to increasing climate stressors.

3. We coupled physiological measurements (thermal tolerance, thermal optima, salinity tolerance, predation rate) with environmental time series data to assess the effects of warming and extreme low salinity events on non-native predators (gastropods) and native prey (oysters) from a coastal ecosystem.

4. In general support of the trophic sensitivity hypothesis, we found that both non-native predators exhibited lower thermal optima relative to native prey, lower salinity tolerance and one predator was less tolerant of warming. However, because warming tolerance is extremely high (i.e. habitat temperature is 7.9-21°C below thermal tolerance), near term warming may first increase predator performance (consumption and growth rates), with negative effects on prey. Low salinity will likely produce heterogeneous effects on predator-prey interactions due to varying watershed sizes among estuaries that control the duration of low salinity events.

5. The trophic sensitivity hypothesis may be a useful framework for understanding community responses to extreme climate change, which portends a decoupling of predator-prey interactions. However, we conclude that this hypothesis must be evaluated in environmental context and that coupling physiological metrics with in situ environmental data offers the best predictive power of near-term climate change impacts on invaded communities. Within our study system, warming is likely to intensify the impacts of both invasive predators, which may greatly reduce the abundance of the native oyster, a species of conservation and restoration focus.


Abstract — Three ecotypes of killer whale occur in partial sympatry in the North Pacific. Individuals assortatively mate within the same ecotype, resulting in correlated ecological and genetic differentiation. A key question is whether this pattern of evolutionary divergence is an example of incipient sympatric speciation from a single panmictic ancestral population, or whether sympatry could have resulted from multiple colonisations of the North Pacific and secondary contact between ecotypes. Here, we infer multilocus coalescent trees from >1000 nuclear single-nucleotide polymorphisms (SNPs) and find evidence of incomplete lineage sorting so that the genealogies of SNPs do not all conform to a single topology. To disentangle whether uncertainty in the phylogenetic inference of the relationships among ecotypes could also result from ancestral admixture events we reconstructed the relationship among the ecotypes as an admixture graph and estimated f4-statistics using TreeMix. The results were consistent with episodes of admixture between two of the North Pacific ecotypes and the two outgroups (populations from the Southern Ocean and the North Atlantic). Gene flow may have occurred via unsampled ‘ghost’ populations rather than directly between the populations sampled here. Our results indicate that because of ancestral admixture events and incomplete lineage sorting, a single bifurcating tree does not fully describe the relationship among these populations. The data are therefore most consistent with the genomic variation among North Pacific killer whale ecotypes resulting from multiple colonisation events, and secondary contact may have facilitated evolutionary divergence. Thus, the present-day populations of North Pacific killer whale ecotypes have a complex ancestry, confounding the tree-based inference of ancestral geography.

Abstract — Three ecotypes of killer whale occur in partial sympatry in the North Pacific. Individuals assortatively mate within the same ecotype, resulting in correlated ecological and genetic differentiation. A key question is whether this pattern of evolutionary divergence is an example of incipient sympatric speciation from a single panmictic ancestral population, or whether sympatry could have resulted from multiple colonisations of the North Pacific and secondary contact between ecotypes. Here, we infer multilocus coalescent trees from >1000 nuclear single-nucleotide polymorphisms (SNPs) and find evidence of incomplete lineage sorting so that the genealogies of SNPs do not all conform to a single topology. To disentangle whether uncertainty in the phylogenetic inference of the relationships among ecotypes could also result from ancestral admixture events we reconstructed the relationship among the ecotypes as an admixture graph and estimated f4-statistics using TreeMix. The results were consistent with episodes of admixture between two of the North Pacific ecotypes and the two outgroups (populations from the Southern Ocean and the North Atlantic). Gene flow may have occurred
Week of 11 October 2016


Abstract – The eastern Pacific warm pool supports reef-building corals, as well as distinct communities of plankton, fishes, marine mammals and birds. This habitat is characterized by warm, low-salinity surface water lying on top of a strong, shallow thermocline. It is bounded by the South Equatorial Current and equatorial cold tongue to the south, cooler and more saline subtropical water to the northwest, and cold eastern boundary currents to the north and south (California and Peru Currents). The continental boundary influences atmospheric forcing by gap winds during winter and by causing the rainy Intertropical Convergence Zone to be located north of the equator and over the warm pool. Patterns of waves, tides and tropical cyclones impinging on coral reefs are described. The structure and variability of water masses and circulation are determined by solar and atmospheric processes, both within and outside of the region. To the west of the Galápagos, surface circulation is predominantly the east-west equatorial currents. Near the coast, surface circulation is modified by the coastal boundary, local winds, eddies, and interaction with eastern boundary currents. Primary productivity depends on oceanic upwelling along the equator and local centers of upwelling and wind mixing in coastal waters. Eastern tropical Pacific surface waters are moderately productive. Phytoplankton productivity is limited by a lack of the micronutrient dissolved iron, except where local coastal processes provide a source, so that macronutrients such as nitrate are never depleted. Seasonal changes in solar forcing, winds, rainfall, surface temperature and salinity, and other environmental characteristics are described, although seasonality in this region is not as pronounced as at higher latitudes. In contrast, interannual variations caused by the El Niño-Southern Oscillation across the entire tropical Indo-Pacific are very important in this region (Chap. 4). Oxygen depletion is extreme below the sharp thermocline, with consequences for mesopelagic and subthermocline benthic organisms. Surface waters are relatively low pH and marginally carbonate-saturated. Climate change is predicted to lead to future oceanographic changes in this region: warming and acidification of surface waters, increased stratification and reduced productivity, and upwelling/mixing of hypoxic waters into the surface layer. These changes are likely to affect organisms and populations living in the eastern tropical Pacific.


Abstract – The seasonal variations and the interactions of the water masses in the tropical Pacific off central Mexico (TPCM) and four surrounding areas were examined based on an extensive new hydrographic database. The regional water masses were redefined in terms of absolute salinity (SA) and conservative temperature (Q) according to the Thermodynamic Equation of Seawater 2010 (TEOS-10). Hydrographic data and the evaporation minus (precipitation + runoff) balance were used to investigate the origin and seasonality of two salinity minima in the area. The shallow (50–100 m) salinity minimum originates with the California Current System and becomes saltier as it extends southeastward and mixes with tropical subsurface waters while the surface salinity minimum extends farther north in the TPCM in summer and fall because of the northward advection of tropical surface waters. The interactions between water masses allow a characterization of the seasonal pattern of circulation of the Mexican Coastal Current (MCC), the tropical branch of the California Current, and the flows through the entrance of the Gulf of California. The seasonality of the MCC inferred from the distribution of the water masses largely coincides with the geostrophic circulation forced by an annual Rossby wave.

**Abstract** – Studying the ontogeny of vocal behavior is crucial to understanding the roles of factors such as social influence or acoustic environment in the development of normal adult vocal repertoires. We investigated the ontogeny of Blainville’s beaked whale (*Mesoplodon densirostris*) clicks using recordings from mother-calf pairs in the Bahamas. Results indicate calves from three months of age echolocate using clicks similar to those of adults. As neonates are not vocalizing immediately after birth, they may be eavesdropping on their mothers’ clicks allowing them to follow during foraging dives shortly after birth, minimizing their time left alone at the surface and vulnerable to predation.


**Abstract** – The dive behavior of gravid leatherback turtles (*Dermochelys coriacea*) was studied during the internesting interval in two western Pacific nesting regions: Papua Barat, Indonesia, and the Solomon Islands in 2006, 2007, and 2010. We used three types of dive data: time-at-depth data (Papua Barat: *N* = 4; Solomon Islands: *N* = 6), intermittent dive data (Papua Barat: *N* = 6) obtained from ARGOS satellite transmitters, and continuous dive data obtained from recovered semi-archival tags (Papua Barat: *N* = 1, Solomon Islands: *N* = 1). All dive data demonstrated that the leatherback turtles routinely dove to deep waters (around 150 m) throughout the internesting interval. The continuous dive data showed that turtles spent 37.3% of their time in routine deep dives and that they stayed in cold waters below the thermocline. Fine-scale monitoring (1-s interval, 0.5 m of resolution) suggested that these routine deep dives were not accompanied with any wiggles (up-and-down undulations in the depth profile) or flat-bottom phases, and they reached deep waters by gliding, which suggests that these dives may have served to conserve energy and/or to thermoregulate. Comparison with the dive behavior in other regions (Costa Rica, French Guiana, Grenada, Malaysia, and St. Croix) suggests that gravid leatherback turtles in all regions except French Guiana assume an energy-saving strategy during the internesting interval that involves gliding to or resting on the sea floor in colder water. The behavioral tactics (dive patterns) they use, however, differ because of bathymetric constraints.


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**Week of 19 September 2016**

**Week of 29 August 2016**

**Week of 15 August 2016**


**Abstract** – The dramatic increase in the application of genomic techniques to non-model organisms (NMOs) over the past decade has yielded numerous valuable contributions to evolutionary biology and ecology, many of which would not have been possible with traditional genetic markers. We review this recent progression with a particular focus on genomic studies of marine mammals, a group of taxa that represent key macroevolutionary transitions from terrestrial to marine environments and for which available genomic resources have recently undergone notable rapid growth. Genomic studies of NMOs utilize an expanding range of approaches, including whole genome sequencing, restriction site-associated DNA sequencing, array-based sequencing of single nucleotide polymorphisms and target sequence probes (e.g., exomes), and transcriptome sequencing. These approaches generate different types and quantities of data, and many can be applied with limited or no prior genomic resources, thus overcoming one traditional limitation of
research on NMOs. Within marine mammals, such studies have thus far yielded significant contributions to the fields of phylogenomics and comparative genomics, as well as enabled investigations of fitness, demography, and population structure. Here we review the primary options for generating genomic data, introduce several emerging techniques, and discuss the suitability of each approach for different applications in the study of NMOs.

**Week of 8 August 2016**


Abstract - Three ecotypes of killer whale occur in partial sympathy in the North Pacific. Individuals assortatively mate within the same ecotype, resulting in correlated ecological and genetic differentiation. A key question is whether this pattern of evolutionary divergence is an example of incipient sympatric speciation from a single panmictic ancestral population, or whether sympatry could have resulted from multiple colonisations of the North Pacific and secondary contact between ecotypes. Here, we infer multi-locus coalescent trees from >1,000 nuclear SNPs and find evidence of incomplete lineage sorting so that the genealogies of SNPs do not all conform to a single topology. To disentangle whether uncertainty in the phylogenetic inference of the relationships among ecotypes could result from ancestral admixture events we reconstructed the relationship among the ecotypes as an admixture graph and estimated f_4 statistics using TreeMix. The results were consistent with episodes of admixture between two of the North Pacific ecotypes and the two outgroups (populations from the Southern Ocean and the North Atlantic). Gene flow may have occurred via unsampled ‘ghost’ populations rather than directly between the populations sampled here. Our results indicate that due to ancestral admixture events and incomplete lineage sorting, a single bifurcating tree does not fully describe the relationship among these populations. The data are therefore most consistent with the genomic variation among North Pacific killer whale ecotypes resulting from multiple colonisation events, and secondary contact may have facilitated evolutionary divergence. Thus, the present-day populations of North Pacific killer whale ecotypes have a complex ancestry, confounding the tree-based inference of ancestral geography.


Abstract – Echolocation signals produced by beaked whales (family: Ziphiidae) include frequency-modulated (FM) pulses that appear to have species-specific characteristics. To date there has been no established evidence that a single species of beaked whale might produce more than one type of FM pulse. In 2014 a group of Blainville’s beaked whales (*Mesoplodon densirostris*) were sighted off of southern California; recordings included FM pulses with significant increases in peak frequency, center frequency, and -10 dB bandwidth relative to FM pulses previously attributed to this species. This research suggests there may be greater variation in received beaked whale FM pulses than previously understood.

**Week of 25 July 2016**


No abstract


Abstract – Humpback whales (*Megaptera novaeangliae*) are known to interfere with attacking killer whales (*Orcinus orca*). To investigate why, we reviewed accounts of 115 interactions between them. Humpbacks initiated the majority of interactions (57% vs. 43%; n = 72), although the killer whales were almost exclusively mammal-eating forms (MEKWs, 95%) vs. fish-eaters (5%; n = 108). When MEKWs approached humpbacks (n = 27), they attacked 85% of the time and targeted only calves. When humpbacks approached killer whales (n = 41),
93% were MEKWs, and ≥87% of them were attacking or feeding on prey at the time. When humpbacks interacted with attacking MEKWs, 11% of the prey were humpbacks and 89% comprised 10 other species, including three cetaceans, six pinnipeds, and one teleost fish. Approaching humpbacks often harassed attacking MEKWs (≥55% of 56 interactions), regardless of the prey species, which we argue was mobbing behavior. Hump-back mobbing sometimes allowed MEKW prey, including non-humpbacks, to escape. We suggest that humpbacks initially responded to vocalizations of attacking MEKWs without knowing the prey species targeted. Although reciprocity or kin selection might explain communal defense of conspecific calves, there was no apparent benefit to humpbacks continuing to interfere when other species were being attacked. Interspecific altruism, even if unintentional, could not be ruled out.

*Week of 18 July 2016*


*Abstract*—The occurrence, distribution, group size and abundance of California coastal stock bottlenose dolphins (*Tursiops truncatus*) were assessed during a boat-based photo-identification study between November 2009 and April 2011 off San Diego, California. A total of 31 photographic surveys were completed and dolphin groups were encountered on 30 (97%) of them. A total of 115 dolphin groups were observed and 346 individuals photographically identified. All groups were sighted within approximately 1-2 km of shore. The mean group size was 8.2 (SE = 0.6) and the average number of dolphins and groups encountered per survey was 31.5 (SE = 4.2) and 3.9 (SE = 0.5), respectively. Low resighting rates (mean = 2.2; SE = 0.8) and an ever-increasing rate of discovery for previously unidentified dolphins were observed. Strikingly, 258 of the 346 identified dolphins during this study were not represented in the prior 1981-2005 photo-identification catalog for San Diego. Dolphins were considered “marked” if they had two or more dorsal fin nicks. Mark-recapture analysis using POPAN as well as closed models in RMark produced abundance estimates of 515 marked dolphins (95% CI = 470-564, SE = 24.0) and 453 marked dolphins (95% CI = 411-524, SE = 28.1), respectively. Differences in encounter rates, group size and number of groups encountered per survey during the 2009-2011 study were apparent when compared to earlier studies in the same area between 1984 and 2005.

*Week of 5 July 2016*


*Abstract*—Effective species conservation and management requires information on species distribution patterns, which is challenging for highly mobile and cryptic species that may be subject to multiple anthropogenic stressors across international boundaries. Understanding species–habitat relationships can improve the assessment of trends and distribution by explicitly allowing high-resolution data on habitats to inform abundance estimation and the identification of protected areas. In this study, we aggregated an unprecedented set of survey data of a marine top predator, the harbor porpoise (*Phocoena phocoena*), collected in the UK (SCANS II, Dogger Bank), Belgium, the Netherlands, Germany, and Denmark, to develop seasonal habitat-based density models for the central and southern North Sea. Visual survey data were collected over 9 yr (2005–2013) by means of dedicated line-transect surveys, taking into account the proportion of missed sightings. Generalized additive models of porpoise density were fitted to 156,630 km of on-effort survey data with 14,356 sightings of porpoise groups. Selected predictors included static and dynamic variables, such as depth, distance to shore and to sandeel (*Ammodyses* spp.) grounds, sea surface temperature (SST), proxies for fronts, and day length. Day length and the spatial distribution of daily SST proved to be good proxies for “season,” allowing predictions in both space and time. The density models captured seasonal distribution shifts of porpoises across international boundaries. By combining the large-scale international SCANS II survey with the more frequent, small-scale national surveys, it has been possible to provide seasonal maps that will be used to assist the EU Habitats and Marine Strategy Frame- work Directives in effectively assessing the conservation status of harbor porpoises. Moreover, our results can facilitate the identification of regions where human
activities and disturbances are likely to impact the population and are especially relevant for marine spatial planning, which requires accurate fine-scale maps of species distribution to assess risks of increasing human activities at sea.

**Week of 20 June 2016**


*Abstract* - Vertebrate vision is mediated by two types of photoreceptors, rod and cone cells. Rods are highly sensitive and confer vision in dim-light, whereas cones are used in bright-light conditions and enable high acuity color vision. Most mammals have dichromatic color vision and employ two cone pigment genes (*SWS1, LWS*). Cone monochromacy occurs when one of the cone opsins (usually *SWS1*) is inactivated and is present in assorted subterranean, nocturnal, and aquatic mammals. Rod monochromacy occurs when both cone photoreceptors are inactivated, resulting in a pure rod retina. The latter condition is extremely rare in mammals and has only been confirmed with genetic evidence in five cetacean lineages, golden moles, armadillos, and sloths. Cetacean taxa with rod monochromacy include Balaenidae (bowhead and right whales), Balaenopteroidea (rorquals plus gray whale), *Metoplodon bidens* (Sowerby’s beaked whale), *Physseter macrocephalus* (sperm whale), and *Kogia breviceps* (pygmy sperm whale). The first genetic evidence for rod monochromacy in these taxa consisted of inactivated copies of both of their cone pigment genes (*SWS1, LWS*). However, other components of the cone phototransduction cascade are also predicted to accumulate inactivating mutations (frameshifts, premature stop codons, splice site mutations) in rod monochromats. Here, we employ genome sequences and exon capture data from four baleen whales (bowhead, two minke whales, fin whale) and five toothed whales (sperm whale, Yangtze River dolphin, beluga, killer whale, bottlenose dolphin) to test the hypothesis that rod monochromacy is associated with the inactivation of seven genes (*GNAT2, GNB3, GNGT2, PDE6C, PDE6H, CNGA3, CNGB3*) in the cone phototransduction cascade. Cone-monochromatic toothed whales that retain a functional copy of *LWS* (beluga, Yangtze River dolphin, killer whale, bottlenose dolphin) also retain intact copies of other cone-specific phototransduction genes, whereas all rod monochromats that were investigated (Antarctic minke whale, common minke whale, fin whale, bowhead whale, sperm whale) have inactivating mutations in five or more genes in the cone phototransduction cascade. The only shared inactivating mutations that were discovered occur in the three *Balaenoptera* species (two minke whales, fin whale), further suggesting that rod monochromacy evolved independently in two clades of baleen whales, Balaenopteroidea and Balaenidae. We estimate that rod monochromacy evolved first in Balaenopteroidea (~28.8 Ma) followed by *P. macrocephalus* (~19.5 Ma) and Balaenidae (~13.0 Ma).


*No abstract*

**Week of 13 June 2016**


*Abstract* - As global change alters multiple environmental conditions, predicting species’ responses can be challenging without understanding how each environmental factor influences organismal performance. Approaches quantifying mechanistic relationships can greatly complement correlative field data, strengthening our abilities to forecast global change impacts. Substantial salinity increases are projected in the San Francisco Estuary, California, due to anthropogenic water diversion and climatic changes, where the critically endangered delta smelt (*Hypomesus transpacificus*) largely occurs in a low salinity zone (LSZ), despite their ability to tolerate a much broader salinity range. In this study, we combined molecular and organismal measures to quantify the physiological mechanisms and sublethal responses involved in coping with salinity changes. Delta

Abstract - Climate change and associated increases in water temperatures may impact physiological performance in ectotherms and exacerbate endangered species declines. We used an integrative approach to assess the impact of elevated water temperature on two fishes of immediate conservation concern in a large estuary system, the threatened longfin smelt (Spirinchus thaleichthys) and endangered delta smelt (Hypomesus transpacificus). Abundances have reached record lows in California, USA, and these populations are at imminent risk of extirpation. California is currently impacted by a severe drought resulting in high water temperatures, conditions that will become more common due to climate change. We exposed fish to environmentally-relevant temperatures (14°C, 20°C) and used RNA-sequencing to examine the transcriptome-wide responses to elevated water temperature in both species. Consistent with having a lower temperature tolerance, longfin smelt exhibited a pronounced cellular stress response, with an upregulation of heat shock proteins, after exposure to 20°C that was not observed in delta smelt. We detected an increase in metabolic rate in delta smelt at 20°C and increased expression of genes involved in metabolic processes and protein synthesis, patterns not observed in longfin smelt. Through examination of responses across multiple levels of biological organization, and linking these responses to habitat distributions in the wild, we demonstrate that longfin smelt may be more susceptible than delta smelt to increases in temperatures and they have little room to tolerate future warming in California. Understanding the species-specific physiological responses of sensitive species to environmental stressors is critical for conservation efforts and managing aquatic systems globally.


Abstract - Three populations of false killer whales (Pseudorca crassidens) have been identified in the U.S. Exclusive Economic Zone of the Hawaiian Archipelago (Hawaiian EEZ): 1) a main Hawaiian Islands (MHI) insular population, 2) a pelagic population, and 3) a Northwestern Hawaiian Islands (NWHI) population. Spatially-explicit stock boundaries are needed to assess and manage each population. New data, primarily satellite telemetry data, were collected that indicate the existing stock boundaries should be refined. These data were used by the False Killer Whale Stock Boundary Revision Working Group to establish revised, scientifically-defensible stock boundaries that appropriately reflect uncertainty and are robust to routine inputs from ongoing data collection. For each stock, several stock boundary options were identified by the Working Group and reviewed by the Pacific Scientific Review Group before the revised stock boundaries were finalized. The MHI insular stock boundary was changed from a uniform 140-km radius around the MHI to a minimum convex polygon bounded around a 72-km radius of the MHI, resulting in a boundary shape that reflects greater offshore use in the leeward portion of the MHI. While the wide-ranging pelagic stock continues to be assessed within the Hawaiian EEZ, the inner stock boundary was reduced from a 40-km to an 11-km radius around the MHI, a result of individuals occurring closer to shore than previously observed. The NWHI stock boundary largely remained the area of the Papahānaumokuākea Marine National Monument extended to include a 50-nmi radius around Kaua‘i, although 2 vertices were removed to widen the eastern portion, accounting for movement outside of the existing boundary. The following report summarizes the stock boundary revision process for the 3 false killer populations. Additionally, because the stock boundary placement affects the line-transect
abundance estimates of the pelagic and NWHI stocks and the proration of false killer whale bycatch, the report also provides updated abundance estimates for pelagic and NWHI false killer whales and outlines a revised approach for bycatch proration.


Abstract - Marine mammal interactions (i.e., hookings and entanglements) with the Hawaii and American Samoa longline fisheries observed during 2009-2013 were compiled, and the number of marine mammal deaths, serious injuries, and non-serious injuries by fishery, species, and management area were assessed. These values form the basis of the mortality and serious injury estimates included in the stock assessment reports of stocks impacted by these fisheries. Injury determinations were made using a nationally standardized process and established criteria for distinguishing serious from non-serious injuries (National Marine Fisheries Service, 2012). In the Hawaii deep-set fishery, 45 marine mammal interactions were observed from 2009 to 2013; most involved false killer whales (53.3%), resulted in death or serious injury (75.6%), and occurred outside the U.S. exclusive economic zone (EEZ) (55.6%). In the Hawaii shallow-set fishery, 43 marine mammal interactions were observed from 2009 to 2013; most involved Risso’s dolphins (39.5%), resulted in death or serious injury (69.8%), and occurred outside the U.S. EEZ (90.7%). In the American Samoa deep-set fishery, 13 marine mammal interactions were observed from 2009 to 2013; most involved rough-toothed dolphins (46.2%), resulted in death or serious injury (92.3%), and occurred within the U.S. EEZ (76.9%).

Week of 9 May 2016

MMTD’s Scripps Institution of Oceanography current and former Doctorates senior author 4 papers of newest issue of Marine Mammal Science – http://onlinelibrary.wiley.com/journal/10.1111/(ISSN)1748-7692/earlyview

- Use of time-at-temperature data to describe dive behavior in five species of sympatric deep-diving toothed whales. Trevor W. Joyce, John W. Durban, Holly Fearnbach, Diane Claridge and Lisa T. Ballance.
- Multi-methods approach to characterizing the magnitude, impact, and spatial risk of Irrawaddy dolphin (Orcaella brevirostris) bycatch in small-scale fisheries in Malampaya Sound, Philippines. Tara Sayuri Whitty.

Week of 2 May 2016


Abstract - The ocean provides ecosystem services (ES) that sustain humanity. Traditional single-issue marine resource management approaches largely failed to protect living resources from human impacts. Ecosystem-based management (EBM) addresses this problem by promoting resilient social-ecological systems that provide desired ES. To implement EBM, an ES approach can be employed in 4 broad steps: 1) characterize major ES, including quantities, values, and stakeholders, 2) identify trade-offs among ES, 3) determine desired ES outcomes, and 4) manage anthropogenic activities to achieve desired outcomes. Here we apply the ES approach to an open ocean ecosystem, the eastern tropical Pacific (ETP), an area of 21 million km² that includes waters of 12 nations and the oceanic commons, using 35 years (1975-2010) of fisheries and economic data, and 20 years (1986-2006) of ship-based research survey data. We examined commercial fisheries, carbon storage, biodiversity, and recreation (particularly sport fishing) as the major provisioning, regulating, supporting, and cultural ES, respectively. Average catch value for the 10 most commercially-fished species was $2.7 billion yr-1 (1991-2010). The value of carbon export to the deep ocean was $12.9 billion yr-1. The lost value of carbon
storage in two fisheries-depleted dolphin populations was $1.6 million (cumulative), and the carbon value of an annual fishery harvest (544,000 mt) was $1.6 million yr⁻¹. Sport fishing expenditures totaled $1.2 billion yr⁻¹, from studies of just three popular destinations. Over 1/3 of the world’s species of cetaceans, seabirds, and marine turtles occur there, with diversity hotspots occurring throughout the region. This study fills several gaps in the assessment of marine and coastal ES by focusing on an oceanic habitat, utilizing long-term datasets to produce an assessment, mapping the spatial distribution of ecological components, and concentrating on an area beyond Europe and the USA. Our results highlight the variety of ES provided by the ETP and offer a new perspective for a system that historically has been dominated by commercial tuna fisheries. By improving our understanding of ETP ES, this study sets the stage for further analysis of trade-offs, which can inform decisions about resource management and biodiversity conservation.


Abstract - We examined the stomach contents of 3 vertically migrating myctophid fish species from the eastern tropical Pacific (ETP) Ocean and used a classification tree to examine the influence of spatial, biological, and oceanographic predictor variables on diet. Myctophum nitidulum (n=299), Symbolophorus reversus (n=199), and Gonichthys tenuiculus (n=82) were collected with dip nets from surface waters, and prey taxa were quantified from bongo net tows from August through November 2006. A classification tree produced splits with longitude and sea surface salinity (SSS), thereby separating 3 geographically and oceanographically distinct regions of the ETP (offshore, nearshore, and intermediate), where diet was similar among the 3 species. Myctophids consumed, primarily, ostracods offshore (76.4% mean percentage by number [MNi]), euphausiids nearshore (45.0%), and copepods (66.6%) in the intermediate region. The offshore region was characterized by a greater abundance of ostracods in the zooplankton community (17.5% by number) and within a deep mixed-layer depth (MLD) (mean 52.6 m, max 93.0 m). SSS was low in the nearshore region (<32.9 psu) and the MLD was shallow. The intermediate region represented a transition zone between the oceanographic condition of the offshore and nearshore regions. Our results indicate that these 3 myctophid species share a similar regional diet that is strongly influenced by longitude, ostracod availability, SSS, and MLD.

Week of 25 April 2016


Abstract - Anthropogenically altered water temperatures (AAWT) have the potential to affect the movement and distribution of marine ectothermic species. Green sea turtles (GSTs) Chelonia mydas are an ectothermic species observed inhabiting 2 sites with AAWT at the northern point of their geographical range in the eastern Pacific. An acoustic receiver array was deployed with temperature loggers at the San Gabriel River, Long Beach, CA, where 2 power plants discharge warm water into the river, and at the 7th St. Basin, Seal Beach, CA, a dredged shallow basin with warmer water compared to surrounding coastal habitats during the summer months. Juvenile GSTs (n = 22, straight carapace length = 45.2 to 96.8 cm) were tagged with acoustic transmitters. Turtles in the basin migrated into the river during winter months when temperatures dropped below 15°C. During the winter, turtles were most frequently detected at the river receiver stations adjacent to and downstream of the power plants. This suggests that GSTs use the warm effluent as a thermal refuge, avoiding colder areas upstream of the power plants and near the river mouth. In the summer, turtles were most frequently detected at receiver stations upstream of the power plants, potentially exploiting areas of the river with higher primary productivity. AAWT sustain the northernmost aggregation of GSTs in the eastern Pacific year round; however, based on GST thermal tolerance, this population is expected to change their movement patterns when the power plants discontinue discharging warm water by 2029.


Abstract - No global synthesis of the status of baleen whales has been published since the 2008 IUCN Red List assessments. Many populations remain at low numbers from historical commercial whaling, which had ceased for all but a few by 1989. Fishing gear entanglement and ship-strikes are the most severe current threats. The
acute and long-term effects of anthropogenic noise and the cumulative effects of multiple stressors are of concern but poorly understood. The looming consequences of climate change and ocean acidification remain difficult to characterize. Southern right, bowhead, and gray whales have been assessed as Least Concern at the species level, but North Atlantic and North Pacific right whales and the Chile-Peru subpopulation of southern right whales are Critically Endangered as are two bowhead whale subpopulations and the western North Pacific subpopulation of gray whales. Some other baleen whale subpopulations are Endangered. Eastern North Pacific blue whales have reportedly recovered, but Antarctic blue whales remain at about 1 percent of pre-exploitation levels. Small isolated subspecies or subpopulations, such as Northern Indian Ocean blue whales, Arabian Sea humpback whales, and Mediterranean Sea fin whales are threatened while most subpopulations of sei, Bryde’s, and Omura’s whales are inadequately monitored and difficult to assess.

**Week of 18 April 2016**


Abstract - Effective conservation of globally distributed marine species relies on identification of demographically independent populations to ensure that management actions are directed at the appropriate scale. This identification is particularly challenging for species with complex life histories when local breeding populations have not been adequately sampled. We used mtDNA to analyze the population structure of loggerhead turtles from a total of 555 samples collected from 12 nesting sites in Japan in the Northwest Pacific, including previously unsampled rookeries in the Ryukyu Archipelago, for a comprehensive coverage of the nesting distribution. We identified a total of 9 haplotypes based on 820 bp of the mtDNA control region, including 5 variants of a single previously described 380 bp haplotype. We discovered that 1 haplotype (CcP1.1) previously rare in the North Pacific is common in the Ryukyu Archipelago. Based on analysis of haplotype frequencies, we found significant differentiation among regionally grouped nesting populations (analysis of molecular variance p < 0.0001, df = 8; pairwise FST ranging from 0.033 to 0.145). Our results provide evidence to support the recognition of 3 management units (MU) within the NW Pacific Regional Management Unit (RMU). These include (1) the Ryukyu MU that includes Okinawa, Okinoerabu and Amami, (2) Yakushima Island MU and (3) a Mainland MU that includes Bousou, Enshu-nada, Shikoku, Kii and Eastern Kyushu. These new data from Japan will provide important baseline data for global genetic stock assessments and contribute to our understanding of the population structure, ecology and life history of this migratory marine species in the northern Pacific.

**Week of 11 April 2016**


Summary - NMFS received a petition from the Animal Welfare Institute, Whale and Dolphin Conservation, Cetacean Society International, and Earth Island Institute to designate the Sakhalin Bay-Amur River beluga whales as depleted under the MMPA. The petition asserts this group of whales constitutes a stock and that this stock is below its OSP and qualifies for a depleted designation. NMFS found the petitioned action may be warranted. NMFS established a status review team (referred to as the Team), to review the status of the beluga whales in the Sakhalin Bay-Amur River portion of the Okhotsk Sea using the best, currently available information. The Team’s review involved two steps. First, to determine whether the Sakhalin Bay-Amur River beluga whales constitute a stock under the MMPA, and then, second, if these whales meet the definition of stock, determine the depletion level for the stock. In regard to the first step, the Team agreed that there was strong evidence for genetic differentiation within the Sea of Okhotsk in both mtDNA and nuclear DNA, between beluga whales that summer in the western Sea of Okhotsk from Sakhalin Bay to Udskaya Bay (west of 145˚E longitude) and those that summer in the northeastern Sea of Okhotsk off the west Kamchatka coast (east
of 145° E longitude). Because of the limited evidence regarding the stock structure of the Sakhalin Bay-Amur River relative to other western Sea of Okhotsk beluga whales, the Team used SEDM procedures to evaluate the available genetic and telemetry data for beluga whales in the western Sea of Okhotsk as they relate to delineating stocks. Using SEDM procedures, eight questions concerning the interpretation of the genetic (mtDNA and nuclear DNA) and telemetry data as well as the similarities with how beluga whale stocks in Alaska have been delineated were addressed. The Team concluded that the movement and mtDNA patterns of the beluga whales in the western Sea of Okhotsk were analogous to beluga whales in Bristol Bay and Norton Sound Alaska, which are defined as demographically independent stocks under the MMPA. The Team concluded that Sakhalin Bay-Amur River whales were either their own stock or they belonged to a stock that also summers in Nikolaya Bay. More genetic and tagging data would be needed to conclude more precisely how belugas in Nikolaya Bay relate to belugas in the Sakhalin Bay – Amur River area.


Abstract - Leatherback turtles (Dermochelys coriacea) undergo substantial cyclical changes in body condition during foraging and nesting. Ultrasoundography has been used to measure subcutaneous fat as an indicator of body condition in many species but has not been applied in sea turtles. To validate this technique in leatherback turtles, ultrasound images were obtained from 36 live-captured and dead-stranded immature and adult turtles from foraging and nesting areas in the Pacific and Atlantic oceans. Ultrasound measurements were compared with direct measurements from surgical biopsy or necropsy. Tissue architecture was confirmed histologically in a subset of turtles. The dorsal shoulder region provided the best site for differentiation of tissues. Maximum fat depth values with the front flipper in a neutral (45°–90°) position demonstrated good correlation with direct measurements. Ultrasound-derived fat measurements may be used in the future for quantitative assessment of body condition as an index of health in this critically endangered species.


Abstract - The three-dimensional configuration of hydrophones in a volumetric array has been shown to address many limitations of the linear arrays for some species (Zimmer, 2013). One author (JB) developed two predecessors to the current prototypes of towed volumetric arrays. Field tests in 2011 and 2012 provided 3-D localization at speeds up to 6-8 knots. These designs provided acoustic bearings to animal groups, without the left/right ambiguity and provided the approximate depth of the animals. However, these designs had poor acoustic performance at higher speeds (likely due to turbulent flow and vibrations) and rotated during turns causing torque on the tow cable and uncertainty in array orientation. Despite the shortcomings of these designs, the concept of a light-weight, towed volumetric array showed merit. We present the results of a project aimed at improving the hydrodynamics of the volumetric array design for towing at faster speeds, up to 10 knots, from large research vessels. Two different designs were selected for the prototypes, henceforth known as the torpedo array and the X-array. We explain the theory behind the design considerations for each prototype, the sea trial results and subsequent modifications, and discuss improvements to future volumetric array designs.


Abstract - Correlations between morphological and genetic data provide evidence to delineate species or evolutionarily significant units, which then become the units to conserve in management plans. Here, we examine the distribution and genetic differentiation of two morphotypes of short-finned pilot whale (Globicephala macrorhynchus) in the Pacific Ocean. Mitochondrial control region sequences from 333 samples were combined with 152 previously published sequences to describe genetic variability globally and population structure in the Pacific. Although genetic variability is low, we found strong differentiation at both broad and
local levels across the Pacific. Based on genetics, two types are distributed throughout the Pacific, one predominantly in the eastern Pacific and the other in the western and central Pacific. In the eastern Pacific Ocean, no correlation was found between distribution and sea surface temperature. The two types have broad latitudinal ranges, suggesting their distributions are likely driven by more complex factors, such as prey distribution, rather than sea surface temperature.


Abstract - This report presents long-term seasonal distribution maps of selected seabird, pinniped and cetacean species off the Pacific coast of Washington. The maps were created to support state-led marine spatial planning and responsible stewardship of natural resources by the Olympic Coast National Marine Sanctuary. They are intended to distinguish persistent areas of high relative density from areas of low relative density, and are useful for identifying ecologically important areas, recognizing and mitigating impacts from human uses and coastal hazards, and improving our understanding of marine environments. Predicted relative density distribution maps were constructed using associative models linking at-sea species observations with environmental covariates. Associative models relied on species observations compiled from federal, state, and non-governmental monitoring programs with data between 1995 and 2014. Environmental variables, such as depth, sea surface temperature, and indices of primary productivity, were processed from long-term archival satellite, oceanographic, and hydrographic databases. The compilation of at-sea species observations represents the first attempt to combine eleven selected survey programs, and is a substantial combination of nearshore and offshore survey effort. As far as we are aware, the compilation prepared for this report is the largest synthesis of recent seabird, pinniped, and cetacean observations in the study area, in terms of both number of observations and number of programs combined. A boosted generalized additive modeling framework was applied to associate seabird and environmental covariate data sets and develop contiguous, accurate predictions of relative density. To improve model performance, the modeling framework allowed for flexible relationships and multi-way interactions between environmental variables while accounting for sampling heterogeneity between and within datasets. Model performance was assessed using cross validation and a range of model fit and bias diagnostics. All models showed good performance based on model performance diagnostics, and expert reviewers agreed all maps were valuable representations of species distributions. Reviewers included ecologists, coastal resource managers, and modelers from multiple agencies and organizations. These maps represent an important step towards improving our understanding of the long-term spatial distributions of selected seabirds, pinnipeds, and cetaceans, identifying persistent hotspots of relative densities, and more effectively planning offshore human activities. The seabird, pinniped, and cetacean predictions are already being used by the Washington Department of Fish and Wildlife to identify ecologically important areas off the Pacific Coast of Washington, and they intend to utilize this information in planning for offshore renewable energy development. Predictive Mapping of Seabirds, Pinnipeds and Cetaceans off the Pacific Coast of Washington 1 The Pacific Northwest depends on a healthy coastal and marine ecosystem to maintain thriving economies and vibrant communities. Marine ecosystems support critical habitats for wildlife and a growing number of ocean activities such as fishing, transportation, aquaculture, recreation, and energy production. Planners, policy makers, and resource managers are being challenged to sustainably balance multiple ocean uses and environmental conservation mandates in a finite space and with limited information. This balancing act is being supported by spatial planning. Marine spatial planning is a planning process that enables integrated, forward-looking, and consistent decision making on the human uses which occur in the oceans and along coasts (Ehler and Douveree, 2009). It can improve marine resource management by planning for human uses in locations that reduce conflict among different activities, and supports a balance among social, economic, and ecological benefits received from ocean resources. Forward-looking coastal states such as Washington are investing in and assuming marine spatial planning as an integral part of managing human uses and activities in the marine environment. In March 2010, the Washington state legislature enacted a marine spatial planning law (RCW §43.372) to address resource use conflicts in waters off Washington. In 2011, a report to the legislature and a workshop on human use data provided guidance for the marine spatial planning process. In 2012, the governor amended the existing law to focus funding on mapping and ecosystem assessments for Washington’s Pacific coast and the legislature provided $3.7 million in the 2013-15 fiscal year biennium to begin marine spatial planning off Washington’s
The funds were appropriated through the Washington Department of Natural Resources Marine Resources Stewardship Account with coordination among the State Ocean Caucus, the four Coastal Treaty Tribes, four coastal Marine Resource Committees and the Washington Coastal Marine Advisory Council. This project was initiated to support Washington’s marine spatial plan.


Abstract - The role of behavioral ecology in improving wildlife conservation and management has been the subject of much recent debate. We aim to answer two foundational questions about the current use of behavioral knowledge in conservation: 1. To what extent is behavioral knowledge used in wildlife conservation and management? 2. How does the use of behavior differ among conservation fields in both frequency and types of use? To answer these questions, we searched the literature for intersections between key fields of animal behavior and conservation biology and created a systematic ‘heat’ map to visualize relative efforts. Our analysis challenges previous suggestions that there is little association between the fields and reveals tremendous variation in the use of different behaviors in conservation. For instance, some behaviors, such as foraging and dispersal, are commonly considered, but other behaviors such as learning, social or anti-predatory behaviors are hardly considered. Our analysis suggests that in many cases awareness of the importance of behavior does not translate into applicable management tools. We suggest that behavioral ecologists should focus on developing research in underutilized intersections of behavior and conservation themes for which preliminary work show a potential for improving conservation and management, on translating behavioral theory into applicable and testable predictions, and on creating systematic reviews to summarize the behavioral evidence within the behavior-conservation intersections for which many studies exist.


Abstract - Stochastic versions of Gompertz, Ricker and various other dynamics models play a fundamental role in quantifying strength of density dependence and studying long term dynamics of wildlife populations. These models are frequently estimated using time series of abundance estimates that are inevitably subject to observation error and missing data. This issue can be addressed with a state-space modeling framework that jointly estimates the observed data model and the underlying stochastic population dynamics (SPD) model. In cases where abundance data are from multiple locations with a smaller spatial resolution (e.g. from mark-recapture and distance sampling studies), models are conventionally fitted to spatially pooled estimates of yearly abundances. Here, we demonstrate that a spatial version of SPD models can be directly estimated from short time series of spatially referenced distance sampling data in a unified hierarchical state-space modeling framework that also allows for spatial variance (covariance) in population growth. We also show that a full range of likelihood based inference, including estimability diagnostics and model selection, is feasible in this class of models using a data cloning algorithm. We further show through simulation experiments that the hierarchical state-space framework introduced herein efficiently captures the underlying dynamical parameters and spatial abundance distribution. We apply our methodology by analysing a time series of line-transact distance sampling data for fin whales (Balaenoptera physalus) off the U.S. west coast. Although there were only seven surveys conducted during the study time frame, 1991-2014, our analysis detected presence of strong density regulation and provided reliable estimates of fin whale densities. In summary, we show that the integrative framework developed herein allows ecologists to better infer key population characteristics such as presence of density regulation and spatial variability in a population's intrinsic growth potential.


Abstract - We outline a framework for informing management of threatened species bycatch based on the use of limit reference points. We use western Pacific (WP) leatherback sea turtles interacting with the California drift gillnet (CDGN) fishery off the U.S. West Coast as an example. WP leatherbacks are Critically Endangered (IUCN Red List) and precipitously declining. They incur fishing and other impacts from multiple countries and in international waters, but most bycatch management decisions are made by national governments – individually or in concert in intergovernmental organizations – so appropriate cumulative mortality limits for
the whole population may be of limited value to decision-making by many domestic agencies. We propose a two-step approach of estimating local limit reference points (LRPs) based on the fraction of the population occurring within a management jurisdiction, and then estimating the probability that these LRPs are being exceeded to inform management decisions. The latter component is particularly useful for making inference about rare-event bycatch, which is prone to severe estimation error when observer coverage is limited and conventional annual ratio-type estimators are used. We present a historical and forecasted time series of local LRP estimates, based on a time series of local leatherback abundance estimates and an LRP estimator, tuned by Management Strategy Evaluation. We estimate two LRPs, one aimed at recovering or maintaining a population above its maximum net productivity level, and another aimed at expediting recovery for a depleted population. Finally, we estimate the probability that mortality in the CDGN fishery has exceeded these LRPs in the past and will do so in the future, based on estimates of catchability (from Bayesian analysis of observer program data), population abundance, and fishing effort forecasts. We find that both local LRPs were likely exceeded by the CDGN fishery in the past, but that with current management measures and declining fishing effort, mortality rates have been reduced so that current and future leatherback mortality in the CDGN fishery is very likely between the two LRPs given current effort. Our analyses can help inform management in several ways, such as by supporting development of input control rules to help ensure that the probability of exceeding an LRP remains below a certain threshold, providing a sense of the amount of monitoring data (e.g., from fishery observer programs) needed to reasonably assess impacts of the fishery, and providing metrics to help evaluate whether fisheries meet international certification standards for sustainability.

**Week of 28 March 2016**


*Abstract* - Fisheries that operate at large spatial scales and with high intensity have the potential to impact highly migratory species, and it is important to characterize threats to specific breeding populations of these species. We used many-to-many mixed-stock analysis (MSA) \( n = 408 \) and microsatellite assignment testing \( n = 397 \) to determine source populations for leatherback turtles \( (Dermochelys coriacea) \) caught as bycatch in the U.S. pelagic longline fishery from 2002 to 2012 in the western North Atlantic. Within the United States, we had bycatch samples from the majority of statistical fishing areas: Gulf of Mexico (GOM), Northeast Distant (NED), Caribbean (CAR), Florida East Coast (FEC), Mid Atlantic Bight (MAB), Northeast Coastal (NEC), South Atlantic Bight (SAB) and Sargasso (SAR). We determined the proportions of turtles from each of nine nesting stocks in the Atlantic in each of the sampled areas. These nesting stocks included Brazil, Costa Rica, Florida, Trinidad, French Guiana, St. Croix, Ghana, Gabon, and South Africa. The MSA revealed that the NED had a lower relative proportion of turtles from Costa Rica than other areas and that the GOM had the highest relative proportion of turtles from Costa Rica. No turtles were assigned to the African rookeries, lending further evidence that turtles from that region forage elsewhere and therefore may not be affected by western North Atlantic fisheries. This work contributes to the ongoing assessment of threats to leatherback turtles in the Regional Management Unit (RMU) of the western North Atlantic, and draws attention to the disproportionate number of turtles from Costa Rica being caught in the Gulf of Mexico; Costa Rica is one of the only populations in the northern Atlantic that is not experiencing significant increases in nest numbers. This approach should be useful in determining population-specific threats to other highly migratory protected species that may depend on segregated foraging areas either within or among species.

**Week of 21 March 2016**


*Abstract* - Hearing sensitivity is a fundamental determinant of a species’ vulnerability to anthropogenic noise, however little is known about the hearing capacities of most conservation dependent species. When audiometric data are integrated with other aspects of species’ acoustic ecology, life history, and characteristic habitat topography and soundscape, predictions can be made regarding probable vulnerability to the negative impacts
of different types of anthropogenic noise. Here we used an adaptive psychoacoustic technique to measure hearing thresholds in the endangered giant panda; a species that uses acoustic communication to coordinate reproduction. Our results suggest that giant pandas have functional hearing into the ultrasonic range, with good sensitivity between 10.0 and 16.0 kHz, and best sensitivity measured at 12.5–14.0 kHz. We estimated the lower and upper limits of functional hearing as 0.10 and 70.0 kHz respectively. While these results suggest that panda hearing is similar to that of some other terrestrial carnivores, panda hearing thresholds above 14.0 kHz were significantly lower (i.e., more sensitive) than those of the polar bear, the only other bear species for which data are available. We discuss the implications of this divergence, as well as the relationship between hearing sensitivity and the spectral parameters of panda vocalizations. We suggest that these data, placed in context, can be used towards the development of a sensory-based model of noise disturbance for the species.

Week of 14 March 2016


This report contains human-caused injury and mortality records of pinnipeds and cetaceans that occur in U.S. west coast waters for the period 2010-2014, for those species evaluated in Pacific region marine mammal stock assessment reports (SARs) (Carretta et al. 2015a). Mortality records, while included in this report, were obviously not evaluated for SI/NSI status. Subsistence and directed takes (i.e., gray whales taken by Russian natives) are not reported here but are reported in SARs published by NMFS. Previous records, including cases from 2007 through 2009, are published in previous reports (Carretta et al. 2013a, 2014, 2015b).

Sources of injury data include strandings, disentanglement networks, the public, researchers, and fishery observer programs. Stranding data includes records of injured marine mammals at sea and ashore. Injury sources include, but are not limited to, vessel strikes, gillnet entanglement, pot and trap gear entanglement, shootings, marine debris entanglement, research related injuries/deaths, hook and line fishery interactions, and power plant water intake entrainment. Most records originate from stranding networks in California, Oregon, and Washington, though a few Alaska records of Eastern North Pacific gray whales (Eschrichtius robustus) are included, because this population is assessed in the Pacific region SARs and occurs along the U.S. west coast. Other marine mammals, such as Steller sea lions (Eumetopias jubatus), occur in California, Oregon, and Washington waters, but they are assessed in Alaska region SARs (Allen and Angliss 2014) and are not included in this report. Injury determinations for Pacific region species/stocks in the central Pacific from Hawaii westward are also included in separate reports (Bradford and Forney 2014).

Week of 29 February 2016


The report of the Joint Marine Mammal Commission (MMC) and NMFS Passive Acoustic Surveying Workshop on the use and development of passive acoustics to inform marine mammal stock assessments is available online at www.MMC.gov.
Executive Summary (portion only) - The National Marine Fisheries Service (NMFS) is responsible for gathering the information needed to support its stock assessments of marine mammals. The distribution and abundance of each stock is the core of those assessments. Data to support stock assessments are traditionally gathered by conducting visual observations during shipboard and/or aerial surveys. Increasingly, however, the Agency is having difficulties providing abundance estimates and other data needed for marine mammal stock assessment, which has spurred NMFS to increase its investment in alternative monitoring methods that may fill some critical data gaps more effectively and efficiently than large-scale ship and aerial surveys alone can achieve.

For the last several years, research teams across NMFS have been investigating the use of advanced survey techniques to fill the stock assessment data-gap or to supplement traditional survey data. Passive acoustic monitoring is a promising approach, which can be pursued within the context of existing ship-based survey efforts or as part of an autonomous monitoring system. Research teams around the world are developing new vehicles, recorders, software, and analytical techniques to study marine mammals, but it is clear that one approach will not adequately address every one of NMFS’s science goals and research requirements for stock assessments. Technological, scientific and funding constraints are hindering the full and efficient use of passive acoustics by NMFS to inform its marine mammal stock assessments.

Week of 22 February 2016


Abstract - Species distribution models are now widely used in conservation and management to predict suitable habitat for protected marine species. The primary sources of dynamic habitat data have been in situ and remotely sensed oceanic variables (both are considered “measured data”), but now ocean models can provide historical estimates and forecast predictions of relevant habitat variables such as temperature, salinity, and mixed layer depth. To assess the performance of modeled ocean data in species distribution models, we present a case study for cetaceans that compares models based on output from a data assimilative implementation of the Regional Ocean Modeling System (ROMS) to those based on measured data. Specifically, we used seven years of cetacean line-transect survey data collected between 1991 and 2009 to develop predictive habitat-based models of cetacean density for 11 species in the California Current Ecosystem. Two different generalized additive models were compared: one built with a full suite of ROMS output and another built with a full suite of measured data. Model performance was assessed using the percentage of explained deviance, root mean squared error (RMSE), observed to predicted density ratios, and visual inspection of predicted and observed distributions. Predicted distribution patterns were similar for models using ROMS output and measured data, and showed good concordance between observed sightings and model predictions. Quantitative measures of predictive ability were also similar between model types, and RMSE values were almost identical. The overall demonstrated success of the ROMS-based models opens new opportunities for dynamic species management and biodiversity monitoring because ROMS output is available in near real time and can be forecast.

Week of 8 February 2016


Abstract -

1. Stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope analysis (SIA) has proven useful in addressing fundamental questions in ecology such as reconstructing trophic interactions, habitat connections and climate regime shifts. The temporal scales over which SIA can be used to address ecological problems vary depending on the protein turnover times of the analysed tissue. Hard, inert tissues, such as teeth, bones and mollusc shells, grow in regular intervals (i.e. daily or annually), and sequential sampling of these growth layers provides a time series of isotopic patterns. As a result, SIA on these tissues is useful for elucidating behaviour and ecology of animals over time, especially those with cryptic life-history stages, such as
marine turtles that retain growth layers in their humerus bones. To date, there exists no standard protocol for the sequential sampling of cortical bone samples taken from fresh, modern samples for SIA.

2. We tested two different methods, micromilling untreated bone cross sections and biopsy coring bone cross sections processed for skeletochronology, for sequentially sampling individual growth layers from marine turtle humerus bones.

3. We present a standard protocol for sequential bone growth layer sampling for SIA, facilitating direct comparison of future studies. We recommend using the micromilling sampling technique on untreated bone cross sections, as it facilitated higher precision sampling of growth layers that were not affected by chemical processing, and minimized sample handling, thereby reducing chances for contamination.

4. This is the first study to present a standardized method to sequentially sample annual bone growth layers for stable isotope analysis and facilitates direct comparison among future studies.

**Week of 25 January 2016**


Summary - Japanese whalers are back in the Southern Ocean, aiming to kill 333 minke whales — ostensibly for the purposes of scientific research — under special permits issued by their government. In our view, the science behind Japan’s whaling activity has not passed a reasonable standard of peer review. The IWC urgently needs to develop a process of scientific review that results in clear decisions that can be respected by all.


Abstract - Climate change is driving rapid changes in environmental conditions and affecting population and species’ persistence across spatial and temporal scales. Integrating climate change assessments into biological resource management, such as conserving endangered species, is a substantial challenge, partly due to a mismatch between global climate forecasts and local or regional conservation planning. Here, we demonstrate how outputs of global climate change models can be down-scaled to the watershed scale, and then coupled with ecophysiological metrics to assess climate change effects on organisms of conservation concern. We employed models to estimate future water temperatures (2010–2099) under several climate change scenarios within the large heterogeneous San Francisco Estuary. We then assessed the warming effects on the endangered, endemic Delta Smelt, Hypomesus transpacificus, by integrating localized projected water temperatures with thermal sensitivity metrics (tolerance, spawning and maturation windows, and sublethal stress thresholds) across life stages. Lethal temperatures occurred under several scenarios, but sublethal effects resulting from chronic stressful temperatures were more common across the estuary (median >60 days above threshold for >50% locations by the end of the century). Behavioral avoidance of such stressful temperatures would make a large portion of the potential range of Delta Smelt unavailable during the summer and fall. Since Delta Smelt are not likely to migrate to other estuaries, these changes are likely to result in substantial habitat compression. Additionally, the Delta Smelt maturation window was shortened by 18–85 days, revealing cumulative effects of stressful summer and fall temperatures with early initiation of spring spawning that may negatively impact fitness. Our findings highlight the value of integrating sublethal thresholds, life history, and in situ thermal heterogeneity into global change impact assessments. As down-scaled climate models are becoming widely available, we conclude that similar assessments at management-relevant scales will improve the scientific basis for resource management decisions.

**Week of 18 January 2016**

Abstract - Recovery of cetacean carcasses provides data on levels of human-caused mortality, but represents only a minimum count of impacts. Counts of stranded carcasses are negatively biased by factors that include at-sea scavenging, sinking, drift away from land, stranding in locations where detection is unlikely, and natural removal from beaches due to wave and tidal action prior to detection. We estimate the fraction of carcasses recovered for a population of coastal bottlenose dolphins (*Tursiops truncatus*), using abundance and survival rate data to estimate annual deaths in the population. Observed stranding numbers are compared to expected deaths to estimate the fraction of carcasses recovered. For the California coastal population of bottlenose dolphins, we estimate the fraction of carcasses recovered to be 0.25 (95% CI = 0.20 – 0.33). During a 12 yr period, 327 animals (95% CI = 253–413) were expected to have died and been available for recovery, but only 83 carcasses attributed to this population were documented. Given the coastal habits of California coastal bottlenose dolphins, it is likely that carcass recovery rates of this population greatly exceed recovery rates of more pelagic dolphin species in the region.


Abstract - Melon-headed whale (*Peponocephala electra*) and Pygmy killer whale (*Feresa attenuata*) are very poorly known species and are often confused with each other. We examined in detail Figure 3 in MARIGO and GIFFONI (2010) who reported that two melon-headed whales were taken in a surface driftnet about 90 nm off Santos, Brazil. We concluded they were in fact pygmy killer whales and explain our reasoning. To aid in future identifications, we illustrate and describe some of the main differences between these two species of small cetaceans. The incident reported by MARIGO and GIFFONI (2010) might represent the ‘tip of the iceberg’ regarding the incidental catches of cetaceans by pelagic drift nets off Brazil. Offshore driftnetting operating along the south-eastern coast of Brazil may threaten pygmy killer whales.


Abstract - Rivers worldwide, particularly in tropical regions, support multiple human uses that can threaten water security and cause species decline. Some tropical rivers are home to obligate freshwater cetaceans (river dolphins) that are vulnerable to exploitation and to upstream and downstream habitat degradation due to limited dispersal opportunities. Assessing vulnerability is complicated by difficulty in reliably estimating abundance, due to the animals’ cryptic nature and complex, dynamic habitat. We compared density estimates from surveys conducted in 1993, 2002 and 2007. Surveys were not part of a coordinated monitoring plan and thus were conducted using slightly different methods in different months, which complicated statistical inference. We used information from the most recent survey to account for bias and uncertainty in earlier estimates and used bootstrap and Bayesian approaches to estimate trends, conditional on a plausible range of process variance associated with seasonal movements. For *Inia*, probability of decline was >0.75, even under the highest seasonal movement levels considered. For *Sotalia*, there was a >0.75 probability of population increase. There are 151 proposals pending in the Amazon for large (>2 MW) hydroelectric developments that would fragment habitat, and reports suggest that *Inia* is experiencing illegal killing for fish bait. In this context, our population trend estimates are cause for concern, but improved monitoring is needed to more reliably assess population status. Based on lessons learned from our analysis, future surveys will be standardized in terms of timing (conducted during the transitional water season) and methodology (using our most recent field protocols) to minimize confounding factors and provide more robust inference about population trends. We provide recommendations for ways to distinguish seasonal movements from annual population trends to guide Amazon river dolphin conservation. Until then, two interpretations exist: either *Inia* is declining, or existing information cannot detect declines unambiguously without additional surveys. Neither explanation bodes well, given the myriad anthropogenic stressors Amazon river dolphins face.


Abstract - Ontogenetic changes in resource use often delimit transitions between life stages. Ecological and individual factors can cause variation in the timing and consistency of these transitions, ultimately affecting
community and population dynamics through changes in growth and survival. Therefore, it is important to
document and understand behavioral and life history polymorphisms, and the processes that drive intraspecific
variation in them. To evaluate juvenile loggerhead sea turtle (Caretta caretta) life history variation and to detect
shifts in habitat and diet that occur during an oceanic-to-neritic ontogenetic shift, we sequentially analyzed the
stable isotope composition of humerus bone growth increments from turtles that stranded dead on Southeastern
U. S. beaches between 1997 and 2013 (n = 84). In one-half of the sampled turtles, growth increment-specific
nitrogen stable isotope (d15N) data showed significant increases in d15N values over each turtle’s life. These
data were used to provide a new line of evidence that juvenile Northwest Atlantic loggerheads exhibit two
major ontogenetic shift patterns: discrete shifts (n = 24), which were completed within one year, and
facultative shifts (n = 14), which were completed over multiple years (up to five). The mean difference in pre-
and post-ontogenetic shift d15N values was 4.3%. Differences in isotopic baselines between neritic and oceanic
habitats of the Northwest Atlantic Ocean make it likely these patterns are driven by a coupled change in both
habitat and diet, and that facultative shifters utilize both neritic and oceanic resources within transitional growth
years. Mean size and age at transition between habitats (54.2 cm straightline carapace length, SCL; 11.98 yr)
was within the range of previous estimates and did not differ between discrete and facultative shifters. Our
results further expand our understanding of loggerhead sea turtle life history polymorphisms and demonstrate
the value of bone tissue analysis to the study of this variation. Sequential analysis of annual skeletal growth
increments provides a valuable method for reconstructing long-term ontogenetic changes in foraging ecology
and habitat use in long-lived, cryptic marine species.

Week of 11 January 2016

Alyson H. Fleming, Casey T. Clark, John Calambokidis, and Jay Barlow. 2015. Humpback whale diets
respond to variance in ocean climate and ecosystem conditions in the California Current. Global Change

Abstract - Large, migratory predators are often cited as sentinel species for ecosystem processes and
climate-related changes, but their utility as indicators is dependent upon an understanding of their
response to environmental variability. Documentation of the links between climate variability,
cecosystem change and predator dynamics is absent for most top predators. Identifying species that
may be useful indicators and elucidating these mechanistic links provides insight into current
ecological dynamics and may inform predictions of future ecosystem responses to climatic change.
We examine humpback whale response to environmental variability through stable isotope analysis of
diet over a dynamic 20-year period (1993–2012) in the California Current System (CCS). Humpback
whale diets captured two major shifts in oceanographic and ecological conditions in the CCS. Isotopic
signatures reflect a diet dominated by krill during periods characterized by positive phases of the
North Pacific Gyre Oscillation (NPGO), cool sea surface temperature (SST), strong upwelling and
high krill biomass. In contrast, humpback whale diets are dominated by schooling fish when the
NPGO is negative, SST is warmer, seasonal upwelling is delayed and anchovy and sardine
populations display increased biomass and range expansion. These findings demonstrate that
humpback whales trophically respond to ecosystem shifts, and as a result, their foraging behavior is a
synoptic indicator of oceanographic and ecological conditions across the CCS. Multi-decadal
examination of these sentinel species thus provides insight into biological consequences of interannual
climate fluctuations, fundamental to advancing ecosystem predictions related to global climate
change.

Week of 14 December 2015


Abstract - Previous studies have reported inactivated copies of six enamel-related genes (AMBN, AMEL,
AMTN, ENAM, KLK4, MMP20) and one dentin-related gene (DSPP) in one or more toothless vertebrates
and/or vertebrates with enamelless teeth, thereby providing evidence that these genes are enamel or tooth-
specific with respect to their critical functions that are maintained by natural selection. Here, we employ available genome sequences for edentulous and enamellless mammals to evaluate the enamel specificity of four genes (WDR72, SLC24A4, FAM83H, C4orf26) that have been implicated in amelogenesis imperfecta, a condition in which proper enamel formation is abrogated during tooth development. Coding sequences for WDR72, SLC24A4, and FAM83H are intact in four edentulous taxa (Chinese pangolin, three baleen whales) and three taxa (aardvark, nine-banded armadillo, Hoffmann's two-toed sloth) with enamellless teeth, suggesting that these genes have critical functions beyond their involvement in tooth development. By contrast, genomic data for C4orf26 reveal inactivating mutations in pangolin and bowhead whale as well as evidence for deletion of this gene in two minke whale species. Hybridization capture of exonic regions and PCR screens provide evidence for inactivation of C4orf26 in eight additional baleen whale species. However, C4orf26 is intact in all three species with enamellless teeth that were surveyed, as well as in 95 additional mammalian species with enamel-capped teeth. Estimates of selection intensity suggest that dN/dS ratios on branches leading to taxa with enamellless teeth are similar to the dN/dS ratio on branches leading to taxa with enamel-capped teeth. Based on these results, we conclude that C4orf26 is tooth-specific, but not enamel-specific, with respect to its essential functions that are maintained by natural selection. A caveat is that an alternative splice site variant, which translates exon 3 in a different reading frame, is putatively functional in Catarrhini and may have evolved an additional role in this primate clade.

Week of 7 December 2015


Abstract - No global synthesis of the status of baleen whales has been published since the 2008 IUCN Red List assessments. Many populations remain at low numbers from historical commercial whaling, which had ceased for all but a few by 1989. Fishing gear entanglement and ship strikes are the most severe current threats. The acute and long-term effects of anthropogenic noise and the cumulative effects of multiple stressors are of concern but poorly understood. The looming consequences of climate change and ocean acidification remain difficult to characterize. North Atlantic and North Pacific right whales are among the species listed as Endangered. Southern right, bowhead, and gray whales have been assessed as Least Concern but some subpopulations of these species - western North Pacific gray whales, Chile-Peru right whales, and Svalbard/Barents Sea and Sea of Okhotsk bowhead whales - remain at low levels and are either Endangered or Critically Endangered. Eastern North Pacific blue whales have reportedly recovered, but Antarctic blue whales remain at about 1% of pre-exploitation levels. Small isolated subspecies or subpopulations, such as northern Indian Ocean blue whales, Arabian Sea humpback whales, and Mediterranean Sea fin whales are threatened while most subpopulations of sei, Bryde’s, and Omura’s whales are inadequately monitored and difficult to assess.

Week of 23 November 2015


Abstract - Blue whales are infrequently reported from New Zealand and their taxonomic status is unclear. Here we present new information on the residency, external morphology, and habitat use of blue whales encountered in New Zealand waters. Thirty-one blue whales were photo-identified around the North and South Islands of New Zealand from 2004-2014 in seven different months of the year. One photographic match was found between June 2011 and March 2013: the first evidence that an individual blue whale has remained in or returned to New Zealand waters in different years and seasons. Observations of the external morphology of blue whales encountered off the South Island confirm that there is a shorter, non-Antarctic form of blue whale occurring near New Zealand. Body
length and proportion, head shape, body condition and skin condition were similar to Australian but not Antarctic blue whales. In 2013, feeding behavior was observed off the South Island’s west coast and strong evidence of feeding was observed off the east coast, the first reported occurrence of feeding for these locations. Feeding behavior was also observed in the Hauraki Gulf in November 2010. Feeding in these widely spread locations, in addition to the recently reported foraging ground in the South Taranaki Bight, suggest that New Zealand coastal waters are a feeding area for blue whales.

**Week of 2 November 2015**


*Abstract* - Fisheries bycatch is a threat to species of marine megafauna across the world’s oceans. Work over the past several decades has greatly advanced our understanding of the species affected, the magnitude and the spatial extent of bycatch. In the same time period, there have been substantial advances in the development of mitigation strategies and best practices to reduce bycatch. In this paper, we take stock of bycatch knowledge and science to address the critical question “Where do we go from here?” First, we review the current state of global bycatch science, including bycatch rate estimation and biological effects of bycatch, and bycatch mitigation practices and gear. We then identify knowledge gaps as well as socio-cultural constraints that hamper effective knowledge transfer or implementation, and discuss emerging transdisciplinary approaches to address these issues. Finally, we discuss the need to consider bycatch in a changing ocean and socio-cultural context where species, ecosystems, and people are responding to multiple stressors and dynamic conditions. As the field of bycatch research moves into the 21st century, a new perspective is needed to develop responsive strategies that effectively address the shifting ecological, social, cultural and economic contexts of the global bycatch seascape.

**Week of 26 October 2015**


*Summary* - This paper reports the first documented inter-seasonal movement for a blue whale in the southeastern Pacific Ocean, establishing a migratory link between a mid-latitude feeding ground in the Corcovado Gulf, Chile and a potential breeding ground in the Eastern Tropical Pacific. This is the longest latitudinal movement reported for a Southern Hemisphere blue whale (5,200 km).


*Summary* - The value of passive acoustics as a tool for studying marine mammals relies on the ability to detect and classify sounds associated with these species. Classification efforts typically focus on a single species, or occasionally on a few species found within a geographic region. In an effort to improve our ability to classify species during shipboard population surveys and other passive acoustic monitoring needs, we have developed an automated whistle classification algorithm that includes all whistling species found within a large geographic region, the California Current. In order to train this whistle classifier, single-species encounters within the California Current and near (Eastern Tropical Pacific) were compiled from archived recordings. Whistles were automatically detected using the ‘Whistle and Moan Detector’ (WMD) within the acoustic data processing software platform, PAMGUARD (Gillespie 2008). Measurements from each whistle contour were automatically extracted using the ROCCA (Real-time Odontocete Call Classification Algorithm) module in PAMGUARD. These data were used to train and test a region specific ROCCA whistle classifier to be used on future surveys. This report presents the data used to develop this California Current whistle classifier and the results from testing the classifier on this training data.

**Week of 19 October 2015**

Summary - Weighing as much as 2,000 pounds and reaching lengths of over seven feet, leatherback turtles are the world’s largest reptile. These unusual sea turtles have a thick, pliable shell that helps them to withstand great depths—they can swim more than one thousand meters below the surface in search of food. And what food source sustains these goliaths? Their diet consists almost exclusively of jellyfish, a meal they crisscross the oceans to find.

Leatherbacks have been declining in recent decades, and some predict they will be gone by the end of this century. Why? Because of two primary factors: human redevelopment of nesting beaches and commercial fishing. There are only twenty-nine index beaches in the world where these turtles nest, and there is immense pressure to develop most of them into homes or resorts. At the same time, longline and gill net fisheries continue to overwhelm waters frequented by leatherbacks.

In The Leatherback Turtle, James R. Spotila and Pilar Santidrián Tomillo bring together the world’s leading experts to produce a volume that reveals the biology of the leatherback while putting a spotlight on the conservation problems and solutions related to the species. The book leaves us with options: embark on the conservation strategy laid out within its pages and save one of nature’s most splendid creations, or watch yet another magnificent species disappear.

Week of 12 October 2015


Summary - A workshop was held May 20 – 21, 2015, in San Diego, California, USA, titled: “Workshop to Assess/Re-Assess IUCN Red Listings for Indo-Pacific Species of Coastal Marine Small Cetaceans.” Species included were Orcaella brevirostris, O. heinsohni, Neophocaena asiaeorientalis, and two of the three Indo-Pacific Sousa species: S. chinensis and S. plumbea. Sousa sahulensis and Neophocaena phocaenoides were not assessed, largely for lack of information about these species.

Red List assessments require estimates of generation time for a pristine population, i.e., one with stable age structure and abundance at carrying capacity such that the annual per-capita population growth rate is \( \lambda = \exp(r) = 1 \). Let this generation time be denoted \( T_0 \). Estimating \( T_0 \) for the above species is the primary goal of this analysis. Additionally, this analysis provides point estimates of the anthropogenic mortality rate required to reduce a population by 30%, 50%, or 80% over three generations (3\( T_0 \)). These reductions warrant Vulnerable, Endangered, or Critically Endangered status, respectively, under the Red List criterion A; IUCN 2012).


No Abstract

Week of 5 October 2015


Abstract - Forecasting species' responses to climate change requires understanding the underlying mechanisms governing environmental stress tolerance, including acclimation capacity and acute stress responses. Current knowledge of these physiological processes in aquatic ectotherms is largely drawn from eurythermal or extreme stenothermal species. Yet many species of conservation concern exhibit tolerance windows and acclimation
capacities in between these extremes. We linked transcriptome profiles to organismal tolerance in a mesothermal endangered fish, the delta smelt (Hypomesus transpacificus), to quantify the cellular processes, sublethal thresholds and effects of thermal acclimation on acute stress responses. Delta smelt initiated rapid molecular changes in line with expectations of theoretical thermal limitation models, but also exhibited diminished capacity to modify the expression of some genes and cellular mechanisms key to coping with acute thermal stress found in eurytherms. Sublethal critical thresholds occurred 4–6 °C below their upper tolerance limits, and thermal acclimation shifted the onset of acute thermal stress and tolerance as predicted. However, we found evidence that delta smelt's limited thermal plasticity may be partially due to an inability of individuals to effectively make physiological adjustments to truly achieve new homeostasis under heightened temperatures, resulting in chronic thermal stress. These findings provide insight into the physiological basis of the diverse patterns of thermal tolerances observed in nature. Moreover, understanding how underlying molecular mechanisms shape thermal acclimation capacity, acute stress responses and ultimately differential phenotypes contributes to a predictive framework to deduce species' responses in situ to changes in selective pressures due to climate change.

Week of 28 September 2015


Abstract -

1. The global distribution of fin whales Balaenoptera physalus is not fully understood. Existing maps can be divided into two conflicting categories: one showing a continuous global distribution and another showing an equatorial hiatus (gap in the global distribution) between approximately 20°N and 20°S. Questions also remain about the seasonal distribution of fin whales.

2. To explore the suggested equatorial hiatus and seasonal distribution patterns, we synthesised information on fin whale distribution in the post-whaling era (1980–2012) from published literature, publicly available reports and studies conducted by various organisations. We created four seasonally stratified maps showing line-transect density estimates, line-transect survey effort, acoustic detections, and sightings.

3. An equatorial hiatus in the global distribution of fin whales during the post-whaling era is supported by numerous line-transect surveys and by the rarity of equatorial acoustic detections and sightings, and corroborated by whaling era reports, morphological analyses, and genetic analyses.

4. Our synthesis of post-whaling era data is consistent with results from other studies indicating that fin whales are more abundant at higher latitudes during warmer months and more abundant at lower latitudes (although these latitudes are still greater than 20°) during colder months. However, our synthesis and results from other studies also indicate that some fin whales in both hemispheres remain in higher latitudes (50°–60° north or south) during colder months and in lower latitudes (to approximately 20°–30° north or south) during warmer months, indicating that seasonal fin whale movements differ from the seasonal migrations of blue whales Balaenoptera musculus and humpback whales Megaptera novaeangliae.

5. Our maps of global fin whale distribution provide a comprehensive picture of current knowledge and highlight important geographical and temporal data gaps. Surveys should be conducted within the identified data gaps in order to increase fine-scale spatial and temporal knowledge of distribution patterns, improve fin whale taxonomy, and identify areas of elevated fin whale densities that may require management of threats, such as ship strikes.


Abstract -

RATIONALE: The sampling of sequential, annually formed bone growth layers for stable carbon (δ13C values) and nitrogen (δ15N values) isotope analysis (SIA) can provide a time series of foraging ecology data. To date, no standard protocol exists for the pre-SIA treatment of cortical samples taken from fresh, modern, bones.

METHODS: Based on the SIA of historical bone, it is assumed that fresh bone samples must be pre-treated with acid prior to SIA. Using an elemental analyzer coupled to an isotope ratio mass spectrometer to measure stable carbon and nitrogen ratios, we tested the need to acidify cortical bone powder with 0.25 M HCl prior to
SIA to isolate bone collagen for the determination of δ13C and δ15N values. We also examined the need for lipid extraction to remove potential biases related to δ13C analysis, based on a C:N ratio threshold of 3.5.

RESULTS: It was found that acidification of micromilled cortical bone samples from marine turtles does not affect their δ15N values, and the small effect acidification has on δ13C values can be mathematically corrected for, thus eliminating the need for pre-SIA acidification of cortical bone. The lipid content of the cortical bone samples was low, as measured by their C:N ratios, indicating that lipid extracting cortical bone samples from modern marine turtles is unnecessary. CONCLUSIONS: We present a standard protocol for testing fresh, modern cortical bone samples prior to SIA, facilitating direct comparison of future studies. Based on the results obtained from marine turtle bones, pre-acidification and lipid removal of cortical bone are not recommended. This is especially useful as there is frequently not enough bone material removed via micromilling of sequential growth layers to accommodate both acid treatment and SIA.

Week of 21 September 2015

doi:10.1371/journal.pone.0136452 (http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0136452)

Abstract - Biological limit reference points (LRPs) for fisheries catch represent upper bounds that avoid undesirable population states. LRPs can support consistent management evaluation among species and regions, and can advance ecosystem-based fisheries management. For transboundary species, LRPs prorated by local abundance can inform local management decisions when international coordination is lacking. We estimated LRPs for western Pacific leatherbacks in the U.S. West Coast Exclusive Economic Zone (WCEEZ) using three approaches with different types of information on local abundance. For the current application, the best-informed LRP used a local abundance estimate derived from nest counts, vital rate information, satellite tag data, and fishery observer data, and was calculated with a Potential Biological Removal estimator. Management strategy evaluation was used to set tuning parameters of the LRP estimators to satisfy risk tolerances for falling below population thresholds, and to evaluate sensitivity of population outcomes to bias in key inputs. We estimated local LRPs consistent with three hypothetical management objectives: allowing the population to rebuild to its maximum net productivity level (4.7 turtles per five years), limiting delay of population rebuilding (0.8 turtles per five years), or only preventing further decline (7.7 turtles per five years). These LRPs pertain to all human-caused removals and represent the WCEEZ contribution to meeting population management objectives within a broader international cooperative framework. We present multi-year estimates, because at low LRP values, annual assessments are prone to substantial error that can lead to volatile and costly management without providing further conservation benefit. The novel approach and the performance criteria used here are not a direct expression of the “jeopardy” standard of the U.S. Endangered Species Act, but they provide useful assessment information and could help guide international management frameworks. Given the range of abundance data scenarios addressed, LRPs should be estimable for many other areas, populations, and taxa.


Summary - A training workshop on best practices to collect data to estimate marine mammal abundance on the Pacific coast of South America was carried out at Salinas, Ecuador, 18-20 August 2015. The activity was conducted in the framework of the cooperation between the USA National Oceanic and Atmospheric Administration (NOAA) and the Permanent Commission for the South Pacific and in implementing the Marine Mammal Action Plan for the Conservation of Marine Mammals in the Southeast Pacific. The lack of information on abundance and population trends for the vast majority of species inhabiting this area is a major gap that deserves attention.

The annual regional oceanographic cruises coordinated by CPPS in four countries (Chile, Colombia, Ecuador and Peru) have been identified as potential platforms for collecting data that can be used to estimate marine mammal abundance. However, large scale assessments require the use of standardized methodologies and expertise. Thus, the workshop objectives were to: 1) Provide training to marine mammal researchers in the region about best practices for collecting data that can be used to estimate abundance; 2) Promote research on
marine mammals with a regional focus, standardizing monitoring techniques and data sharing; 3) Strengthen the bonds of cooperation with NOAA researchers with experience in marine mammal population assessments in the eastern Pacific; 4) Define the basic requirements for the creation of a regional long-term program to assess marine mammal populations in the Southeast Pacific. The workshop was attended by 23 people from 5 countries and included representatives from governmental research institutions, universities, and NGO’s. The current data collection practices in the four countries were reviewed. Regional expertise was shared about using line-transect methodology to estimate the abundance of river dolphins and baleen whales in coastal areas. Personnel from the SWFCS shared their expertise about data collection protocols used during their marine mammal and ecosystem assessment surveys in the Eastern tropical Pacific and on west coast of the USA. These procedures have been extensively used and tested. Numerous publications are available about these protocols. Participants also received information about the basics of line-transect sampling theory.

On the second day, participants had the opportunity to apply data collection protocols and use new equipment during five hours of field training on board a yacht rented for this purpose. Trainees filled out sightings and effort logs and estimated group sizes, distance to sightings, and angle to sightings.

On the final day of the workshop, participants discussed the field training and agreed on the best data collection procedures. Specifically, they reached agreement on equipment, data recording, observers and effort, protocols for sightings, estimating group size, passing and closing protocols, and topics for future workshops. Finally, participants made recommendations for CPPS, the individual countries, and researchers about the best procedures to collect data on future marine mammal surveys in the Southeast Pacific.

**Week of 14 September 2015**


*Description* - This new edition of Marine Mammals of the World describes and illustrates newly discovered and rarely photographed species, making it the most comprehensive and up-to-date marine mammal identification guide available. This edition continues to meet the research-focused needs of marine biologists and conservation biologists by providing a tremendous influx of new photos, taking advantage of advances in digital and auto-focusing photography, and the emergence of marine mammal studies and "whalewatching" around the world. The book encompasses cetacean, pinniped, and sirenian species, as well as extinct species, and describes basic biology and taxonomic groupings of marine mammals.

**Week of 7 September 2015**


*Abstract* - Limit reference points (LRPs) for catch, which correspond to thresholds to undesirable population or ecosystem states, offer a consistent, objective approach to management evaluation and prioritization across fisheries, species, and jurisdictions. LRPs have been applied successfully to manage catch of some marine megafauna (elasmobranchs, marine reptiles, seabirds, and marine mammals) in some jurisdictions, such as the use of Potential Biological Removal (PBR) to manage incidental mortality of marine mammals under the U.S. Marine Mammal Protection Act. However, implementation of ecosystem-based management is still in its infancy globally, and LRPs have not yet been widely adopted for marine megafauna, particularly for incidental catch. Here, guidelines are proposed for estimating catch LRPs for marine megafauna, with particular attention to resolving common technical and political challenges, including (1) identifying management units, population thresholds, and risk tolerances that align with common conservation goals and best practices, (2) choosing catch LRP estimators, (3) estimating input parameters such as abundance and productivity, (4) handling uncertainty, and (5) dealing with mismatches between management jurisdictions and population boundaries. The problem of cumulative impacts across sectors is briefly addressed. These guidelines, grounded in marine policy, science, precedent, and lessons learned, should facilitate wider application of catch LRPs in evaluation and management of fisheries impacts on marine megafauna, in support of global commitments to conserve biodiversity and manage fisheries responsibly.

Abstract - Although the acoustic structure of mammal vocal signals often varies according to the social context of emission, relatively few mammal studies have examined acoustic variation during intersexual advertisement. In the current study male giant panda bleats were recorded during the breeding season in three behavioural contexts: vocalising alone, during vocal interactions with females outside of peak oestrus, and during vocal interactions with peak-oestrous females. Male bleats produced during vocal interactions with peak-oestrous females were longer in duration and had higher mean fundamental frequency than those produced when males were either involved in a vocal interaction with a female outside of peak oestrus or vocalising alone. In addition, males produced bleats with higher rates of fundamental frequency modulation when they were vocalising alone than when they were interacting with females. These results show that acoustic features of male giant panda bleats have the potential to signal the caller’s motivational state, and suggest that males increase the rate of fundamental frequency modulation in bleats when they are alone to maximally broadcast their quality and promote close-range contact with receptive females during the breeding season.

Week of 24 August 2015


Summary - The Marine Mammal Protection Act (MMPA) requires the National Oceanic and Atmospheric Administration (NOAA), National Marine Fisheries Service (NMFS), to document human-caused mortality, non-serious injury (NSI), and serious injury (SI) of marine mammals a part of assessing marine mammal stocks and to evaluate human-caused injury and mortality levels in the context of potential biological removal (PBR) levels calculated under the MMPA (Wade 1998). NMFS defines SI as “any injury that will likely result in mortality.” While documenting mortality is straightforward, distinguishing NSI from SI requires reliable data on injury severity and animal condition, often in challenging environments where thorough examination of injuries is not possible. NMFS updated its SI designation and reporting process in 2012, using guidance from previous workshops (Angliss and DeMaster 1998, Andersen et al. 2008), expert opinion, and analysis of historic injury cases to develop new criteria for distinguishing SI from NSI (NMFS 2012a, 2012b; NOAA 2012; Moore et al. 2013).

This report contains updated records of human-caused injury and mortality to pinnipeds and cetaceans from 2009 to 2013 for marine mammal populations that occur in U.S. west coast waters and which are evaluated in Pacific region marine mammal stock assessment reports (SARs) (Carretta et al. 2013a, 2013b). Mortality records, while included in this report, were obviously not evaluated for SI/NSI status. Subsistence and directed takes (i.e., gray whales taken by Russian natives) are not reported here but are reported in SARs published by NMFS. Previous records, including cases from 2007 and 2008, are published in previous reports (Carretta et al. 2013a, 2014).

Sources of injury data include strandings, disentanglement networks, and fishery observer programs. Stranding network data includes records of injured marine mammals at sea and ashore reported by the public, as well as researchers. Injury sources include, but are not limited to, vessel strikes, gillnet entanglement, pot and trap gear entanglement, shootings, marine debris entanglement, research-related injuries/deaths, hook and line fishery interactions, and power plant water intake entainment. Most records originate from stranding networks in California, Oregon, and Washington, though a few Alaska records of Eastern North Pacific gray whales (Eschrichtius robustus) are included, because this population is assessed in the Pacific region SARs and occurs along the U.S. west coast. Other marine mammals, such as Steller sea lions (Eumetopias jubatus), occur in California, Oregon, and Washington waters, but they are assessed in Alaska region SARs (Allen and Angliss 2014) and are not included in this report. Injury determinations for Pacific region species/stocks in the central Pacific from Hawaii westward are also included in separate reports.

Summary - Under the 1994 amendments to the Marine Mammal Protection Act (MMPA), the National Marine Fisheries Service (NMFS) and the U.S. Fish and Wildlife Service (USFWS) are required to publish Stock Assessment Reports for all stocks of marine mammals within U.S. waters, to review new information every year for strategic stocks and every three years for non-strategic stocks, and to update the stock assessment reports when significant new information becomes available.

Pacific region stock assessments include those studied by the Southwest Fisheries Science Center (SWFSC, La Jolla, CA), the Pacific Islands Fisheries Science Center (PIFSC, Honolulu, HI), the National Marine Mammal Laboratory (NMML, Seattle, WA), and the Northwest Fisheries Science Center (NWFSC, Seattle, WA).

The 2014 Pacific marine mammal stock assessments include revised reports for 11 Pacific marine mammal stocks under NMFS jurisdiction, including six “strategic” stocks: Hawaiian monk seal, Southern Resident killer whale, Main Hawaiian Islands Insular false killer whale, Hawaii Pelagic false killer whale, California/Oregon/Washington sperm whale, and Western North Pacific gray whale. New abundance estimates are available for three stocks in the Pacific Islands region and five U.S. west coast stocks. New estimates of abundance for the California/Oregon/Washington stock of sperm whales are based on a Bayesian trend analysis that utilizes previously collected line-transect data (Moore and Barlow, 2014), resulting in a more stable time series of abundance estimates. Mortality and serious injury estimates of California/Oregon/Washington sperm whales in California drift gillnets are updated, based on pooling additional years of data (>5 years) to reduce bias and improve precision in mean annual bycatch estimates (Carretta and Moore 2014). The combination of new abundance estimates and pooling of bycatch estimates over a longer time period for this stock of sperm whales results in mean annual bycatch estimates that no longer exceed PBR. In addition, a new stock assessment report for Western North Pacific gray whales is presented for the first time, prompted by new data showing that gray whales previously photographed in the western North Pacific utilize U.S. and Mexican waters.

Week of 3 August 2015


Abstract - Conventional aircraft have been used for photogrammetry studies of free ranging whales, but are often not practical in remote regions or not affordable. Here we report on the use of a small, unmanned hexacopter (APH-22; Aerial Imaging Solutions) as an alternative method for collecting photographs to measure killer whales (Orcinus Orca) at sea. We deployed and retrieved the hexacopter by hand during 60 flights (average duration 13.2 min, max 15.7 min) from the upper deck of an 8.2 m boat, utilizing the aircraft’s vertical takeoff and landing (VTOL) capability. The hexacopter was quiet and stable in flight, and therefore could be flown at relatively low altitudes without disturbing whales. The payload was a Micro Four-Thirds system camera that was used to obtain 18920 still images from an altitude of 35–40 m above the whales. Tests indicated a ground-resolved distance of <1.4 cm across the full extent of a flat and undistorted field of view, and an onboard pressure altimeter enabled measurements in pixels to be scaled to true size with an average accuracy of 5 cm. As a result, the images were sharp enough to differentiate individual whales using natural markings (77 whales in total) and preliminary estimates resolved differences in whale lengths ranging from 2.6 to 5.8 m. This first application at sea demonstrated the APH-22 hexacopter to be a safe and cost-effective platform for collecting photogrammetry images to fill key scientific data gaps about whales, and we anticipate this utility will extend to studies of other wildlife species.

Abstract - Somatic growth rates of green turtles (Chelonia mydas) are affected by foraging success and influence their survival and reproduction. Gorgona National Park (GNP) in the Colombian Pacific (2°58’03” N, 78°10’49”W) is an insular foraging site that offers a unique opportunity to study the black (occurring only in the eastern Pacific) and yellow (with western Pacific nesting beach origins) morphotypes of green turtles during their juvenile phase. A total of 995 turtles were captured and marked between October 2003 and December 2012. Recapture rates were low (20 black morphotype and 13 yellow morphotype turtles) but suggested that at least some turtles remain in the area for extended periods (>5 years). Mean growth rate was slightly higher for black morphotype (mean 0.92 ± 0.24 cm/y) than yellow morphotype turtles (mean 0.74 ± 0.26 cm/y), and both morphotypes displayed a non-monotonic growth pattern. Black morphotype turtles grew faster at intermediate sizes, similar to black turtles at other locations in the eastern Pacific, whereas yellow morphotype turtles had slowest growth at intermediate sizes. Our data underscore the importance of GNP as a foraging habitat for C. mydas individuals from distinct nesting populations and indicate that these morphotypes have different growth patterns while residing at the same foraging site.


Abstract - Global climate change during the Late Pleistocene periodically encroached and then released habitat during the glacial cycles, causing range expansions and contractions in some species. These dynamics have played a major role in geographic radiations, diversification and speciation. We investigate these dynamics in the most widely distributed of marine mammals, the killer whale (Orcinus orca), using a global data set of over 450 samples. This marine top predator inhabits coastal and pelagic ecosystems ranging from the ice edge to the tropics, often exhibiting ecological, behavioural and morphological variation suggestive of local adaptation accompanied by reproductive isolation. Results suggest a rapid global radiation occurred over the last 350 000 years. Based on habitat models, we estimated there was only a 15% global contraction of core suitable habitat during the last glacial maximum, and the resources appeared to sustain a constant global effective female population size throughout the Late Pleistocene. Reconstruction of the ancestral phylogeography highlighted the high mobility of this species, identifying 22 strongly supported long-range dispersal events including interoceanic and interhemispheric movement. Despite this propensity for geographic dispersal, the increased sampling of this study uncovered very few potential examples of ancestral dispersal among ecotypes. Concordance of nuclear and mitochondrial data further confirms genetic cohesiveness, with little or no current gene flow among sympatric ecotypes. Taken as a whole, our data suggest that the glacial cycles influenced local populations in different ways, with no clear global pattern, but with secondary contact among lineages following long-range dispersal as a potential mechanism driving ecological diversification.

Week of 20 July 2015


Abstract - Boat-based photo-identification research has been carried out on bottlenose dolphins in eastern North Pacific coastal waters off northern Baja California, Mexico and southern and central California, USA from 1981 to 2001. Within these waters, bottlenose dolphins routinely travel back and forth between coastal locations while generally staying within a narrow corridor extending only 1–2 km from the shore. Inter-area match rates for 616 dolphins photo-identified between 1981–2000 in four California coastal study areas (CCSAs) of Ensenada, San Diego, Orange County and Santa Barbara averaged 76%. To explore possible southern range limits for these dolphins, photo-identification surveys were carried out in the coastal waters off San Quintín, Baja California, Mexico between April–August 1990 (n=8 surveys) and July 1999 to June 2000 (n=12 surveys). The 207 individual dolphins identified off San Quintín were compared to the 616 dolphins identified in the CCSAs. The inter-area match rate between San Quintín and the CCSAs was 3.4% (n=7 dolphins). This low rate contrasts sharply with the much higher average match rate of 76% observed between the CCSAs. These differences in match rates suggest that both a California coastal stock and coastal Northern Baja California stock may exist, with only a limited degree of mixing between them.

**Abstract** - In the southern North Sea, harbour porpoise occurrence increased in recent years after a phase of low abundances during earlier decades. Only very few studies on porpoise presence in the southern German North Sea exist so far. As anthropogenic activities will strongly increase in this part of the North Sea during the next years it is most important to assess population level effects. This study focuses on the analysis of temporal and spatial trends in porpoise density in this area of recent change. Dedicated aerial line-transect distance sampling surveys were conducted in the southern German North Sea between May 2002 and June 2013 to assess porpoise density and distribution. Statistical inferences on porpoise population trends were made using a Markov Chain Monte Carlo (MCMC) technique. Two approaches were chosen to test for a trend in porpoise density and an additional model focused on the change in density of calves. During 55,820 km of survey effort 4377 porpoises including 140 calves were recorded. A significant effect of increasing spatial aggregation from the lower density areas in the south-eastern German Bight to hot spot areas in the western parts was detected. For the western part of the study area a significant increase in porpoise density between 2002 and 2013 was detected. Seasons were significantly different with highest porpoise density in spring and successively decreasing densities in summer and autumn. From 2008 onwards high densities were also observed in summer. Calf density increased during the study period and was significantly higher in the west. On the basis of this extensive and unique dataset on porpoise occurrence in the southern German North Sea the findings clearly show that especially the south-western German North Sea serves as habitat of increasing importance for porpoises throughout the last decade. Definite reasons still remain unresolved. Changes in prey abundance or less favourable conditions in other areas could be important factors, which may also have caused a southward shift from high density areas in northern waters. On this baseline, further integrative approaches might lead to a sound understanding of the effect of anthropogenic activities on the future development of porpoise populations.


**Summary** - Our Living Oceans habitat report provides a comprehensive summary of habitat information for all fishery and protected species under the purview of NOAA’s National Marine Fisheries Service. The report provides information on habitat science, trends, and research needs nationally and on a region-specific basis. The report also provides a conceptual framework for understanding habitat-use patterns of marine species. It also identifies gaps in the available data and information, and describes how these gaps can be addressed through additional research. As with previous reports in the Our Living Oceans series, this publication and the data presented are the result of the collective efforts of National Marine Fisheries Service staff from around the country.

**Week of 13 July 2015**


**Abstract** - The link between ocean temperature and spatial and temporal distribution patterns of 8 species of small cetaceans off Southern California was examined during the period 1979–2009. Averages and anomalies of sea-surface temperatures (SSTs) were used as proxies for SST fluctuations on 3 temporal scales: seasonal, El Niño–Southern Oscillations (ENSO), and Pacific Decadal Oscillations (PDO). The hypothesis that cetacean species assemblages and habitat associations in southern California waters co-vary with these periodic changes in SST was tested by using generalized additive models. Seasonal SST averages were included as a predictor in the models for Dall’s porpoise (*Phocoenoides dalli*), and common dolphins (*Delphinus spp.*), northern right whale dolphin (*Lissodelphis borealis*), and Risso’s dolphin (*Grampus griseus*). The ENSO index was included as a predictor for northern right whale, long-beaked common (*Delphinus capensis*), and Risso’s dolphins. The
PDO index was selected as a predictor for Dall’s porpoise and Pacific white-sided (Lagenorhynchus obliquidens), common, and bottlenose (Tursiops truncatus) dolphins. A metric of bathymetric depth was included in every model, and seafloor slope was included in 5 of the 9 models, an indication of a distinctive spatial distribution for each species that may represent niche or resource partitioning in a region where multiple species have overlapping ranges. Temporal changes in distribution are likely a response to changes in prey abundance or dispersion, and these patterns associated with SST variation may foreshadow future, more permanent shifts in distribution range that are due to global climate change.

Week of 29 June 2015

No abstract.

http://onlinelibrary.wiley.com/journal/10.1111/(ISSN)1748-7692/earlyview

Abstract - Reproductive parameters were estimated and compared for eastern North Pacific populations of common dolphins using specimen and photogrammetric data. Age and length data for Delphinus capensis and D. delphis specimens recovered as bycatch or strandings were used to estimate the postnatal growth rates needed to estimate age for calves measured in aerial photographs. Bayesian methods propagated uncertainty among models and revealed that the 2009 cohort of calves had birth dates centered on 6 March 2009 for D. capensis and 12 December 2008 for D. delphis. The evidence for discrete calving seasons suggests a mechanism of reproductive isolation has evolved between species. Photogrammetric data and Bayesian methods were also used to estimate the average length at which calves swim independently: 145.1 cm (≈ 11.1 mo) in D. capensis and 140.1 cm (≈ 14.0 mo) in D. delphis, and the proportion of calves (calves/dolphins counted): 0.045 in D. capensis and 0.069 in D. delphis. The latter parameter was converted to an index of calf production (calf/female dolphin) that was >50% lower than pregnancy rates suggesting few births occurred during the study year. Comparisons of regional differences in calf production suggest variability in habitat use patterns within the study area.

Week of 22 June 2015

Feist, Blake E., Marlene A. Bellman, Elizabeth A. Becker, Karin A. Forney, Michael J. Ford, and Phillip S. Levin. 2015. Potential overlap between cetaceans and commercial groundfish fleets that operate in the California Current Large Marine Ecosystem. NOAA Professional Paper NMFS 17, 27 p. doi:10.7755/PP.17

Abstract – Cetacean populations are confronted by many anthropogenic threats, including commercial whaling, noise, vessel collisions, gear entanglement, exploitative competition, habitat disturbance, and global climate change. Evidence indicates that commercial fishing activities can have both direct (e.g., gear entanglement and bycatch) and indirect (e.g., prey reduction and noise) effects on cetaceans. However, few studies have addressed the potential vulnerability of a given cetacean species to an entire fishing fleet that operates over a large marine ecosystem. In this study, we overlaid spatially explicit multiyear predicted mean densities of 11 cetacean species and 1 species guild within the California Current Large Marine Ecosystem with data for commercial fishing effort of the fixed-gear, at-sea hake mid-water trawl, and bottom trawl fleets of the west coast groundfish fishery. We quantified the exposure of each species to each fleet type by multiplying the predicted mean cetacean density by the measured fishing fleet effort. We found large interspecific and interfleet variability in the overlap between cetaceans and fishing fleets. Although many of the species had relatively low overlap rates, others had substantial exposure to some of the fishing fleets, particularly those species with more nearshore distributions. Direct mortality from these fleets has been documented to be low, but our results indicate that there is opportunity for fisheries interactions with some cetacean species, particularly in the fixed-gear fleet. Our analyses make up an important first step in generating formal risk assessments for quantification of the impacts of various fishing fleets on populations of cetacean species that occur in the California Current.

Abstract - Plankton nets are widely used to sample phytoplankton, zooplankton and small nektonic animals. Here I present a step-by-step guide to designing plankton nets that fit the objectives of a study, the logistics of sampling, and the available budget. The primary three key parameters to determine in net design are mesh size, mouth diameter, and overall net length. These “key three” are related by the Open-Area Ratio (OAR), the ratio of effective filtering area to mouth area, which can be used to optimize sustained filtration performance for a target tow volume. Mesh size is determined first, which provides the expected porosity of the net and is primarily based on the smallest retained plankton size. Mouth size is then constrained according to avoidance capabilities of the target organisms and operational logistics. Overall net length is then set to achieve a target tow volume by meeting the minimum required OAR. All three factors can affect cost. Using this process, an array of potential net configurations can be evaluated. A case study is used to demonstrate this design process.

Week of 15 June 2015


Abstract - Conservation biologists frequently use data from the same or related species collected in diverse geographic locations to guide interventions in situations where its applicability is uncertain. There are dangers inherent to this approach. The nesting habitats of critically endangered hawksbill sea turtles (Eretmochelys imbricata) cover a broad geographic global range. Based on data collected in the Caribbean and Indo-Pacific, conservationists assume hawksbills prefer open-coast beaches near coral reefs for nesting, and that individual hawksbills are highly consistent in nest placement, suggesting genetic factors partially account for variation in nest-site choice. We characterized nest-site preferences of hawksbills in El Salvador and Nicaragua, where >80% of nesting activity occurs for this species in the eastern Pacific, and >90% of hawksbill clutches are relocated to hatcheries for protection. We found hawksbills preferred nest sites with abundant vegetation on dynamic beaches within mangrove estuaries. Nests in El Salvador were located closer to the ocean and to the woody vegetation border than nests in Nicaragua, suggesting female hawksbills exhibit local adaptations to differences in nesting habitat. Individual hawksbills consistently placed nests under high percentages of overstory vegetation, but were not consistent in nest placement related to woody vegetation borders. We suggest conservation biologists use caution when generalizing about endangered species that invest in specific life-history strategies (e.g., nesting) over broad ranges based on data collected in distant locations when addressing conservation issues.


Abstract - Aerial surveys are often used to estimate wildlife abundance. The probability of detecting an animal during a survey involves two processes: (1) availability bias when animals present in the search area are not available for detection and (2) perception bias, when some animals potentially visible to observers are missed. Estimating these two sources of bias can lead to improved abundance estimates. However, to date, no marine turtle aerial survey has quantified both biases. To improve in-water marine turtle abundance estimates from aerial counts we estimated: (1) perception bias using independent tandem observers and mark recapture models, and (2) availability bias by quantifying the effect of turtle diving behaviour and environmental conditions on the detection probability of turtles. We compared unadjusted and adjusted abundance estimates to evaluate the effects of these detection biases in aerial surveys. Adjusted data produced a substantially higher estimate of turtles than the unadjusted data. Adjusting for availability bias increased the estimates 18.7 times; adjusting for perception bias resulted in a further 5% increase. These results emphasize the need to consider availability and perception corrections to obtain robust abundance estimates. This approach has application for aerial surveys for other marine wildlife including marine mammals and large sharks.
**Week of 8 June 2015**


Abstract - Passive acoustic monitoring is quickly becoming a standard component of shipboard cetacean population surveys. Power supplies on survey vessels are often electronically noisy and result in poor quality recordings. An independent battery-powered voltage supply is regularly necessary for high quality recordings. Here we describe the design of a simple system to provide independent, single-sided 12 V power for a towed hydrophone system, such as the Southwest Fisheries Science Center’s (SWFSC) Acoustic Recording System (ARS, Rankin et al. 2011) and hydrophone arrays. This system allows for simultaneous use of one battery bank while charging a depleted battery bank. This multi-battery bank system was successfully field tested by SWFSC for four and a half months during the 2014 California Current Cetacean and Ecosystem Assessment Survey (CalCurCEAS), and is based upon an original design Pacific Islands Fisheries Science Center (PIFSC) has been using since 2011.

**Week of 1 June 2015**


Abstract - In July 2012, a mass-stranding of loggerhead sea turtles (Caretta caretta) along the Pacific coast of Baja California, Mexico, coupled with a report of significant bycatch in the gillnet fishery of Baja California Sur, prompted the National Marine Fisheries Service (NMFS), in January 2013, to formally identify Mexico for its lack of an effective regulatory program to end or reduce North Pacific loggerhead turtle bycatch in the gillnet fishery operating in the Gulf of Ulloa pursuant to the High Seas Driftnet Fishing Moratorium Protection Act (Moratorium Protection Act). As indicated in the statute, Mexico had two years to develop a regulatory program that would reduce or eliminate loggerhead turtle bycatch in the region comparable in effectiveness to the United States. In April 2015, Mexico provided the United States with its regulatory measures, which included the implementation of a 90-loggerhead turtle per season mortality cap, development of a spatially tiered reserve system in part of the area where loggerhead bycatch is known to occur, and establishment of an observer program with vessel monitoring and video surveillance system. This report presents a comparability analysis to assess if the management measures are “comparable to measures required in the United States,” which is a requirement under the Moratorium Protection Act if a country is to be positively certified. NMFS will consider whether the program is comparable in effectiveness, taking into account different conditions that could bear on the feasibility and efficacy of comparable measures. Here we provide analyses of effectiveness based on several components of Mexico’s regulatory framework, including an analysis of the maximum loggerhead mortalities per year in U.S. vs. Mexican fisheries that interact with North Pacific loggerhead turtles, spatial and temporal comparisons of time/area closures and restrictions, fisheries gear modifications, observer programs, and enforcement of regulations. We found that, while Mexico is to be commended on their development of new measures to reduce loggerhead bycatch - especially the 90 turtle mortality cap, there are several aspects of Mexico’s regulations that are inconsistent with relevant ongoing management in U.S. fisheries. This Technical Report represents one element of a broader suite of considerations Agency leadership will use in their decision making to determine if Mexico’s regulatory measures are comparable relative to the Moratorium Protection Act certification process for Mexico.

**Week of 25 May 2015**

Emily T. Griffiths and Jay Barlow. 2015. Equipment Performance Report for the Drifting Acoustic Spar
Abstract - The Drifting Acoustic Spar Buoy Recorder (or DASBR) is an autonomous Passive Acoustic Monitoring (PAM) system developed at the Southwest Fisheries Science Center (SWFSC) to provide a practical, low-cost option for collecting high-quality marine acoustic data. Most autonomous recording systems (such as Cornell’s Pop-ups and SIO’s HARPS) are bottom mounted and therefore limited to shelf and slope waters. Fixed moorings in deep pelagic waters are generally too expensive for common use. Hydrophone arrays towed behind research vessels are often used to acoustically detect odontocetes in deeper waters, but they are not ideal. Ship time for towed array surveys is expensive, while ship and water flow noise prevent the collection of ambient noise data using towed arrays. Drifting recording units, such as DASBRs, are not limited to shallow waters, can record deep within the water column, and are isolated from ship noise and flow noise. Here we present the results of three DASBR field tests including two Passive Acoustic Sea Trials (PAST 2013 & PAST 2014) and the 2014 NOAA R/V Lasker shakedown mission trial. We discuss bioacoustic detections of marine mammals and alterations to the original design that were required to prepare the DASBRs for subsequent long-term deployments.


Abstract - Most spatial marine management techniques (e.g., marine protected areas) draw stationary boundaries around often mobile marine features, animals, or resource users. While these approaches can work for relatively stationary marine resources, to be most effective marine management must be as fluid in space and time as the resources and users we aim to manage. Instead, a shift towards dynamic ocean management is suggested, defined as management that rapidly changes in space and time in response to changes in the ocean and its users through the integration of near real-time biological, oceanographic, social and/or economic data. Dynamic management can refine the temporal and spatial scale of managed areas, thereby better balancing ecological and economic objectives. Temperature dependent habitat of a hypothetical mobile marine species was simulated to show the efficiency of dynamic management, finding that 82.0 to 34.2 percent less area needed to be managed using a dynamic approach. Dynamic management further complements existing management by increasing the speed at which decisions are implemented using predefined protocols. With advances in data collection and sharing, particularly in remote sensing, animal tracking, and mobile technology, managers are poised to apply dynamic management across numerous marine sectors. Existing examples demonstrate that dynamic management can successfully allow managers to respond rapidly to changes on-the-water, however to implement dynamic ocean management widely, several gaps must be filled. These include enhancing legal instruments, incorporating ecological and socioeconomic considerations simultaneously, developing ‘out-of-the-box’ platforms to serve dynamic management data to users, and developing applications broadly across additional marine resource sectors.


Abstract - Habitat change is a major driver of species distribution and persistence, but there have been few recorded extinction events for terrestrial mammals across Canada. Currently, we are observing the decline, extirpation, and perhaps extinction of several evolutionarily significant units of woodland caribou (Rangifer tarandus caribou), an iconic and cultural keystone species. We used an extensive set of caribou locations (5 subpopulations, 102 animals, 270,808 GPS-collar locations) collected over 11 years within the Central Mountain Designatable Unit to develop species distribution models that quantified avoidance by caribou of anthropogenic and natural disturbance features. Those empirical relationships allowed us to measure the loss of habitat over a 22-year period and correlate habitat change with measured population decline. The disturbance
responses for caribou were complex and varied by season and subpopulation. We modelled a zone of influence for roads (1.75 km), seismic and pipelines (2.5 km), oil and gas features (4.25 km), cutblocks (5.5 km), burns (8.0 km), and coal mines (3.0 km). When the distribution models for each subpopulation were applied to the respective seasonal ranges, we measured a maximum loss in high-quality habitat of 65.9%. The reduction in habitat was strongly correlated with the annual multiplicative growth rate of 5 subpopulations of caribou. At current rates of habitat loss and population decline, these caribou, a significant component of Canada’s biodiversity, are unlikely to persist. Although the factors leading to extinction are complex, the cumulative impacts of industrial development are a correlate if not causative factor.

**Week of 20 April 2015**


*Abstract* - Shearwaters are ideal for monitoring ocean conditions in the California Current because these predators are abundant, conspicuous, and responsive to oceanographic variability. Herein we evaluated black-vented (*Puffinus opisthomelas*), Buller’s (*P. bulleri*), flesh-footed (*P. carneipes*), pink-footed (*P. creatopus*), short-tailed (*P. tenuirostris*), and sooty (*P. griseus*) shearwaters as fishery-independent indicators of predatory or prey fish availability. We analyzed four years (1996, 2001, 2005, 2008) of monthly (August–November) National Oceanic and Atmospheric Administration seabird surveys, and United States Geological Survey Pacific Coast Fisheries Database catch, from the California coast to 200 nm offshore. An ordination of shearwater abundance and fish catch revealed that the shearwaters and 11 fish/squid species were significantly correlated with one or more of three principal components, which explained 86% of the variation and revealed distinct species assemblages. We evaluated multiple linear regression models for 19 fisheries using five shearwater metrics: density, aggregation, and behavior (traveling, stationary, feeding), three oceanographic indices, and latitude. Eight of these models had a shearwater metric as the primary predictor. In particular, feeding black-vented shearwater abundance explained 75% of dolphinfish (*Coryphaena hippurus*) longline catch. This research illustrates the utility of shearwaters as ecosystem indicators, with direct application for predicting fishery catch of commercial importance.


*Executive Summary:* The green turtle (*Chelonia mydas*) was listed under the ESA on July 28, 1978. Breeding populations of the green turtle in Florida and along the Pacific Coast of Mexico were listed as endangered; all other populations were listed as threatened. In 2007, the National Marine Fisheries Service (NMFS) and the U.S. Fish and Wildlife Service (USFWS); together the Services completed a 5-year review for the green turtle. A 5-year review is an assessment of a listed species to determine whether its status has changed since the time of its listing such that it should be delisted or classified differently than its current status. The Services concluded that new information available since the completion of the previous reviews indicated a possible separation of populations by ocean basins but that a more in-depth analysis was needed to determine the application of the distinct population segment (DPS) policy. Based on the new information and the need for further analysis under the DPS policy, the Services recommended that no change in listing status was warranted in 2007. However, they committed to fully assemble and analyze all relevant information in accordance with the DPS policy. On February 16, 2012, the Services received a petition from the Association of Hawaiian Civic Clubs to identify the Hawaiian green turtle population as a DPS and delist the DPS under the Endangered Species Act of 1973, as amended (ESA; 16 U.S.C. § 1531 et seq.). On August 1, 2012, NMFS (with USFWS concurrence) determined that the petition presented substantial information indicating that the petitioned action may be warranted and initiated a status review to determine whether the petitioned action is warranted. The Services decided to review the Hawaiian population in the context of examining green turtles globally with regard to application of the DPS policy and in light of significant new information since the listing of the species in 1978. This is consistent with the recommendation in the 2007 review. The Services convened a status review team (SRT) in November 2012 to review the best available scientific information, determine whether DPSs exist, and assess the extinction risk for any identified DPS. In accordance with the DPS policy, a population may be defined as a DPS if it is both discrete and significant relative to its
taxon. With regard to discreteness, the SRT evaluated genetic evidence, tagging (flipper and passive integrated transponder (PIT) tags) and satellite telemetry data, demographics information, oceanographic features, and geographic barriers. It determined that there are 11 discrete population segments for green turtles globally. These discrete population segments are markedly separated from each other as a consequence of ecological, behavioral, and oceanographic factors, and based on genetic and morphological evidence. The SRT then considered whether each of the 11 identified discrete population segments is significant relative to its taxon. The SRT determined that each of the 11 discrete population segments were biologically and ecologically significant. They each represent a large portion of the species range, whose loss would result in a significant gap in distribution of the species. Each discrete population segment is genetically unique; the loss of any one discrete population segment would represent a significant loss of genetic diversity. Further, some DPSs represent unique ecological settings influenced by local ecological and physical factors, some exhibit unique morphological or other demographic characteristics, and others have unique movement patterns. Therefore, the SRT concluded that the 11 identified population segments are both discrete from other conspecific population segments and significant to the species, Chelonia mydas. Although DPS is a legal term and the SRT recognizes that these population segments are not technically DPSs until or unless they are designated as such in a rulemaking process, for lack of a better term, we refer to these units as DPSs throughout the report. The SRT identified the following 11 green turtle DPSs distributed globally: (1) North Atlantic DPS (2) Mediterranean DPS (3) South Atlantic DPS (4) Southwest Indian DPS (5) North Indian DPS (6) East Indian - West Pacific DPS (7) Central West Pacific DPS (8) Southwest Pacific DPS (9) Central South Pacific DPS (10) Central North Pacific DPS (11) East Pacific DPS. After the 11 DPSs were identified, the SRT assessed the extinction risk for each DPS. Six critical assessment elements were considered and quantified in this assessment: (1) abundance; (2) population growth rate or productivity; (3) spatial structure; (4) diversity / resilience; (5) threats (as represented by the five factors in section 4(a)(1) of the ESA); and (6) conservation efforts. Each SRT voting member ranked the importance of each of the population elements (first four above) by assigning them a value from 1 to 5, with 1 representing a very low risk. They ranked the influence of the five factors (threats) on the status of the DPS by assigning a value of 0 (neutral) to −2, and ranked the influence of conservation efforts on the status of the DPS by assigning a value of 0 to 2. The SRT noted that none of these elements is entirely independent, and did not attempt to use the values applied to each element by each SRT member to arrive at extinction risk. In the next step, the SRT reviewed information on threats and extinction risk to portions of the ranges for each DPS that, at present, have substantially higher risk than other parts of the DPS and evaluated if these are significant. A portion of the range of a species is considered to be a significant portion of its range (SPR) if it’s contribution to the viability of the species is so important that, if green turtles were extirpated within it, the remaining portion of the population would be in danger of extinction. Only two DPSs were found to have potential SPRs, the Central North Pacific DPS, and the East Indian-West Pacific DPS. Finally, each SRT voting member gave their expert opinion on the likelihood that each DPS would reach a critical risk threshold (quasi-extinction) within 100 years by spreading 100 points across several risk categories for each DPS. For DPSs that were determined to have potential SPRs, the SRT conducted two votes for the risk of extinction: One for the entire DPS, and one for the DPS that would remain if the SPR is lost. A summary of the SRT’s discussions of the critical assessment elements, overall risk of extinction, and conclusions on SPR for each DPS is found in the DPS-specific sections (Sections 5–15) of this report.


Abstract - The US Endangered Species Act (ESA) allows protection of any species that is at risk in all or ‘a significant portion of its range’ (SPOIR). Because this provision is open to many possible interpretations, the agencies responsible for implementing the ESA recently published a SPOIR policy. The policy is based on a framework we developed that asks a simple question: ‘If the portions of the range that are currently at risk were lost, would the entire species, at that point, be threatened or endangered?’ If so, the portion of the range is significant. Some commentators have argued that the policy departs from goals the ESA was originally intended to accomplish. We disagree: biologists and managers struggling to implement provisions of the ESA in complex, realworld situations need practical guidance, and we believe our framework provides that. In particular, it avoids as much as possible normative considerations in evaluating ‘significance’ in terms of human values; instead, we focus on significance to the species, which is consistent with the ESA focus on preventing extinctions, as well as with the mandate that listing determinations be based ‘solely’ on scientific information. However, we agree with some critics that a crucial factor in implementation of the policy will be how historical versus current concepts of range are reconciled. We believe that historical distribution and abundance are important, not as specific restoration goals, but as reference points that characterize conditions under which we are confident the species was viable.

Abstract - We inferred the population densities of blue whales (Balaenoptera musculus) and shortbeaked common dolphins (Delphinus delphis) in the Northeast Pacific Ocean as functions of the water-column’s physical structure by implementing hierarchical models in a Bayesian framework. This approach allowed us to propagate the uncertainty of the field observations into the inference of species-habitat relationships and to generate spatially explicit population density predictions with reduced effects of sampling heterogeneity. Our hypothesis was that the large-scale spatial distributions of these two cetacean species respond primarily to ecological processes resulting from shoaling and outcropping of the pycnocline in regions of wind-forced upwelling and eddy-like circulation. Physically, these processes affect the thermodynamic balance of the water column, decreasing its volume and thus the height of the absolute dynamic topography (ADT). Biologically, they lead to elevated primary productivity and persistent aggregation of low-trophic-level prey. Unlike other remotely sensed variables, ADT provides information about the structure of the entire water column and it is also routinely measured at high spatial-temporal resolution by satellite altimeters with uniform global coverage. Our models provide spatially explicit population density predictions for both species, even in areas where the pycnocline shoals but does not outcrop (e.g. the Costa Rica Dome and the North Equatorial Countercurrent thermocline ridge). Interannual variations in distribution during El Niño anomalies suggest that the population density of both species decreases dramatically in the Equatorial Cold Tongue and the Costa Rica Dome, and that their distributions retrack to particular areas that remain productive, such as the more oceanic waters in the central California Current System, the northern Gulf of California, the North Equatorial Countercurrent thermocline ridge, and the more southern portion of the Humboldt Current System. We posit that such reductions in available foraging PLOS habitats during climatic disturbances could incur high energetic costs on these populations, ultimately affecting individual fitness and survival.


Abstract - To further describe movement patterns and distribution of East Pacific green turtles (Chelonia mydas agassizii) and to determine threat levels for this species within the Eastern Pacific. In order to do this we combined published data from existing flipper tagging and early satellite tracking studies with data from an additional 12 satellite tracked green turtles (1996-2006). Three of these were tracked from their foraging grounds in the Gulf of California along the east coast of the Baja California peninsula to their breeding grounds in Michoacán (1337-2928 km). In addition, three post-nesting females were satellite tracked from Colola beach, Michoacán to their foraging grounds in southern Mexico and Central America (941.3-3020 km). A further six turtles were tracked in the Gulf of California within their foraging grounds giving insights into the scale of ranging behaviour. Turtles undertaking long-distance migrations showed a tendency to follow the coastline. Turtles tracked within foraging grounds showed that foraging individuals typically ranged up to 691.6 km (maximum) from release site location. Additionally, we carried out threat analysis (using the cumulative global human impact in the Eastern Pacific) clustering pre-existing satellite tracking studies from Galapagos, Costa Rica, and data obtained from this study; this indicated that turtles foraging and nesting in Central American waters are subject to the highest anthropogenic impact. Considering that turtles from all three rookeries were found to migrate towards Central America, it is highly important to implement conservation plans in Central American coastal areas to ensure the survival of the remaining green turtles in the Eastern Pacific. Finally, by combining satellite tracking data from this and previous studies, and data of tag returns we created the best available distributional patterns for this particular sea turtle species, which emphasized that conservation measures in key areas may have positive consequences on a regional scale.


Abstract - Conservation biologists frequently use data from the same or related species collected in diverse geographic locations to guide interventions in situations where its applicability is uncertain. There are dangers inherent to this approach. The nesting habitats of critically endangered hawksbill sea turtles (Eretmochelys
imbricata) cover a broad geographic global range. Based on data collected in the Caribbean and Indo-Pacific, conservationists assume hawksbills prefer open-coast beaches near coral reefs for nesting, and that individual hawksbills are highly consistent in nest placement, suggesting genetic factors partially account for variation in nest-site choice. We characterized nest-site preferences of hawksbills in El Salvador and Nicaragua, where >80% of nesting activity occurs for this species in the eastern Pacific, and >90% of hawksbill clutches are relocated to hatcheries for protection. We found hawksbills preferred nest sites with abundant vegetation on dynamic beaches within mangrove estuaries. Nests in El Salvador were located closer to the ocean and to the woody vegetation border than nests in Nicaragua, suggesting female hawksbills exhibit local adaptations to differences in nesting habitat. Individual hawksbills consistently placed nests under high percentages of overstory vegetation, but were not consistent in nest placement related to woody vegetation borders. We suggest conservation biologists use caution when generalizing about endangered species that invest in specific life-history strategies (e.g., nesting) over broad ranges based on data collected in distant locations when addressing conservation issues.


**Abstract** - none. This report covers the Stock Delineation Guidelines Initiative.

**Week of 8 March 2015**


[http://dx.doi.org/10.1890/14-0059.1](http://dx.doi.org/10.1890/14-0059.1)

**Abstract** - Fisheries bycatch is a global threat to marine megafauna. Environmental laws require bycatch assessment for protected species, but this is difficult when bycatch is rare. Low bycatch rates, combined with low observer coverage, may lead to biased, imprecise estimates when using standard ratio estimators. Bayesian model-based approaches incorporate uncertainty, produce less volatile estimates, and enable probabilistic evaluation of estimates relative to management thresholds. Here, we demonstrate a pragmatic decision-making process that uses Bayesian model-based inferences to estimate the probability of exceeding management thresholds for bycatch in fisheries with <100% observer coverage. Using the California drift gillnet fishery as a case study, we (1) model rates of rare-event bycatch and mortality using Bayesian Markov chain Monte Carlo estimation methods and 20 years of observer data; (2) predict unobserved counts of bycatch and mortality; (3) infer expected annual mortality; (4) determine probabilities of mortality exceeding regulatory thresholds; and (5) classify the fishery as having low, medium, or high bycatch impact using those probabilities. We focused on leatherback sea turtles (Dermochelys coriacea) and humpback whales (Megaptera novaeangliae). Candidate models included Poisson or zero-inflated Poisson likelihood, fishing effort, and a bycatch rate that varied with area, time, or regulatory regime. Regulatory regime had the strongest effect on leatherback bycatch, with the highest levels occurring prior to a regulatory change. Area had the strongest effect on humpback bycatch. Cumulative bycatch estimates for the 20-year period were 104–242 leatherbacks (52–153 deaths) and 6–50 humpbacks (0–21 deaths). The probability of exceeding a regulatory threshold under the U.S. Marine Mammal Protection Act (Potential Biological Removal, PBR) of 0.113 humpback deaths was 0.58, warranting a “medium bycatch impact” classification of the fishery. No PBR thresholds exist for leatherbacks, but the probability of exceeding an anticipated level of two deaths per year, stated as part of a U.S. Endangered Species Act assessment process, was 0.0007. The approach demonstrated here would allow managers to objectively and probabilistically classify fisheries with respect to bycatch impacts on species that have population-relevant mortality reference points, and declare with a stipulated level of certainty that bycatch did or did not exceed estimated upper bounds.

**Week of 23 February 2015**


Abstract - Microorganisms in terrestrial and marine ecosystems are essential to environmental sustainability. In the marine environment, invertebrates often depend on metabolic cooperation with their endosymbionts. Coral reefs, one of the most important marine ecosystems, are based on the symbiosis between a broad diversity of dinoflagellates of the genus Symbiodinium and a wide phyletic diversity of hosts (i.e., cnidarian, molluscan, poriferan). This diversity is reflected in the ecology and physiology of the symbionts, yet the underlying biochemical mechanisms are still poorly understood. We examined metabolite profiles of four cultured species of Symbiodinium known to form viable symbioses with reef-building corals, S. microadriaticum (cp-type A194), S. minutum (cp-type B184), S. psugmophillum (cp-type B224) and S. trenchii (cp-type D206). Metabolite profiles were shown to differ among Symbiodinium species and were found to be affected by their physiological response to growth in different temperatures and light regimes. A combined Random Forests and Bayesian analysis revealed that the four Symbiodinium species examined primarily differed in their production of sterols and sugars, including a C29 stanol and the two sterols C28 Δ5 and C28Δ5,22, as well as differences in metabolite abundances of a hexose and inositol. Inositol levels were also strongly affected by changes in temperature across all Symbiodinium species. Our results offer a detailed view of the metabolite profile characteristic of marine symbiotic dinoflagellates of the genus Symbiodinium, and identify patterns of metabolites related to several growth conditions.


Abstract - The central North Pacific Ocean includes diverse temperate and tropical pelagic habitats. Studies of the abundance and distribution of cetaceans within these dynamic marine ecosystems have generally been patchy or conducted at coarse spatial and temporal scales, limiting their utility for pelagic conservation planning. Habitat-based density models provide a tool for identifying pelagic areas of importance to cetaceans, because model predictions are spatially explicit. In this study, we present habitat-based models of cetacean density that were developed and validated for the central North Pacific. Spatial predictions of cetacean densities and measures of uncertainty were derived based on data collected during 15 large-scale shipboard cetacean and ecosystem assessment surveys conducted from 1997 to 2012. We developed generalized additive models using static and remotely sensed dynamic habitat variables, including distance to land, sea-surface temperature (SST), standard deviation of SST, surface chlorophyll concentration, sea-surface height (SSH), and SSH root-mean-square variation. The resulting models, developed using new grid-based prediction methods, provide finer scale information on the distribution and density of cetaceans than previously available. Habitat-based abundance estimates around Hawaii are similar to those derived from standard line-transect analyses of the same data and provide enhanced spatial resolution to inform management and conservation of pelagic cetacean species.

Week of 16 February 2015


Abstract - Quantifying the distribution and abundance of predators is integral to many ecological studies, but can be difficult in remote settings such as Antarctica. Recent advances in the development of unmanned aerial systems (UAS), particularly vertical takeoff and landing (VTOL) aircraft, have provided a new tool for studying the distribution and abundance of predator populations. We detail our experience and testing in selecting a VTOL platform for use in remote, windy, perennially overcast settings, where acquiring cloud-free high-resolution satellite images is often impractical. We present results from the first use of VTOLs for estimating abundance, colony area, and density of krill-dependent predators in Antarctica, based upon 65 missions flown in 2010/2011 (n = 28) and 2012/2013 (n = 37). We address concerns over UAS sound affecting wildlife by comparing VTOL-generated noise to ambient and penguin-generated sound. We also report on the utility of VTOLs for missions other than abundance and distribution, namely to estimate size of individual leopard seals. Several characteristics of small, battery-powered VTOLs make them particularly useful in wildlife applications: (1) portability, (2) stability in flight, (3) limited launch area requirements, (4) safety, and (5) limited sound
when compared to fixed-wing and internal combustion engine aircraft. We conclude that of the numerous UAS available, electric VTOLs are among the most promising for ecological applications.


Abstract - When paired with dart biopsying, quantifying cortisol in blubber tissue may provide an index of relative stress levels (i.e., activation of the hypothalamus-pituitary-adrenal axis) in free-ranging cetacean populations while minimizing the effects of the act of sampling. To validate this approach, cortisol was extracted from blubber samples collected from beach-stranded and by caught short-beaked common dolphins using a modified blubber steroid isolation technique and measured via commercially available enzyme immunoassays. The measurements exhibited appropriate quality characteristics when analyzed via a bootstrapped stepwise parallelism analysis (observed/expected = 1.03, 95%CI: 0.96 – 1.08) and showed no evidence of matrix interference with increasing sample size across typical biopsy tissue masses (75–150mg; r2 = 0.012, p = 0.78, slope = 0.022ng cortisol deviation/U tissue extract added). The relationships between blubber cortisol and eight potential cofactors namely, 1) fatality type (e.g., stranded or bycaught), 2) specimen condition (state of decomposition), 3) total body length, 4) sex, 5) sexual maturity state, 6) pregnancy status, 7) lactation state, and 8) adrenal mass, were assessed using a Bayesian generalized linear model averaging technique. Fatality type was the only factor correlated with blubber cortisol, and the magnitude of the effect size was substantial: beach-stranded individuals had on average 6.1-fold higher cortisol levels than those of bycaught individuals. Because of the differences in conditions surrounding these two fatality types, we interpret this relationship as evidence that blubber cortisol is indicative of stress response. We found no evidence of seasonal variation or a relationship between cortisol and the remaining cofactors.

**Week of 9 February 2015**


Abstract - This study describes and compares the pelagic distribution and migratory patterns of the two subspecies of Gould’s Petrel (Pterodroma leucoptera), and contrasts data obtained from tracking birds at sea using geolocators with observational data (shipboard sightings, by-catch records and beachcast specimens). While breeding, tracked individuals of both subspecies (P. l. leucoptera and P. l. caledonica) foraged within the Tasman Sea and south of the Australian continent, with forays west into the Indian Ocean before laying. After breeding, both subspecies migrated to distinct non-breeding ranges within the eastern tropical Pacific Ocean. Observational data identified the general pattern of migration and foraging areas of the species, whereas data from geolocators provided details of routes and timing of migration, core foraging ranges, and marked spatial and temporal segregation between the two subspecies. However, by attaching geolocators only to established breeders, as is typical of studies of small and medium-sized seabirds, these devices failed to identify that nonbreeding birds (pre-breeders and adults that are deferring breeding) may not follow the same migratory schedules or have the same at-sea distribution. We conclude that integrating data from electronic tracking with observational data substantially improves our understanding of the pelagic distribution of seabird populations.


Abstract - Identifying the appropriate ‘Unit to Conserve’ (UTC) is critical to the success of any management scheme. While the need to define the UTC appropriate to the IWC’s Catch Limit Algorithm (CLA) has long been recognized by its Scientific Committee, little progress has been made on this issue. The CLA was rigorously tested prior to its adoption. However, most of those original performance trials focused on single-population scenarios or two-population scenarios with no ongoing dispersal. None of the trials considered the
performance of the CLA across a range of dispersal rates. In this study, the performance of the CLA under a variety of population structure scenarios is examined. This is the first study to investigate the levels of connectivity (i.e. dispersal rate) for which populations require separate management to meet the conservation goals of the CLA. All the trials consisted of two populations that were managed as a single stock for 100 years. Both historical and modern hunts were spatially-biased so that population 1 was the primary target of hunting. Parameters that varied among trials were the relative carrying capacities (K) of the populations, the dispersal rate between them, maximum sustainable yield rate (MSYR1+), and the precision in simulated abundance estimates. All of these parameters had strong effects on the conservation performance of the CLA.

Trials with a low MSYR1+ (1%) generally ended with the abundance of population 1 below 0.54K, regardless of the dispersal rate or relative carrying capacities of the two populations. The same was true of trials in which the carrying capacity of population 1 represented only 10% of the total landscape carrying capacity and the CV of the abundance estimates was low, even when dispersal between populations was high (5 × 10–3yr–1) and MSYR1+ was 4%. The results suggest that the appropriate UTCs under the RMP are likely to exchange dispersers at high enough rates that they will be difficult to delineate using existing methods. These results also highlight the value of spatially-diffuse hunting patterns that avoid potential overhunting of unrecognised stocks.

Week of 2 February 2015


Week of 19 January 2015

Andrew D. Foote and Phillip A. Morin. 2015. Letter to the Editor in response to Moura et al. Sympatric speciation in killer whales? Heredity doi:10.1038/hdy.2014.120.

In a recent study published in Heredity, Moura et al. (2014) claim their phylogenomic analysis of historical biogeography indicates that killer whale ecotypes found in the largest ocean basin, the North Pacific, diverged in sympatry. We contend that Moura et al.’s inference of divergence within the Pacific Ocean do not equate to divergence in sympatry, and discuss alternative interpretations of their results. Both the mitochondrial and nuclear phylogenies from Moura et al. are compatible with several biogeographical histories of varying complexity, and the most likely history under one evolutionary model may not necessarily be the true history. The data, however, will allow further investigation of some of this uncertainty and the comparison of different models including those that consider gene flow upon secondary contact, providing further insight into the diversification process of killer whales.


Abstract: Targeted environmental monitoring reveals contamination by known chemicals, but may exclude potentially pervasive but unknown compounds. Marine mammals are sentinels of persistent and bioaccumulative contaminants due to their longevity and high trophic position. Using nontargeted analysis, we constructed a mass spectral library of 327 persistent and bioaccumulative compounds identified in blubber from two ecotypes of common bottlenose dolphins (Tursiops truncatus) sampled in the Southern California Bight. This library of halogenated organic compounds (HOCs) consisted of 180 anthropogenic contaminants, 41 natural products, 4 with mixed sources, 8 with unknown sources, and 94 with partial structural characterization and unknown sources. The abundance of compounds whose structures could not be fully elucidated highlights
the prevalence of undiscovered HOCs accumulating in marine food webs. Eighty-six percent of the identified compounds are not currently monitored, including 133 known anthropogenic chemicals. Compounds related to dichlorodiphenyltrichloroethane (DDT) were the most abundant. Natural products were, in some cases, detected at abundances similar to anthropogenic compounds. The profile of naturally occurring HOCs differed between ecotypes, suggesting more abundant offshore sources of these compounds. This nontargeted analytical framework provided a comprehensive list of HOCs that may be characteristic of the region, and its application within monitoring surveys may suggest new chemicals for evaluation.

Week of 22 December 2014


Week of 15 December 2014


Abstract - The eared grebe Podiceps nigricollis shows seasonal variation in the relative size of the major flight muscles that lift and lower the wing: respectively, supracoracoideus (s) and pectoralis (p). S/p ratios are low (~0.07–0.12) when grebes are in flying condition, higher (~0.11–0.15) when staging and flightless, and extreme (to 0.29) when starving. Shifts were driven by changes in the protein content in the pectoralis; intramuscular fat had little effect. S/p ratios also vary seasonally in the red knot Calidris canutus and are higher in birds newly arrived in breeding areas than at other times. If that increase was an adaptive response to promote wing-lifting in association with various breeding behaviors as suggested, one would expect it to result from an absolute increase in the post-arrival size of the supracoracoideus, which was not observed. Instead, we propose that it is unrelated to enhancing the upstroke but results from a decrease in the size of the pectoralis, which is a consequence of the greater rate at which this muscle is catabolized in times of exertion and stress, as at the end of a long migration or during starvation. Fuller data on the size, morphology and physiology of individual muscles at various stages of the annual cycle and migration will help to clarify how ratio changes are achieved, and evaluate potential adaptive significance. http://onlinelibrary.wiley.com/doi/10.1111/jav.00506/abstract.


Abstract - A clear understanding of population structure is essential for assessing conservation status and implementing management strategies. A small, non-migratory population of humpback whales in the Arabian Sea is classified as “Endangered” on the IUCN Red List of Threatened Species, an assessment constrained by a lack of data, including limited understanding of its relationship to other populations. We analyzed 11 microsatellite markers and mitochondrial DNA sequences extracted from 67 Arabian Sea humpback whale tissue samples and compared them to equivalent datasets from the Southern Hemisphere and North Pacific. Results show that the Arabian Sea population is highly distinct; estimates of gene flow and divergence times suggest a Southern Indian Ocean origin but indicate that it has been isolated for approximately 70,000 years, remarkable for a species that is typically highly migratory. Genetic diversity values are significantly lower than those obtained for Southern Hemisphere populations and signatures of ancient and recent genetic bottlenecks were identified. Our findings suggest this is the world’s most isolated humpback whale population, which, when combined with low population abundance estimates and anthropogenic threats, raises concern for its survival. We recommend an amendment of the status of the population to Critically Endangered on the IUCN Red List.

Week of 8 December 2014

*Abstract:* Simultaneous sightings and acoustic detections of sei whales (*Balaenoptera borealis*) are scarce, and there are few published data describing their vocalizations. Analysis of recordings from directional frequency analysis and recording sonobuoys in the presence of sei whales in the Southern Ocean in March 2013 identified both downsweep and upsweep calls. Sound frequencies within all calls were between 34 and 87 Hz with an average call duration of 1.1 s. These very low-frequency sounds share characteristics with sei whale calls recorded near the Hawaiian Islands and off Cape Cod in winter and summer, respectively, but are the first documented sei whale calls in the Southern Ocean that are clearly less than 100 Hz.

**Week of 1 December 2014**


*Abstract* - Reports of killer whales (*Orcinus orca*) preying on large whales have been relatively rare, and the ecological significance of these attacks is controversial. Here we report on numerous observations of killer whales preying on neonate humpback whales (*Megaptera novaeangliae*) off Western Australia (WA) based on reports we compiled and our own observations. Attacking killer whales included at least 19 individuals from three stable social groupings in a highly connected local population; 22 separate attacks with known outcomes resulted in at least 14 (64%) kills of humpback calves. We satellite-tagged an adult female killer whale and followed her group on the water for 20.3 h over six separate days. During that time, they attacked eight humpback calves, and from the seven known outcomes, at least three calves (43%) were killed. Overall, our observations suggest that humpback calves are a predictable, plentiful, and readily taken prey source for killer whales and scavenging sharks off WA for at least 5 mo/yr. Humpback “escorts” vigorously assisted mothers in protecting their calves from attacking killer whales (and a white shark, *Carcharodon carcharias*). This expands the purported role of escorts in humpback whale social interactions, although it is not clear how this behavior is adaptive for the escorts.

**Week of 3 November 2014**


*Abstract* - Climate, behavior, ecology and oceanography shape patterns of biodiversity in marine faunas in the absence of obvious geographic barriers. Marine turtles are an example of highly migratory creatures with deep evolutionary lineages and complex life histories that span both terrestrial and marine environments. Previous studies have focused on the deep isolation of evolutionary lineages (>3mya) through vicariance; however little attention has been given to the pathways of colonization of the eastern Pacific and the processes that have shaped diversity within the most recent evolutionary time. We sequenced 770 bp of the mtDNA control region to examine the stock structure and phylogeography of 550 green turtles from eight different rookeries in the central and eastern Pacific. We found significant differentiation between the geographically separated nesting populations and identified five distinct stocks (*F*_ST* = 0.08 – 0.44, *p*<0.005). Central and eastern Pacific *Chelonia mydas* form a monophyletic group containing 3 sub-clades, with Hawaii more closely related to the eastern Pacific than western Pacific populations. The split between sampled central/eastern and western Pacific haplotypes was estimated at 0.336 mya, suggesting that the Pacific region west of Hawaii has been a more formidable barrier to gene flow in *C.mydas* than the East Pacific Barrier. Our results suggest that the eastern Pacific was colonized from the western Pacific via the Central North Pacific and that the Revillagigedos Islands provided a stepping-stone for radiation of green turtles from the Hawaiian Archipelago to the eastern Pacific. Our results fit with a broader paradigm that has been described for marine biodiversity, where oceanic islands, such as Hawaii and Revillagigedos, rather than being peripheral “graveyards”, serve as sources and recipients of diversity and provide a mechanism for further radiation.

**Week of 27 October 2014**

Abstract - We assessed scarring patterns as evidence of fisheries interactions for three populations of false killer whales in Hawai‘i. Bycatch of the pelagic population in the tuna longline fishery exceeds their Potential Biological Removal level. Scarring was assessed by seven evaluators as consistent, possibly consistent, or not consistent with fisheries interactions, and average scores computed. Scores were highest for scarred main Hawaiian Island (MHI) false killer whales, followed by pelagic and Northwestern Hawaiian Island (NWHI) individuals. Considering only whales for which the majority of evaluators scored scarring as consistent revealed significant differences among populations in the percentage of individuals scarred; MHI: 7.5%, pelagic: 0%, NWHI: 0%. Assessment by social cluster for the MHI population showed that 4.2% of Cluster 1, 7.1% of Cluster 2, and 12.8% of Cluster 3 individuals had such scarring, although differences between clusters were not statistically significant. There was a significant sex bias; all sexed individuals (n = 7) with injuries consistent with fisheries interactions were female. The higher proportion of MHI individuals with fisheries-related scarring suggests that fisheries interactions are occurring at a higher rate in this population. The bias towards females suggests that fisheries-related mortality has a disproportionate impact on population dynamics.


Abstract - From 1948 to 1979, the USSR conducted extensive illegal whaling worldwide. Data from the North Pacific (NP) were analyzed to correct falsified International Whaling Commission catch records, and to investigate the distribution of sperm whales (NP catch = 157,680). Information was available on the distribution of 123,264 sperm whale catches. Among a number of areas defined by the Soviet whalers the largest catches were in the three main regions: 31,395 in the Eastern Region (ER), 29,518 in the Central Region (CR), 19,313 in the Western Region (WR); an additional 23,090 catches were made at the Kuril land stations. Other areas with substantial catches included the Aleutians (5,945) and Commander Islands (1,448), Bering Sea (3,170), Olyutorsky Bay (3,094), and other parts of the pelagic NP (6,049). Four main areas of concentration included: a large pelagic area (30-50°N) in the ER, including the Gulf of Alaska and western coast of North America; the northeastern and southwestern CR; and the southern Kurils. Some of the distribution was similar to 19th century catches, notably in the “Japan Ground” (in the pelagic western Pacific) and the “Coast of Japan Ground”. Many females were caught in Olyutorsky Bay and around the Commander Islands. There was also a division in catch composition at Amchitka Pass (Aleutians), with family groups to the west and mature males to the east. The extensive illegal catches of females removed a significant portion of the reproductively mature population, which likely continues to impact recovery of NP sperm whales today.

This paper is Open Access and a pdf can be downloaded for free at:


Abstract - Blubber progesterone levels were measured in biopsy samples and used to predict the pregnancy status of 507 female common dolphins (204 long-beaked common dolphins, Delphinus capensis, and 303 short-beaked common dolphins, D. delphis). Samples were collected in the coastal waters of the eastern North Pacific between central California, USA and the southern end of Baja California, Mexico. The percentage of females pregnant was similar between the two species: 22.1% (n = 45) of D. capensis and 28.1% (n = 85) of D. delphis. For both species we found strong geographic patterns in pregnancy, suggesting that some areas were more conducive for pregnant females. A sizable drop in percent pregnant from early (38.8%, n = 133) to late (25.3%, n = 91) autumn was found in D. delphis but not in D. capensis. The potential for sample selectivity was examined via biopsies collected either from a large research ship or from a small, rigid-hull inflatable boat (RHIB) launched from the larger ship. An analysis of “Tandem Biopsy Sampling”, replicate biopsy effort on the same schools from each vessel/platform, yielded little evidence that disproportionately more pregnant female common dolphins were biopsied from one platform versus the other. This result plus an analysis of pregnancy status relative to the duration of biopsy operations failed to uncover strong evidence of unaccounted
sampling bias with respect to pregnancy state. In total, these results demonstrate the utility of blubber progesterone concentrations to assess pregnancy status in free-ranging cetaceans and they highlight potential factors associated with population-level variation in dolphin pregnancy rates.


Abstract - Climatic variation alters biochemical and ecological processes, but it is difficult both to quantify the magnitude of such changes, and to differentiate long-term shifts from inter-annual variability. Here, we simultaneously quantify decade-scale isotopic variability at the lowest and highest trophic positions in the offshore California Current System (CCS) by measuring d15N and d13C values of amino acids in a top predator, the sperm whale (Physeter macrocephalus). Using a time series of skin tissue samples as a biological archive, isotopic records from individual amino acids (AAs) can reveal the proximate factors driving a temporal decline we observed in bulk isotope values (a decline of 1 %) by decoupling changes in primary producer isotope values from those linked to the trophic position of this toothed whale. A continuous decline in baseline (i.e., primary producer) d15N and d13C values was observed from 1993 to 2005 (a decrease of 4% for d15N source-AAs and 3% for d13C essential-AAs), while the trophic position of whales was variable over time and it did not exhibit directional trends. The baseline d15N and d13C shifts suggest rapid ongoing changes in the carbon and nitrogen biogeochemical cycling in the offshore CCS, potentially occurring at faster rates than long-term shifts observed elsewhere in the Pacific. While the mechanisms forcing these biogeochemical shifts remain to be determined, our data suggest possible links to natural climate variability, and also corresponding shifts in surface nutrient availability. Our study demonstrates that isotopic analysis of individual amino acids from a top marine mammal predator can be a powerful new approach to reconstructing temporal variation in both biochemical cycling and trophic structure.

Week of 20 October 2014


Abstract – An adult female long-beaked common dolphin Delphinus capensis live-stranded in La Jolla, California, USA, on July 30, 2012 and subsequently died on the beach. Computed tomography and magnetic resonance imaging revealed gas bubble accumulation in the vasculature, organ parenchyma, mandibular fat pads, and subdermal sheath as well as a gas-filled cavity within the liver, mild caudal abdominal effusion, and fluid in the uterus. Gross examination confirmed these findings and also identified mild ulcerations on the palate, ventral skin, and flukes, uterine necrosis, and multifocal parenchymal cavitations in the brain. Histological review demonstrated necrosis and round clear spaces interpreted as gas bubbles with associated bacterial rods within the brain, liver, spleen, and lymph nodes. Anaerobic cultures of the lung, spleen, liver, bone marrow, and abdominal fluid yielded Clostridium perfringens, which was further identified as type A via a multiplex PCR assay. The gas composition of sampled bubbles was typical of putrefaction gases, which is consistent with the by-products of C. perfringens, a gas-producing bacterium. Gas bubble formation in marine mammals due to barotrauma, and peri- or postmortem offgassing of supersaturated tissues and blood has been previously described. This case study concluded that a systemic infection of C. perfringens likely resulted in production of gas and toxins, causing tissue necrosis.


Abstract – Fishing, farming and ranching provide opportunities for predators to prey on resources concentrated by humans, a behavior termed depredation. In the Gulf of Alaska, observations of sperm whales depredating on fish caught on demersal longline gear dates back to the 1970s, with reported incidents increasing in the mid-1990s. Sperm whale depredation provides an opportunity to study the spread of a novel foraging behavior within a population. Data were collected during National Marine Fisheries Service longline surveys using demersal longline gear in waters off Alaska from 1998 to 2010. We evaluated whether observations of
Abstract -- The requirement to monitor listed species in European designated sites is challenging for long-lived mobile species that only temporarily occupy protected areas. We use a 21 year time series of bottlenose dolphin photo-identification data to assess trends in abundance and conservation status within a Special Area of Conservation (SAC) in Scotland. Mark–recapture methods were used to estimate annual abundance within the SAC from 1990 to 2010. A Bayesian mark–recapture model with a state-space approach was used to estimate overall population trends using data collected across the populations’ range. Despite inter-annual variability in the number of dolphins within the SAC, there was a >99% probability that the wider population was stable or increasing. Results indicate that use of the SAC by the wider population has declined. This is the first evidence of long-term trends in the use of an EU protected area by small cetaceans in relation to changes in overall population status. Our results highlight the importance of adapting the survey protocols used in long-term photo-identification studies to maintain high capture probabilities and minimise sampling heterogeneity. Crucially, these data demonstrate the value of collecting data from the wider population to assess the success of protected areas designated for mobile predators.

Week of 29 September 2014


Abstract -- Relatively little is known about cetaceans inhabiting the waters of the Mariana Islands in the western Pacific. We use mitochondrial DNA (mtDNA) sequences obtained from biopsy samples to investigate the genetic diversity and structure of four species of delphinids found near the Mariana Islands – short-finned pilot whales (SFPWs; Globicephala macrocephalus; n=47), spinner dolphins (Stenella longirostris longirostris; n=95), bottlenose dolphins (Tursiops truncatus; n=15), and melon-headed whales (MHWs; Peponocephala electra; n=2). We found evidence of genetic differentiation between islands for SFPWs, but not for spinner dolphins. Sample sizes were too small to investigate differentiation within the other two species. SFPWs around the Marianas possess haplotype similar to also common in the South Pacific, North Atlantic, Indian Ocean, and of off southern Japan. Both spinner dolphins and MHWs possess haplotypes common throughout the Pacific. The spinner dolphins exhibit high haplotypic diversity similar to that observed in the Society Islands of French Polynesia, suggesting they are not as genetically isolated as Hawaiian spinner dolphins. We did not find any T. aduncus haplotypes among the bottlenose dolphin samples, instead finding that two-thirds of the animals possess T. truncatus haplotypes while the remaining one-third share a single Fraser’s dolphin (Lagenodolephis hosei) haplotype. Photo-identification data confirm that the five samples with Fraser’s dolphin haplotypes come from five different individuals, all of which appear morphologically to be bottlenose dolphins. This result suggests that there has been extensive introgression of Fraser’s dolphin mtDNA into the Mariana Islands bottlenose dolphin gene pool.


ABSTRACT: Population abundance and trends are informative metrics for assessing population status and basing management decisions, but it can be challenging to estimate these metrics for species that are difficult to detect. We used a Bayesian hierarchical approach to improve estimates of abundance and trends for sperm

Week of 6 October 2014


Abstract -- The requirement to monitor listed species in European designated sites is challenging for long-lived mobile species that only temporarily occupy protected areas. We use a 21 year time series of bottlenose dolphin photo-identification data to assess trends in abundance and conservation status within a Special Area of Conservation (SAC) in Scotland. Mark–recapture methods were used to estimate annual abundance within the SAC from 1990 to 2010. A Bayesian mark–recapture model with a state-space approach was used to estimate overall population trends using data collected across the populations’ range. Despite inter-annual variability in the number of dolphins within the SAC, there was a >99% probability that the wider population was stable or increasing. Results indicate that use of the SAC by the wider population has declined. This is the first evidence of long-term trends in the use of an EU protected area by small cetaceans in relation to changes in overall population status. Our results highlight the importance of adapting the survey protocols used in long-term photo-identification studies to maintain high capture probabilities and minimise sampling heterogeneity. Crucially, these data demonstrate the value of collecting data from the wider population to assess the success of protected areas designated for mobile predators.
whales *Physeter macrocephalus* in the California Current based on 6 surveys conducted from 1991 to 2008. The method consists either of a regression trend or Markov process model for true abundance in the study area and an observation model used to estimate detection probability (in our case, based on line-transect distance sampling methods). Our approach improves upon models that we have applied to other cetacean species by incorporating direct estimates of sampling variance in the number of groups encountered (to reduce estimates of process variance) and by using an alternative to the commonly used Horvitz-Thompson-like estimator to better deal with covariate-dependent detection probability estimation when sample sizes are small. Our abundance estimates were much less variable through time than previously published estimates; this has important implications for management under the US Marine Mammal Protection Act. We were unable to precisely estimate overall abundance trends for sperm whales in the study area, but we estimated a high probability that small-group abundance, likely representing adult male abundance, has increased.

*Week of 22 September 2014*


*Abstract* - Understanding the causes and consequences of variability in trophic status is important for interpreting population dynamics and for identifying important habitats for protected species like marine turtles. In the northwest atlantic Ocean, many leatherback turtles (*Dermochelys coriacea*) from distinct breeding stocks throughout the Wider caribbean region migrate to canadian waters sea- sonally to feed, but their trophic status during the migratory and breeding cycle and its implications have not yet been described. In this study, we used stable carbon and nitrogen isotope analyses of bulk skin to characterize the trophic status of leatherbacks in atlantic canadian waters by identify- ing trophic patterns among turtles and the factors influencing those patterns. δ15N values of adult males and females were significantly higher than those of turtles of unknown gender (i.e., presumed to be subadults), and δ15N increased significantly with body size. We found no significant dif- ferences among average stable isotope values of turtles according to breeding stock origin. Significant inter-annual variation in δ15N among cohorts probably reflects broad- scale oceanographic variability that drives fluctuations in stable isotope values of nutrient sources transferred through several trophic positions to leatherbacks, variation in base-line isotope values among different overwintering habitats used by leatherbacks, or a combination of both. Our results demonstrate that understanding effects of demographic and physiological factors, as well as oceanographic conditions, on trophic status is key to explaining observed patterns in population dynamics and for identifying important habitats for widely distributed, long-lived species like leatherbacks.

*Week of 8 September 2014*


*Abstract* - The Northern North Carolina Estuarine System (NNCES) stock of the common bottlenose dolphin (*Tursiops truncatus*) has a small population size and low Potential Biological Removal level (PBR). Levels of serious injury and mortality due to commercial fisheries interactions may exceed the PBR. In addition, the prior abundance estimate, from a survey in 2006, is no longer valid for computing the PBR for the stock after 2014. To obtain a new abundance estimate, we conducted a capture-mark-recapture survey of the NNCS stock in the Pamlico-Albemarle Estuarine Complex (PAEC) from 15 June to 27 July 2013. The PAEC is the primary summer habitat for the stock. We surveyed 4,779 km of trackline, encountering 128 dolphin groups. We took 30,991 photographs, from which 471 individual dolphins were identified from distinctive nicks and notches on dorsal fins. Because dolphins in the most southern portion of the summer habitat overlap with the Southern North Carolina Estuarine System (SNCES) stock in July, some photographed dolphins could have been members of the SNCES stock. We developed a decision tree to identify dolphins that may have belonged to the SNCES stock, thereby allowing us to estimate abundance using all dolphins and then excluding those that
might belong to the SNCES stock. We then calculated lower (823; 95% posterior interval (PI) = 733-931) and upper (873; 95% PI = 775-989) bounds on the abundance estimate based on habitat-use assumptions from the decision tree. Both estimates were obtained using closed capture-mark-recapture models and a novel method to correct for dolphins with indistinctive fins.


No abstract

Week of 25 August 2014


Abstract - Cataloging biodiversity is critical to conservation efforts because accurate taxonomy is often a precondition for protection under laws designed for species conservation, such as the U.S. Endangered Species Act (ESA). Traditional nomenclatural codes governing the taxonomic process have recently come under scrutiny because taxon names are more closely linked to hierarchical ranks than to the taxa themselves. A new approach to naming biological groups, called phylogenetic nomenclature (PN), explicitly names taxa by defining their names in terms of ancestry and descent. PN has the potential to increase nomenclatural stability and decrease confusion induced by the rank-based codes. But proponents of PN have struggled with whether species and infraspecific taxa should be governed by the same rules as other taxa or should have special rules. Some proponents advocate the wholesale abandonment of rank labels (including species); this could have consequences for the implementation of taxon-based conservation legislation. I examined the principles of PN as embodied in the PhyloCode (an alternative to traditional rank-based nomenclature that names biological groups based on the results of phylogenetic analyses and does not associate taxa with ranks) and assessed how this novel approach to naming taxa might affect the implementation of species-based legislation by providing a case study of the ESA. The latest version of the PhyloCode relies on the traditional rank-based codes to name species and infraspecific taxa; thus, little will change regarding the main targets of the ESA because they will retain rank labels. For this reason, and because knowledge of evolutionary relationships is of greater importance than nomenclatural procedures for initial protection of endangered taxa under the ESA, I conclude that PN under the PhyloCode will have little impact on implementation of the ESA.

http://www.nmfs.noaa.gov/pr/sars/region.htm

no abstract

Week of 4 August 2014

http://dx.doi.org/10.1016/j.jembe.2014.04.025

Abstract - To conduct conservation of migratory species, such as marine turtles, it is important to understand the population structure throughout the entire distribution of the species. We study the genetic composition of the leatherback turtles, Dermochelys coriacea foraging in waters off Argentina by analyzing 763 bp sequences of the mtDNA control region in order to determine the nesting origin of these animals. A total of 40 samples were collected from adult leatherbacks (mean 143.5; 180–123 cm curved carapace length) captured (10%) in fisheries or encountered as strandings (90%). Based on analysis of mtDNA sequences we detected 4 haplotypes,
the most common (n=26) being DC1.1, and the other rarer DC1.3 (n=4), DC13.1 (n=2), and DC1.4 (n=1). The genetic diversity was evaluated through the haplotype (0, 3712 ± 0, 1000) and nucleotide diversities (0, 000521 ± 0, 000553). Bayesian Mixed Stock Analysis (MSA) showed that the Buenos Aires foraging leatherbacks come primarily from the West African rookeries (Ghana and Gabon, mean estimate = 69% and 14% respectively). MSA results are consistent with those from mark–recapture studies, since four leatherbacks captured in Argentinean waters were adult females that were originally tagged on the nesting beaches in Gabon, West Africa. Our findings demonstrate the connection between nesting and foraging areas in the South Atlantic and illustrate the importance of the Malvinas ecoregion to the survival of migratory marine vertebrates, such as leatherbacks.


Abstract – no abstract.

Week of 14 July 2014


Abstract - Simple Bayesian statistical models are introduced to estimate the proportion of identifiable individuals and group sizes in photographic identification, or photo-ID, studies of animals that are found in groups. The models require a simple random photographic sampling of animals, where the photographic captures are treated as sampling with replacement within each group. The total number of images, including those that cannot be identified, and the number of images that contain identifiable individuals are used to make inference about the proportion of identifiable individuals within each group and as the population when a number of groups are sampled. The numbers of images for individuals within each group are used to make inference about the group size. Based on analyses of simulated and real data, the models perform well with respect to accuracy and precision of posterior distributions of the parameters. Widths of posterior intervals were affected by the number of groups sampled, sampling duration, and the proportion of identifiable individuals in each group that was sampled. The structure of the models can accommodate covariates, which may affect photographic efficiency, defined in this study as the probability of photographically capturing individuals.

Week of 16 June 2014


Abstract - The Pacific Coast of the Baja California Peninsula (BCP), Mexico, is a hotspot for foraging loggerhead turtles Caretta caretta originating from nesting beaches in Japan. The BCP region is also known for anthropogenic sea turtle mortality that numbers thousands of turtles annually. To put the conservation implications of this mortality into biological context, we conducted aerial surveys to determine the distribution and abundance of loggerhead turtles in the Gulf of Ulloa, along the BCP Pacific Coast. Each year from 2005 to 2007, we surveyed ca. 3700 km of transect lines, including areas up to 140 km offshore. During these surveys, we detected loggerhead turtles at the water’s surface on 755 occasions (total of 785 loggerheads in groups of up to 7 turtles). We applied standard line-transect methods to estimate sea turtle abundance for survey data collected during good to excellent sighting conditions, which included 447 loggerhead sightings during ~6400 km of survey effort. We derived the proportion of time that loggerheads
were at the surface and visible to surveyors based on in situ dive data. The mean annual abundance of 43,226 loggerhead turtles (CV = 0.51, 95% CI range = 15,017 to 100,444) represents the first abundance estimate for foraging North Pacific loggerheads based on robust analytical approaches. Our density estimate confirms the importance of the BCP as a major foraging area for loggerhead turtles in the North Pacific. In the context of annual mortality estimates of loggerheads near BCP, these results suggest that up to 11% of the region’s loggerhead population may perish each year due to anthropogenic and/or natural threats. We calculate that up to 50% of the loggerhead turtles residing in the BCP region in any given year will die within 15 yr if current mortality rates continue. This underscores the urgent need to minimize anthropogenic and natural mortality of local loggerheads.

**Week of 26 May 2014**


*Abstract* - False killer whales (*Pseudorca crassidens*) are large Delphinids typically found in deep water far offshore. However, in the Hawaiian Archipelago there are two resident island-associated populations of false killer whales, one in the waters around the main Hawaiian Islands (MHI) and one in the waters around the Northwestern Hawaiian Islands (NWHI). We use mitochondrial DNA (mtDNA) control region sequences and genotypes from 16 nuclear (nucDNA) microsatellite loci from 206 individuals to examine levels of differentiation among the two island-associated populations and offshore animals from the central and eastern North Pacific. Both mtDNA and nucDNA exhibit highly significant differentiation between populations, confirming limited gene flow in both sexes. The mtDNA haplotypes exhibit a strong pattern of phylogeographic concordance, with island-associated populations sharing three closely related haplotypes not found elsewhere in the Pacific. However, nucDNA data suggests that NWHI animals are at least as differentiated from MHI animals as they are from offshore animals. The patterns of differentiation revealed by the two marker types suggest that the island-associated false killer whale populations likely share a common colonization history, but have limited contemporary gene flow.


*Abstract* - Capture-recapture methods are frequently employed to estimate abundance of cetaceans using photographic techniques and a variety of statistical models. However, there are many unresolved issues regarding the selection and manipulation of images that can potentially impose bias on resulting estimates. To examine the potential impact of these issues we circulated a test data set of dorsal fin images from bottlenose dolphins to several independent research groups. Photo-identification methods were generally similar, but the selection, scoring, and matching of images varied greatly amongst groups. Based on these results we make the following recommendations. Researchers should: (1) determine the degree of marking, or level of distinctiveness, and use images of sufficient quality to recognize animals of that level of distinctiveness; (2) ensure that markings are sufficiently distinct to eliminate the potential for “twins” to occur; (3) stratify data sets by distinctiveness and generate a series of abundance estimates to investigate the influence of including animals of varying degrees of markings; and (4) strive to examine and incorporate variability among analysts into capture-recapture estimation. In this paper we summarize these potential sources of bias and provide recommendations for best practices for using natural markings in a capture-recapture framework.

**Week of 05 May 2014**


Abstract - Hong Kong has one of the last remaining nesting populations of endangered green turtles (*Chelonia mydas*) in southern China. Because nesting individuals are vital to sustain populations, this study characterizes and reports essential baseline information about nesting pattern, postnesting movement, and genetic composition of green turtles nesting in Hong Kong to provide a basis for effective scientific-based management of this migratory species. The number of nesters observed in Hong Kong was relatively low compared with other rookeries in southern China, but the nesting pattern in terms of clutch size and interesting interval was comparable with that of other nearby rookeries. These nesters are likely a remnant of a small population previously depleted as a result of historical harvesting of eggs in Hong Kong. Based on available DNA sequences and literature, we identified two mtDNA haplotypes, CmP18 (which is also common in the rookery in Taiwan) and a novel endemic haplotype (CmP116). We found significant differentiation based on haplotype frequencies between populations in Hong Kong and Lanyu, Taiwan, indicating that these nesting populations are demographically isolated. Loss of these populations would therefore result in loss of genetic diversity for this species in the region. Satellite tracking of the local nesters revealed postnesting movement to foraging habitats in Vietnam and Hainan Island. International cooperation and consistent dedicated research are of paramount importance to conservation and recovery of green turtle assemblages in the region.

**Week of 28 April 2014**


No abstract

**Week of 21 April 2014**


Abstract - We used stable isotope (δ13C, δ15N, δ34S) analysis in combination with satellite telemetry to evaluate the foraging areas chosen by 88 loggerhead turtles *Caretta caretta* nesting in southwestern Florida. Nine turtles were tracked and skin-sampled in more than one nesting season to evaluate within-individual consistency in foraging sites and stable isotope values. Turtles migrated to 5 regions: Caribbean, Florida Keys, West Florida Shelf, northern Gulf of Mexico, and Yucatan Peninsula. The stable isotope ratios across these foraging grounds ranged from −21.16 to −7.69 ‰ for δ13C, 3.27 to 13.99 ‰ for δ15N, and 1.91 to 20.64 ‰ for δ34S. We compared bulk skin tissue stable isotope values for all turtles by bioregion, year, body size, depth of putative foraging area, and linear distance from the closest shore; among these factors, only bioregion showed a significant effect on isotope values. There were subtle regional differences in mean δ13C, δ15N, and δ34S, and an apparent north-south isotopic shift aligning with ocean currents adjacent to the Florida Keys. The influence of coastal topography and shifting biogeographic boundaries such as the Loop Current may cause strong ocean water mixing that results in the observed similarities in stable isotope values among regions. These results indicate that stable isotopes alone may be an inadequate tool for identifying fine-scale (<100 km) residency of sea turtles within this ocean region.

**Week of 14 April 2014**


Overview - Bycatch of marine mammals, sea turtles, and seabirds is reported for two gillnet fisheries in 2012: 1) the California (CA) swordfish and thresher shark drift gillnet fishery, and 2) the CA halibut and white
seabass set gillnet fishery, based on fishery observer data collected in 2012. Bycatch estimates are generated using ratio estimation methods. Observations in the CA swordfish and thresher shark drift gillnet fishery included 83 sets during 15 fishing trips, from an estimated 445 sets fished by all vessels (18.7% observer coverage). Observed bycatch included 5 short-beaked common dolphins (Delphinus delphis), one northern right whale dolphin (Lissodelphis borealis), and six California sea lions (Zalophus californianus). Additionally, one leatherback sea turtle (Dermochelys coriacea) was reported released alive and we provide an estimate of entanglements of this species in 2012. Estimated bycatch is 26 (CV=0.78) short-beaked common dolphins, five (CV=1.01) northern right whale dolphins, and 32 (CV=0.60) California sea lions. The estimated number of leatherback turtle entanglements in 2012 is five (CV=1.09), based on the observation of one entangled turtle and 18.7% observer coverage. Observations in the CA halibut and white seabass set gillnet fishery included 75 days of fishing, from an estimated 1,360 days fished by all vessels (5.5% observer coverage). Observed bycatch included 18 California sea lions, one pelagic cormorant (Phalacrocorax pelagicus), and three unidentified cormorants (Phalacrocorax sp). Estimated bycatch is 326 (CV=0.33) California sea lions, 18 (CV=0.98) pelagic cormorants and 54 (CV=0.72) unidentified cormorants. Two additional fisheries observed in 2012 did not have any recorded bycatch of marine mammals, seabirds, or sea turtles. The CA yellowtail, barracuda, and white seabass drift gillnet fishery had very low observer coverage, with three observed sets during one fishing trip, from an estimated 141 trips fished (0.7% observer coverage). The CA pelagic longline fishery, which operates outside of the U.S. Exclusive Economic Zone, was also observed in 2012, with 100% observer coverage and no observed bycatch.


**No Abstract**

**Week of 7 April 2014**

De Beukelaer, S., Miller, C., Moore, T.J., Kathey, S., and Grimmer K.. 2014. Monterey Bay National Marine Sanctuary Vessel Traffic Analysis 2009-2012. Monterey Bay National Marine Sanctuary Technical Report, 44 pp. **Executive Summary** - Monterey Bay National Marine Sanctuary (MBNMS) staff and stakeholders sought to have a better understanding of vessel compliance with the International Maritime Organization (IMO) recommended tracks within the MBNMS that were established in 2000. Three different analyses using Automated Information System (AIS) ship traffic data were completed to address this question. The Naval Postgraduate School (NPS) reviewed daily AIS data from September 2009-2012 and found that annually less than 8 individual cargo vessels deviated more than 3 nautical miles inshore of the northbound recommended track for vessels 300 gross tons and above and only one tanker was found deviating from that northbound track in that time-period. A further refinement of the analysis of the tanker traffic would be facilitated by access to data on the association and contents of each vessel because Western States Petroleum Association (WSPA) tankers carry crude oil, black oil, or other persistent liquid cargo in bulk and have agreed to stay more than 50 nautical miles offshore. The Southwest Fisheries Science Center of the National Marine Fisheries Service completed density maps for 2009 AIS data and found that tankers are using the recommended tracks, particularly those designated for vessels carrying hazardous cargo in bulk with an especially higher density using the southbound track. The 2009 data analysis by the Southwest Fisheries Science Center indicated higher densities of cargo vessels in the northbound recommended track for vessels 300 gross tons and above than in the other three tracks. MBNMS began conducting random daily reviews of AIS data on October 1, 2012 and staff contact the United States Coast Guard (USCG) when a deviation of more than 3 nautical miles inshore of the northbound recommended track for vessels 300 gross tons and above is noted. The USCG verifies the AIS data and contacts the vessel if they determine that the AIS data do reflect a deviation. These three AIS analyses do indicate that a great majority of the vessels that transit through the MBNMS are complying with the IMO recommended tracks.

**Week of 31 March 2014**

**Mark S. Lowry,** Richard Condit, Brian Hatfield, Sarah G. Allen, Ryan Berger, Patricia A. Morris, Burney J. Le Boeuf, and J. Reiter. 2014. Abundance, Distribution, and Population Growth of the Northern Elephant Seal

Abstract - We report on the distribution and abundance of the northern elephant seal (Mirounga angustirostris) in the United States from 1991 to 2010. Pup production (i.e., births) was the principal metric used to characterize abundance, distribution, and population growth of the U.S. population and of each rookery in the U.S. Birth estimates were obtained from the literature and estimated from recent counts of adult females or counts of pups made during ground and aerial photographic surveys conducted during the pupping-breeding season at all rookeries in central California and the Channel Islands in southern California. A total of 40,684 pups were estimated to have been born at 11 rookeries in the U.S. in 2010. The two most productive rookeries as of 2010 were San Miguel Island (16,208 pups) and San Nicolas Island (10,882 pups). The Piedras Blancas rookery was not established in 1991 but has since grown to be the fourth largest rookery as of 2010. Rookeries grew most rapidly initially, presumably due to high immigration rates; then increased moderately, eventually becoming stable; and some declined in size. Since 1988, the U.S. population has been growing at an average annual rate of 3.8%. The multiplicative factor needed to estimate total population size from pup production is estimated at 4.4. Total U.S. population size in 2010 was estimated at 179,000 individuals. Using conservative estimates for population growth of northern elephant seals in Mexico, we estimate that the total population in Mexico and the U.S. in 2010 was between 210,000 and 239,000 individuals.

Week of 24 March 2014


Abstract - Recent research on ocean health has found large predator abundance to be a key element of ocean condition. Fisheries can impact large predator abundance directly through targeted capture and indirectly through incidental capture of nontarget species or bycatch. However, measures of the global nature of bycatch are lacking for air-breathing megafauna. We fill this knowledge gap and present a synoptic global assessment of the distribution and intensity of bycatch of seabirds, marine mammals, and sea turtles based on empirical data from the three most commonly used types of fishing gears worldwide. We identify taxa-specific hotspots of bycatch intensity and find evidence of cumulative impacts across fishing fleets and gears. This global map of bycatch illustrates where data are particularly scarce—in coastal and small-scale fisheries and ocean regions that support developed industrial fisheries and millions of small-scale fishers—and identifies fishing areas where, given the evidence of cumulative hotspots across gear and taxa, traditional species or gear-specific bycatch management and mitigation efforts may be necessary but not sufficient. Given the global distribution of bycatch and the mitigation success achieved by some fleets, the reduction of air-breathing megafauna bycatch is both an urgent and achievable conservation priority.

Week of 17 March 2014


Abstract - Previous underwater recordings made in New Zealand have identified a complex sequence of low frequency sounds that have been attributed to blue whales based on similarity to blue whale songs in other areas. Recordings of sounds with these characteristics were made opportunistically during the Southern Ocean Research Partnership's recent Antarctic Blue Whale Voyage. Detections of these sounds occurred all around the South Island of New Zealand during the voyage transits from Nelson, New Zealand to the Antarctic and return. By following acoustic bearings from directional sonobuoys, blue whales were visually detected and confirmed as the source of these sounds. These recordings, together with the historical recordings made northeast of New Zealand, indicate song types that persist over several decades and are
indicative of the year-round presence of a population of blue whales that inhabits the waters around New Zealand. Measurements of the four-part vocalizations reveal that blue whale song in this region has changed slowly, but consistently over the past 50 years. The most intense units of these calls were detected as far south as 53°S, which represents a considerable range extension compared to the limited prior data on the spatial distribution of this population.

**Week of 10 March 2014**


http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0090464

*Abstract* - For biological populations that form aggregations (or clusters) of individuals, cluster size is an important parameter in line-transect abundance estimation and should be accurately measured. Cluster size in cetaceans has traditionally been represented as the total number of individuals in a group, but group size may be underestimated if group members are spatially diffuse. Groups of false killer whales (*Pseudorca crassidens*) can comprise numerous subgroups that are dispersed over tens of kilometers, leading to a spatial mismatch between a detected group and the theoretical framework of line-transect analysis. Three stocks of false killer whales are found within the U.S. Exclusive Economic Zone of the Hawaiian Islands (Hawaiian EEZ): an insular main Hawaiian Islands stock, a pelagic stock, and a Northwestern Hawaiian Islands (NWHI) stock. A ship-based line-transect survey of the Hawaiian EEZ was conducted in the summer and fall of 2010, resulting in six systematic-effort visual sightings of pelagic (*n* = 5) and NWHI (*n* = 1) false killer whale groups. The maximum number and spatial extent of subgroups per sighting was 18 subgroups and 35 km, respectively. These sightings were combined with data from similar previous surveys and analyzed within the conventional line-transect estimation framework. The detection function, mean cluster size, and encounter rate were estimated separately to appropriately incorporate data collected using different methods. Unlike previous line-transect analyses of cetaceans, subgroups were treated as the analytical cluster instead of groups because subgroups better conform to the specifications of line-transect theory. Bootstrap values (*n* = 5,000) of the line-transect parameters were randomly combined to estimate the variance of stock-specific abundance estimates. Hawai’i pelagic and NWHI false killer whales were estimated to number 1,552 (CV = 0.66; 95% CI = 479–5,030) and 552 (CV = 1.09; 95% CI = 97–3,123) individuals, respectively. Subgroup structure is an important factor to consider in line-transect analyses of false killer whales and other species with complex grouping patterns.

**Week of 3 March 2014**


*Abstract* - Woodland caribou (*Rangifer tarandus caribou*) are a species of increasing conservation concern across North America. Throughout much of boreal Canada, human developments, including forestry and energy development, are now accepted causes of the decline in the number and distribution of caribou. One of the hypothesised mechanisms for the decline is altered predator–prey dynamics. We quantified the impacts of a variety of industrial activities on gray wolf (*Canis lupus*) and caribou interactions at a regional scale. We used animal locations collected with global positioning system collars and field data to examine how a range of industrial developments influenced the movements of wolves. We quantified the speed of wolf movements and the tortuosity of movement paths at two spatiotemporal scales across forested boreal and mountainous environments occupied by woodland caribou. Habitat and disturbance features better explained wolf movements during the weekly scale. In general, linear movements increased during winter, which paralleled past studies that suggested linear travel by wolves was associated with deep snow and the increased maintenance and patrol of territories. Wolves decreased movement rates but not sinuosity within close proximity to disturbance features, thus implying behaviours near such features were more closely associated with prey searching and hunting. Alternatively, wolves increased movement rates and linear travel through areas with high densities of linear and non-linear industrial features; this response suggested that wolves avoided spending time in high-risk areas associated with human activities. Results of this study further our
understanding of wolf distribution and behaviour in habitats supporting populations of caribou within a matrix of industrial developments.

**Week of 24 February 2014**


*Abstract* - Recent research on ocean health has found large predator abundance to be a key element of ocean condition. Fisheries can impact large predator abundance directly through targeted capture and indirectly through incidental capture of non-target species, or bycatch. However, measures of the global nature of bycatch are lacking for air-breathing megafauna. We fill this knowledge gap and present the first global assessment of the distribution and intensity of bycatch of seabirds, marine mammals, and sea turtles based on empirical data from the three most commonly used types of fishing gears worldwide. We identify taxa-specific hotspots of bycatch intensity and find evidence of cumulative impacts across fishing fleets and gears. This global map of bycatch illustrates where data are particularly scarce - in coastal and small-scale fisheries and in ocean regions that support developed industrial fisheries and millions of small-scale fishers – and identify fishing areas where, given the evidence of cumulative hotspots across gear and taxa, traditional species or gear-specific bycatch management and mitigation efforts may be necessary, but not sufficient. Given the global distribution of bycatch and the mitigation success achieved by some fleets, the reduction of air-breathing megafauna bycatch is both an urgent and achievable conservation priority.

**Week of 10 February 2014**


*Abstract* - We present genetic and morphological evidence supporting the recognition of a previously synonymized species of *Mesoplodon* beaked whale in the tropical Indo-Pacific, *Mesoplodon hotalula*. Although the new species is closely-related to the rare ginkgo-toothed beaked whale *M. ginkgodens*, we show that these two lineages can be differentiated by maternally (mitochondrial DNA), biparentally (autosomal), and paternally (Y chromosome) inherited DNA sequences, as well as by morphological features. The reciprocal monophyly of the mtDNA genealogies and the largely parapatric distribution of these lineages is consistent with reproductive isolation. The new lineage is currently known from at least seven specimens: Sri Lanka (1), Gilbert Islands, Republic of Kiribati (1+), Palmyra Atoll, Northern Line Islands, U.S.A. (3), Maldives (1), and Seychelles (1). The type specimen (Sri Lanka) was described as a new species, *M. hotalula*, in 1963, but later synonymized with *M. ginkgodens*. This discovery brings the total number of *Mesoplodon* species to 15, making it, by far, the most speciose yet least known genus of cetaceans.


*Abstract* - Numerous methods are available for analysis of avian vocalizations, but few research efforts have compared recent methods for calculating and evaluating similarity among calls, particularly those collected in the field. This manuscript compares a suite of methodologies for analyzing flight calls of New World warblers, investigating the effectiveness of four techniques for calculating call similarity: (1) spectrographic cross-correlation, (2) dynamic time warping, (3) Euclidean distance between spectrogram-based feature measurements, and (4) random forest distance between spectrogram-based feature measurements. We tested these methods on flight calls, which are short, structurally simple vocalizations typically used during
nocturnal migration, as these signals may contain important ecological or demographic information. Using the four techniques listed above, we classified flight calls from three datasets, one collected from captive birds and two collected from wild birds in the field. Each dataset contained an equal number of calls from four warbler species commonly recorded during acoustic monitoring: American Redstart, Chestnut-sided Warbler, Hooded Warbler, and Ovenbird. Using captive recordings to train the classification models, we created four similarity-based classifiers which were then tested on the captive and field datasets. We show that these classification methods are limited in their ability to successfully classify the calls of these warbler species, and that classification accuracy was lower on field recordings than captive recordings for each of the tested methods. Of the four methods we compared, the random forest technique had the highest classification accuracy, enabling correct classification of 67.6% of field recordings. To compare the performance of the automated techniques to manual classification, the most common method used in flight call research, human experts were also asked to classify calls from each dataset. The experts correctly classified approximately 90% of field recordings, indicating that although the automated techniques are faster, they remain less accurate than manual classification. However, because of the challenges inherent to these data, such as the structural similarity among the flight calls of focal species and the presence of environmental noise in the field recordings, some of the tested automated classification techniques may be acceptable for real-world applications. We believe that this comparison of broadly applicable methodologies provides information that will prove to be useful for analysis, detection and classification of short duration signals. Based on our results, we recommend that a combination of feature measurements and random forest classification can be used to assign flight calls to species, while human experts oversee the process.

Week of 3 February 2014


Abstract - Temporal variability in species distribution remains a major source of uncertainty in managing protected marine species, particularly in ecosystems with significant seasonal or interannual variation, such as the California Current Ecosystem (CCE). Spatially explicit species-habitat models have become valuable tools for decision-makers assisting in the development and implementation of measures to reduce adverse impacts (e.g., from fishery bycatch, ship strikes, anthropogenic sound), but such models are often not available for all seasons of interest. Broad-scale migratory patterns of many of the large whale species are well-known, while seasonal distribution shifts of small cetaceans are typically less well understood. Within the CCE, species-habitat models have been developed based on six summer-fall surveys conducted during 1991-2008. In this study, we evaluate whether the between-year oceanographic variability can inform species predictions during winter-spring periods. Generalized additive models were developed to predict abundance of four cetacean species genera known to have year-round occurrence in the CCE: common dolphins (Delphinus spp.), Pacific white-sided dolphin (Lagenorhynchus obliquidens), northern right whale dolphin (Lissodelphis borealis), and Dall’s porpoise (Phocoenoides dalli). Predictor variables included a combination of temporally dynamic, remotely sensed environmental variables and geographically fixed variables. Across-season predictive ability was evaluated relative to aerial surveys conducted in winter-spring 1991-92, using observed:predicted density ratios, nonparametric Spearman rank correlation tests, and visual inspection of predicted and observed distributions by species. Seasonal geographic patterns of species density were captured effectively for most species, although some model limitations were evident, particularly when the original summer-fall data did not adequately capture winter-spring habitat conditions.


Abstract - Cetacean interactions (i.e., hookings and entanglements) with the Hawaii and American Samoa longline fisheries observed during 2007-2011 were compiled, and the number of cetacean deaths, serious injuries, and non-serious injuries by fishery, species, and management area were assessed. These values form the basis of the mortality and serious injury estimates included in the stock assessment reports of stocks impacted by these fisheries. Injury determinations were made using a revised process for distinguishing
serious from non-serious injuries (National Marine Fisheries Service, 2012). In the Hawaii deep-set fishery, 50 cetacean interactions were observed from 2007 to 2011; most involved false killer whales (48.0%), resulted in death or serious injury (73.5%), and occurred outside the U.S. exclusive economic zone, or EEZ (54.0%). In the Hawaii shallow-set fishery, 46 cetacean interactions were observed from 2007 to 2011; most involved Risso’s dolphins (45.7%), resulted in death or serious injury (77.2%), and occurred outside the U.S. EEZ (91.3%). In the American Samoa deep-set fishery, 14 cetacean interactions were observed from 2007 to 2011; most involved rough-toothed dolphins (42.9%), resulted in death or serious injury (92.9%), and occurred within the U.S. EEZ (85.7%).


Abstract - Accurate estimates of the annual numbers of nesting females are critical for assessing sea turtle populations. There has been a significant increase in nesting by Kemp’s ridley (Lepidochelys kempii) turtles at Padre Island National Seashore (PAIS) and nearby beaches in Texas, USA. There were 4 nests observed in Texas during 1995 and a record of 209 in 2012. However, it is unclear how many clutches are laid by the same female turtles. We use a genetic approach to infer the number of individual nesters from genotypes determined from dead embryos and hatchlings sampled from clutches. Mitochondrial DNA sequencing was combined with nuclear DNA analysis at 10 microsatellite loci to match genotypes for nesters and offspring of unknown parentage in over 50% of the unassigned nests. Our results indicate that traditional methods, based on observed tagged turtles, have underestimated the number of Kemp’s ridleys nesting in Texas. We demonstrate how genetic approaches can be incorporated into population assessments when direct census of adult animals is not feasible. This approach also provides a basis to apply Capture-Mark-Recapture techniques to impact assessment of events, such as the recent oil spill, on the population via sampling of nests to identify and track individual nesters over time.


Abstract - Population connectivity and spatial distribution are fundamentally related to ecology, evolution, and behavior. Here we combined powerful genetic analysis with high quality simulations of particle dispersal in an ocean circulation model to investigate the distribution of green turtles foraging at the remote Palmyra Atoll National Wildlife Refuge, Central Pacific. We analyzed mitochondrial sequences from turtles (n = 349) collected there over five years (2008 - 2012). Genetic analysis assigned natal origins almost exclusively (~97%) to the West Central and South Central Pacific combined Regional Management Units. Further, our modeling results indicated that turtles could potentially drift to Palmyra Atoll via surface currents along a near-Equatorial swathe traversing the Pacific. Comparing findings from genetics and modeling highlighted the complex impacts of ocean currents and behavior on natal origins. Although the Palmyra feeding ground was highly differentiated genetically from others in the Indo-Pacific, there was no significant differentiation among years, sexes, or stage-classes at the Refuge. Understanding the population distribution of this foraging population advances knowledge of green turtles and contributes to effective conservation planning for this threatened species.

Week of 27 January 2014


Abstract - At least ten species of beaked whales inhabit the North Pacific, but little is known about their abundance, ecology, and behavior, as they are elusive and difficult to distinguish visually at sea. Six of these species produce known species-specific frequency modulated (FM) echolocation pulses: Baird’s, Blainville’s, Cuvier’s, Deraniyagala’s, Longman’s, and Stejneger’s beaked whales. Additionally, one described FM pulse (BWC) from Cross Seamount, Hawai‘i, and three unknown FM pulse types (BW40, BW43, BW70) have been identified from almost 11 cumulative years of autonomous recordings at 24 sites
throughout the North Pacific. Most sites had a dominant FM pulse type with other types being either absent or limited. There was not a strong seasonal influence on the occurrence of these signals at any site, but longer time series may reveal smaller, consistent fluctuations. Only the species producing BWC signals, detected throughout the Pacific Islands region, consistently showed a diel cycle with nocturnal foraging. By comparing stranding and sighting information with acoustic findings, we hypothesize that BWC signals are produced by ginkgo-toothed beaked whales. BW43 signal encounters were restricted to Southern California and may be produced by Perrin’s beaked whale, known only from Californian waters. BW70 signals were detected in the southern Gulf of California, which is prime habitat for Pygmy beaked whales. Hubb’s beaked whale may have produced the BW40 signals encountered off central and southern California; however, these signals were also recorded off Pearl and Hermes Reef and Wake Atoll, which are well south of their known range.


Abstract - Fisheries bycatch is a critical source of mortality for rapidly declining populations of leatherback turtles, Dermochelys coriacea. We integrated use-intensity distributions for 135 satellite-tracked adult turtles with longline fishing effort to estimate predicted bycatch risk over space and time in the Pacific Ocean. Areas of predicted bycatch risk did not overlap for eastern and western Pacific nesting populations, warranting their consideration as distinct management units with respect to fisheries bycatch. For western Pacific nesting populations, we identified several areas of high risk in the north and central Pacific, but greatest risk was adjacent to primary nesting beaches in tropical seas of Indo-Pacific islands, largely confined to several exclusive economic zones under the jurisdiction of national authorities. For eastern Pacific nesting populations, we identified moderate risk associated with migrations to nesting beaches, but the greatest risk was in the South Pacific Gyre, a broad pelagic zone outside national waters where management is currently lacking and may prove difficult to implement. Efforts should focus on these predicted hotspots to develop more targeted management approaches to alleviate leatherback bycatch.


Abstract - Previous genetic studies have demonstrated that natal homing shapes the stock structure of marine turtle nesting populations. However, widespread sharing of common haplotypes based on short segments of the mitochondrial control region often limits resolution of the demographic connectivity of populations. Recent studies employing longer control region sequences to resolve haplotype sharing have focused on regional assessments of genetic structure and phylogeography. Here we synthesize available control region sequences for loggerhead turtles from the Mediterranean Sea, Atlantic, and western Indian Ocean basins. These data represent six of the nine globally significant regional management units (RMUs) for the species and include novel sequence data from Brazil, Cape Verde, South Africa and Oman. Genetic tests of differentiation among 42 rookeries represented by short sequences (380 bp haplotypes from 3,486 samples) and 40 rookeries represented by long sequences (.800 bp haplotypes from 3,434 samples) supported the distinction of the six RMUs analyzed as well as recognition of at least 18 demographically independent management units (MUs) with respect to female natal homing. A total of 59 haplotypes were resolved. These haplotypes belonged to two highly divergent global lineages, with haplogroup I represented primarily by CC-A1, CC-A4, and CC-A11 variants and haplogroup II represented by CC-A2 and derived variants. Geographic distribution patterns of haplogroup II haplotypes and the nested position of CCA11.6 from Oman among the Atlantic haplotypes invoke recent colonization of the Indian Ocean from the Atlantic for both global lineages. The haplotypes we confirmed for western Indian Ocean RMUs allow reinterpretation of previous mixed stock analysis and further suggest that contemporary migratory connectivity between the Indian and Atlantic Oceans occurs on a broader scale than previously hypothesized. This study represents a valuable model for conducting comprehensive international cooperative data management and research in marine ecology.

Abstract - A total of 56 vaquitas (Phocoena sinus) were examined to evaluate their sexual dimorphism and isometric and/or allometric growth in 35 external characteristics. Absolute and relative (to total length) measurements and growth rates were compared between sexually immature and mature females and males. T-tests and analysis of variance (ANOVA) and covariance (ANCOVA) were used to evaluate sexual dimorphism. Sexual dimorphism in the vaquita was detected in the total length, head region (from blowhole to tip of upper jaw), anterior section of the body (from dorsal fin to tip of upper jaw), dorsal fin and the genital and anal regions. Fluke width is relatively larger in mature males than immature males, but in females this relative metric does not change during their development. In addition, males present a higher dorsal fin. These somatic changes are probably related to the swimming capacity (speed, agility, maneuvering) during the breeding season and/or foraging activities. A linear model of growth was used to determine possible proportional changes with respect to total body length through the development of 33 external characteristics. The anterior region of the body and the flippers were relatively larger in immature individuals than in mature ones.

Week of 20 January 2014


Abstract - Humpback whales (Megaptera novaeangliae) in the Southeastern Atlantic Ocean (BSB stock) are distributed in winter along the western coast of the African continent, from Gulf of Guinea to western South Africa. Recent data suggest that this stock is sub-structured with a sub-stock that breeds in Gabon and possibly in other areas of Gulf of Guinea through Angola (B1), and a sub-stock using the west coast of South Africa as a winter migration corridor and summer feeding ground (B2). The location of the breeding ground for B2 whales remains unknown. This work re-evaluates the spatial and temporal population structure of humpback whales on the west coast of Africa using a combination of maternally and bi-parentally inherited markers. A total of 2018 samples representing B1 and B2 regions were amplified, sexed, genotyped and sequenced. The results revealed a subtle but significant genetic differentiation at spatial and temporal scales between B1 and B2, even with high gene flow and current interchange between the two regions. Differences in site fidelity and sex ratio between the two sub-stocks were found. The existence of some spatial and/or temporal segregation for the breeding grounds in the Gulf of Guinea together with the possible maternally directed site-fidelity to specific feeding grounds, some animals from Gabon travelling offshore to feeding grounds and others travelling coastwise to feed off West South Africa could be an explanation for the nature of the genetic differentiation found in this study. Further genetic sampling in other areas of the winter range and the strategic deployment of satellite tags could help clarify the situation.

Summary – Based on morphology, genetics, and distribution, we conclude that there are differences at the ESU, subspecies or species level between Peru (and northern Chile), and the western South Atlantic (Brazil, Uruguay, Argentina, and the Falkland Islands), and eastern South Pacific (southern Chile) fur seals. We propose that A. a. gracilis is a junior synonym of A. a. australis. The English common name should remain the South American fur seal on the South Atlantic mainland and the Falkland Islands. Following Berta and Churchill (2012) the Peru/northern fur seal is an unnamed subspecies with the Peruvian fur seal as its English common name. However, additional studies are needed on Peruvian and Galapagos fur seals to determine their taxonomic status and relationship to other fur seals.

Week of 13 January 2014

Galletti Vernazzani, B., Cabrera, E., and Brownell, R. L., Jr. 2014. Eastern South Pacific southern right whale

No Abstract

Week of 6 January 2014


Abstract - Biological and fisheries data were analysed to assess the impact of fisheries mortality on a Critically Endangered subpopulation of <100 humpback dolphins Sousa chinensis in the eastern Taiwan Strait (ETS). Substantial interactions between ETS S. chinensis (hereafter Sousa) and fishing gear are known to cause dolphin mortality. In 2009, a total of 6318 motorised fishing vessels were operating from ports within Sousa habitats. An average of 32 fishing craft per kilometer was observed along a 200 km stretch of Sousa habitat. Based on a photo-identification catalogue, >30% of the ETS Sousa subpopulation exhibited injuries caused by fishing gear. Three individuals were photographed with fishing gear attached to their bodies, and 1 dolphin was found dead with fresh injuries caused by fishing gear. To ensure recovery of ETS Sousa, mortality due to human causes should be reduced to <1 individual every 7 yr. Fisheries bycatch is the most serious threat to these dolphins and needs to be eliminated as soon as possible to avoid extinction. Preventing the use of trammel nets, other gillnets and trawling throughout their habitat would be the single most effective conservation measure for ETS Sousa in the short term. Other fishing methods are available, and using the most selective, sustainable fishing methods available will benefit not only dolphins but also fish stocks, seabirds and other species, as well as the fishing industry, which depends on these species for its long-term viability. However, in the short term, there are costs associated with switching to more selective fishing gear.

Week of 2 December 2013


Abstract - Identifying the appropriate ‘Unit to Conserve’ (UTC) is critical to the success of any management scheme. While the need to define the UTC appropriate to the IWC’s Catch Limit Algorithm (CLA) has long been recognised by its Scientific Committee, little progress has been made on this issue. The CLA was rigorously tested prior to its adoption. However, most of those original performance trials focused on single-population scenarios or two-population scenarios with no ongoing dispersal. None of the trials considered the performance of the CLA across a range of dispersal rates. In this study, the performance of the CLA under a variety of population structure scenarios is examined. This is the first study to investigate the levels of connectivity (i.e. dispersal rate) for which populations require separate management to meet the conservation goals of the CLA. All the trials consisted of two populations that were managed as a single stock for 100 years. Both historical and modern hunts were spatially-biased so that population 1 was the primary target of hunting. Parameters that varied among trials were the relative carrying capacities (K) of the populations, the dispersal rate between them, maximum sustainable yield rate (MSYR1+), and the precision in simulated abundance estimates. All of these parameters had strong effects on the conservation performance of the CLA. Trials with a low MSYR1+ (1%) generally ended with the abundance of population 1 below 0.54K, regardless of the dispersal rate or relative carrying capacities of the two populations. The same was true of trials in which the carrying capacity of population 1 represented only 10% of the total landscape carrying capacity and the CV of the abundance estimates was low, even when dispersal between populations was high (5 × 10–3 yr−1) and MSYR1+ was 4%. The results suggest that the appropriate UTCs under the RMP are likely to exchange dispersers at high enough rates that they will be difficult to delineate using existing methods. These results also highlight the value of spatially-diffuse hunting patterns that avoid potential overhunting of unrecognised stocks.


**Overview** - This assessment is significant in that it is the first time subpopulation-level listings for Leatherback turtles are recognized by IUCN along with the global assessment of all subpopulations combined. Based on Red List criteria and categories, East Pacific, West Pacific, Southwest Atlantic, and Southwest Indian Ocean subpopulations were listed as “Critically Endangered,” Northwest Atlantic leatherbacks were listed as “Least Concern,” and Northeast Indian Ocean and Southeast Atlantic subpopulations were listed as “Data Deficient”. Globally, leatherback status is now “Vulnerable.”

*Week of 25 November 2013*

Hyung-Soon Yim and 54 co-authors (including Phil Morin). 2013. Minke whale genome and aquatic adaptation in cetaceans. Nature Genetics. doi.10.1038/ng.2835

*Abstract* - The shift from terrestrial to aquatic life by whales was a substantial evolutionary event. Here we report the whole-genome sequencing and *de novo* assembly of the minke whale genome, as well as the whole-genome sequences of three minke whales, a fin whale, a bottlenose dolphin and a finless porpoise. Our comparative genomic analysis identified an expansion in the whale lineage of gene families associated with stress-responsive proteins and anaerobic metabolism, whereas gene families related to body hair and sensory receptors were contracted. Our analysis also identified whale-specific mutations in genes encoding antioxidants and enzymes controlling blood pressure and salt concentration. Overall the whole-genome sequences exhibited distinct features that are associated with the physiological and morphological changes needed for life in an aquatic environment, marked by resistance to physiological stresses caused by a lack of oxygen, increased amounts of reactive oxygen species and high salt levels.


*Abstract* - Hundreds of southern right whale calves *Eubalaena australis* died on their calving ground at Peninsula Valdés, Argentina from 2003 through 2011. During this period, the number of dead calves increased at a much greater rate than that of living calves over the preceding 32 yr, and with greater inter-annual variation. High mortality events occurred late in the calving seasons of 2005 and 2007, early in the seasons of 2008 and 2009, and were equally divided between early and late in 2010 and 2011. Calves that died late in the seasons of 2005 and 2007 were at least a meter longer (mean 7.3 m) than newborns, indicating that they had grown and presumably were healthy before dying. An unusual number of large calves (>6 m) died early in the seasons of 2008 and 2009, suggesting that a population-wide process (e.g. nutritional stress) affected many mothers including older, larger mothers that tend to give birth to larger calves early in the season. Many tissue samples have been collected and analyzed, but no consistent lesions, pathologic processes or elevated levels of algal biotoxins have been identified to explain these recent mortality events. Here, we document the high mortality events, place them in historical context and describe ongoing efforts to identify their causes. As of 2010, the southern right whale sub-population that calves off Peninsula Valdés was estimated to be less than 20% of its initial size before whaling; the ongoing high mortality of calves will significantly affect its recovery.

*Week of 12 November 2013*


*Abstract* - Sea turtle populations disperse widely across oceans and migrate between terrestrial nesting habitat and distant feeding and developmental habitats. Understanding population stock structure is important for accurately assessing threats such as mortality from fishery bycatch and for defining specific demographic
units of conservation concern. We compared 776-bp mtDNA control region haplotypes from 389 juvenile loggerhead turtles sampled as bycatch in the U.S. pelagic longline fishery in the western North Atlantic Northeast Distant (NED) region to haplotype frequencies observed in 23 genetically distinct nesting stocks representing the 4 Distinct Population Segments (DPS) that have been identified throughout the Atlantic Ocean and Mediterranean Sea. We used Bayesian mixed-stock analysis to produce stock composition estimates for juvenile loggerhead turtles that use pelagic habitat in the central North Atlantic. We found that nearly all of the loggerheads caught in NED waters belonged to the Northwest Atlantic DPS (mean = 99.2%), with the majority coming from the large eastern Florida rookeries (mean = 84.0%). We also detected contributions from the western Florida rookeries (mean = 11.7%) and Mexico (mean = 3.5%) but found little evidence of contributions from the rookeries of the South Atlantic, Northeast Atlantic or Mediterranean DPSs. These results will help improve specific threats assessments and are relevant to ongoing development of conservation plans that are aligned to the recent DPS listings for loggerheads.


Abstract - The productive North Pacific waters of the Gulf of Alaska, Aleutian Islands and Bering Sea support a high density of fish-eating “Resident” type killer whales (Orcinus Orca), which overlap in distribution with commercial fisheries, producing both direct and indirect interactions. To provide a spatial context for these interactions, we analyzed a 10-year dataset of 3,058 whale photoidentifications from 331 encounters within a large (linear ~4,000 km) coastal study area to investigate the ranging and social patterns of 532 individually identifiable whales photographed in more than one encounter. Although capable of large-scale movements (maximum 1,443 km), we documented ranges generally <200 km, with high site fidelity across summer sampling intervals and also re-sightings during a winter survey. Bayesian analysis of pairwise associations identified four defined clusters, likely representing groupings of stable matrilines, with distinct ranging patterns, that combined to form a large network of associated whales that ranged across most of the study area. This provides evidence of structure within the Alaska stock of Resident killer whales, important for evaluating ecosystem and fisheries impacts. This network included whales known to depredate groundfish from longline fisheries, and we suggest that such large-scale connectivity has facilitated the spread of depredation.


Week of 04 November 2013


Abstract - In Australia, the olive ridley sea turtle Lepidochelys olivacea has received little research attention and monitoring. The Australian populations are relatively small and their distribution is limited to remote areas in the northern part of the country. Previous global genetic studies of olive ridley populations showed that the Australian breeding population at the McCluer Group of islands, Northern Territory, is genetically distinct from other olive ridley populations breeding in the Indo-Pacific. However, nothing is known about the genetic stock structure among Australian olive ridley rookeries found across northern Australia. High predation of eggs by feral pigs, dogs and monitor lizards Varanus spp. is believed to have severely impacted the number of nesting females at some rookeries. Of particular concern is the small nesting population on the western Cape York Peninsula, and without immediate conservation action this population could face extinction. The results presented here establish that there are at least 2 independent management units (stocks) of olive ridley turtles nesting in Australia and emphasise the importance of conserving the
genetically distinct small breeding population nesting along the western Cape York Peninsula. In addition, results from 44 turtles caught in ghost nets across the Gulf of Carpentaria revealed that 45% of the haplotypes (32% of all ghost net samples) had not been observed at any rookery in Australia or SE Asia. This research highlights the need for better information on olive ridley population structure in the region and for urgent conservation action for the western Cape York population.


Summary:
1. Animal-borne instruments provide researchers with valuable data to address important questions on wildlife ecology and conservation. However, these devices have known impacts on animal behaviour and energetics. Tags deployed on migrating animals may reduce reproductive output through increased energy demands or cause phenological mismatches of foraging and nesting events. For marine organisms, the only tagging guidelines that exist are based on lift and thrust impacts on birds – concepts that do not translate well to aquatic animals. Herein, we provide guidelines on assessing drag from animal-borne instruments and discuss the ecological impacts on marine organisms. Of particular concern is the effect of drag from instruments to the welfare of the animals and for the applicability of collected data to wild populations.
2. To help understand how drag from electronic tags affects marine animals in the wild, we used marine turtles as model aquatic organisms and conducted wind tunnel experiments to measure the fluid drag of various marine turtle body types with and without commercially available electronic tags (e.g. satellite, TDR, video cameras). We quantified the drag associated with carrying biotelemetry devices of varying frontal area and design (squared or tear drop shaped) and generated contour plots depicting percentage drag increase as a framework for evaluating tag drag by scientists and wildlife managers. Then, using concepts of fluid dynamics, we derived a universal equation estimating drag impacts from instruments across marine taxa.
3. The drag of the marine turtle casts was measured in wind speeds from 2 to 30 m/s, equivalent to 01–19 m/s in seawater. The drag coefficient (CD) of the marine turtles ranged from 011 to 022, which is typical of other large, air-breathing, marine vertebrates. The CD of tags in reference to the turtle casts was 091’018 and most tags caused minimal additional drag (<5%) to adult animals, but the same devices increased the drag for juveniles significantly (>100%). The sensitivity of aquatic animals to instrument drag is a dynamic relationship between the fluid flow patterns, or CD, and the frontal area ratio of the animal and tag.
4. In this paper, we have outlined methods for quantifying the drag costs from animal-borne instrumentation considering the instrument retention time (time to release from the animal) and the activity of the instrumented animal. With this valuable tool, researchers can quantify the drag costs from animal-borne instrumentation and choose appropriate tags for their intended study organism and question. Reducing drag will ultimately reduce the impact on the instrumented animals and lead to greater biological realism in the collected data.


Abstract - Stressors associated with human activities interact in complex ways to affect marine ecosystems, yet we lack spatially explicit assessments of cumulative impacts on ecologically and economically key components such as marine predators. Here we develop a metric of cumulative utilization and impact (CUI) on marine predators by combining electronic tracking data of eight protected predator species (n=685 individuals) in the California Current Ecosystem with data on 24 anthropogenic stressors. We show significant variation in CUI with some of the highest impacts within US National Marine Sanctuaries. High variation in underlying species and cumulative impact distributions means that neither alone is sufficient for effective spatial management. Instead, comprehensive management approaches accounting for both cumulative human impacts and trade-offs among multiple stressors must be applied in planning the use of
marine resources.

**Week of 29 October 2013**


**Abstract** - Stage durations are integral to wildlife population models that can inform management, as they influence age at maturation and stage-specific survival rates. To refine oceanic stage duration estimates for western North Atlantic loggerhead sea turtles *Caretta caretta*, skeletochronological analysis was conducted on humeri collected in the Azores islands and along the US Atlantic coast. Complementary skeletal growth increment-specific stable isotope analysis was also performed for a subset of the humeri, to identify the skeletal growth mark associated with the shift from oceanic to neritic habitat through stable nitrogen isotope ($\delta^{15}N$) values and the presence of turtles in inshore waters. Although the transitional growth mark in this sub-sample corresponded to a range of sizes similar to those described in previous studies, mean size at recruitment (55.3 cm straightline carapace length [SCL]) for these turtles was larger than previously estimated. Similarly, while the range of ages at recruitment — corresponding both with the transitional growth mark and those yielded by fitting smoothing splines to SCL-at-age data—overlapped almost fully with earlier estimates, the mean age estimate (12.4 yr) differed from previous studies. Validated back-calculation of somatic growth rates from skeletal growth marks yielded means and ranges that encompassed those of previous loggerhead growth studies in this geographic area. Generalized additive models and generalized additive mixed models used to assess the potential influence of discrete and continuous covariates on back-calculated growth rates spanning 1984 to 2009 indicated significant effects of age, SCL, calendar year, and $\delta^{15}N$, but none for sex or location.


**Abstract** - Two populations of false killer whales, *Pseudorca crassidens*, are recognized from Hawaiian waters: the Hawaiian insular population, an island-associated population found around the main Hawaiian Islands; and the Hawai’i pelagic population, found in offshore waters. This species has not been previously documented near the Northwestern Hawaiian Islands. During a 2010 large-vessel survey throughout the Exclusive Economic Zone (EEZ) surrounding the Hawaiian Islands, false killer whales from 11 encounters were individually photo-identified, and photos were compared among encounters and with a catalog of false killer whales from the main Hawaiian Islands. Individuals from three of the encounters, all in the Northwestern Hawaiian Islands within the eastern part of the Papahānaumokuākea Marine National Monument, were the only ones documented that matched with false killer whales previously seen around the main Hawaiian Islands, and the matches were to individuals documented off Kaua’i in 2008 that were of unknown population membership. Two individuals from one of these three 2010 encounters were instrumented with satellite tags attached to dorsal fins, and their movements were documented over 4.6 and 52 days. Movements of the tagged individuals ranged from French Frigate Shoals to Middle Bank (between Nihoa and Ni’ihau) and included shallow nearshore waters and deep waters to 147 km from land. Combined, the photo-identification and satellite-tagging results suggest that there is a second island-associated population of this species in Hawai’i that primarily uses the Northwestern Hawaiian Islands, with a range that overlaps with that of the main Hawaiian Islands insular population.


**Abstract** - Accurate identification of units for conservation is particularly challenging for marine species as obvious barriers to gene flow are lacking. Bryde's whales (*Balaenoptera spp.*) are subject to multiple human-mediated stressors, including fisheries bycatch, ship strikes and scientific whaling by Japan. For effective management, a clear understanding of how populations of each Bryde's whale species are genetically
structured across their range is required. We conducted a population-level analysis of mtDNA control region sequences with 56 new samples from Oman, Maldives, and Bangladesh, plus published sequences from Java and the Northern Pacific. Nine diagnostic characters in the mitochondrial control region and a maximum parsimony phylogenetic analysis identified 2 genetically recognized subspecies of Bryde's whale: the larger, offshore form, *Balaenoptera edeni brydei*, and the smaller, coastal form, *Balaenoptera edeni edeni*. Genetic diversity and differentiation indices, combined with a reconstructed maximum parsimony haplotype network, indicate strong differences in the genetic diversity and population structure within each subspecies. Discrete population units are identified for *B. e. brydei* in the Maldives, Java and the Northwest Pacific and for *B. e. edeni* between the Northern Indian Ocean (Oman and Bangladesh) and the coastal waters of Japan.


Abstract - Hong Kong holds one of the last remaining nesting populations of endangered green turtles (*Chelonia mydas*) in southern China. Bearing in mind that nesting individuals are vital to sustain populations, this study characterizes and reports essential baseline information about the nesting pattern, post-nesting movement and genetic composition of green turtles nesting in Hong Kong in order to provide a basis for effective scientific-based management of this migratory species. While the number of nesters observed in Hong Kong was relatively low compared with other rookeries in southern China, the nesting pattern in terms of clutch size and inter-nesting interval was comparable to that of other nearby rookeries. These nesters are likely a remnant of the small population previously deplited as a result of the historical harvesting of eggs in Hong Kong. Based on the available DNA sequences and literature, we identified two mtDNA haplotypes: CmP18 which is also common in the rookery in Taiwan and a novel endemic haplotype (CmP116), and found significant differentiation based on haplotype frequencies between Hong Kong and Lanyu, Taiwan (FST=0.90, p<0.001), indicating that these nesting populations are demographically isolated. Loss of these populations would therefore result in loss of genetic diversity for this species in the region. Satellite tracking of the local nesters revealed post-nesting movement to foraging habitats in Vietnam and Hainan Island. International cooperation and consistent dedicated research are of paramount importance to the conservation and recovery of the green turtle assemblages in the region.


Abstract - The difficulties associated with detecting population boundaries have long constrained the conservation and management of highly mobile, wide-ranging marine species, such as killer whales (*Orcinus orca*). In this study, we use data from 26 nuclear microsatellite loci and mitochondrial DNA sequences (988 bp) to test a priori hypotheses about population subdivisions generated from a decade of killer whale surveys across the northern North Pacific. A total of 462 remote skin biopsies were collected from wild killer whales primarily between 2001 and 2010 from the northern Gulf of Alaska to the Sea of Okhotsk, representing both the piscivorous “resident” and the mammal-eating “transient” (or Bigg’s) killer whales. Divergence of the 2 ecotypes was supported by both mtDNA and microsatellites. Geographic patterns of genetic differentiation were supported by significant regions of genetic discontinuity, providing evidence of population structuring within both ecotypes and corroborating direct observations of restricted movements of individual whales. In the Aleutian Islands (Alaska), subpopulations, or groups with significantly different mtDNA and microsatellite allele frequencies, were largely delimited by major oceanographic boundaries for resident killer whales. Although Amchitka Pass represented a major subdivision for transient killer whales between the central and western Aleutian Islands, several smaller subpopulations were evident throughout the eastern Aleutians and Bering Sea. Support for seasonally sympatric transient subpopulations around Unimak Island suggests isolating mechanisms other than geographic distance within this highly mobile top predator.


Abstract - Research has suggested killer whale (Orcinus orca) predation may affect cetacean vocal behavior; however, few data exist to test this hypothesis. Data collected during 40,976 km of visual and acoustic shipboard surveys in the tropical Pacific Ocean, including 1,232 detections of 13 species, were examined to determine if changes in dolphin vocal activity could be attributed to the presence of killer whales. Generalized linear models and Random Forest analyses were used to test the hypothesis that dolphin vocal activity was related to the distance and time to the nearest killer whale sighting. Both results show that dolphin vocalizations were inversely correlated with the temporal proximity of killer whales (P < 0.05). Despite the relative rarity of killer whales in the tropics, they appear to influence vocal behavior of nearby dolphin schools. This disruption in communication may not significantly impact interactions necessary for survival in tropical waters where killer whale density is low. However, in temperate climates, where increased productivity supports a greater abundance of killer whales, this interruption in communication may have a greater impact. The lower incidence of whistling dolphins in temperate waters may be related to the greater abundance of killer whales in these areas.


Abstract - The interactions of numerous abiotic and biotic factors experienced by sea turtle embryos during incubation affect their survival. In this study we determined the hatching and emergence success of green turtles Chelonia mydas from nests on 4 beaches on the Galápagos Islands, one of the most important rookeries for green turtles in the eastern Pacific Ocean. Mean (+SD) hatching and emergence success for the 1039 nests examined were 46.0 ± 33.4 and 45.6 ± 33.4%, respectively. These values are relatively low compared to other green turtle populations worldwide. We evaluated the effects of beach, year, day of oviposition, carapace length and width of female, nest position, nest habitat, and nest chamber depth on hatching and emergence success with binomial generalized additive models with fixed effects. We found variation in hatching and emergence success was significant among beaches, years, day of oviposition, and nest habitat. Predation by feral pigs and beetles and destruction of earlier nests by nesting females were the most important causes of embryo mortality. Efforts to keep threats at minimum levels, particularly controlling pigs near Isabela beaches, should be considered a major conservation objective. This study highlights important differences among beaches within a rookery and emphasizes the need to continue improving management strategies to protect green turtles and their critical habitats. Quantitative information provided here can be used as a basis for long-term studies in the Galápagos and for comparison to other sea turtles rookeries.

Week of 30 September 2013


Week of 16 September 2013

Abstract - Identifying evolutionary divergent taxonomic units, e.g. species and subspecies, is important for conservation and evolutionary biology. The ‘type D’ killer whale, Orcinus Orca, is a rarely observed morphotype with a pelagic, circumpolar subantarctic distribution, making dedicated research and therefore taxonomic study extremely difficult to date. In this study, we used DNA target enrichment hybridisation capture coupled to high throughput sequencing, to obtain the first DNA sequence from the only known museum specimen of this recently described morphotype. The high coverage, complete mitogenome sequence was compared to a previously published global dataset of 139 individuals, indicating that this type is highly divergent to all previously genetically sequenced killer whale forms. The estimated divergence time (390,000 years ago) from its most recent common ancestor with other extant killer whale lineages was the second oldest split within the killer whale phylogeny. This study provides the first genetic support of type D potentially being a distinct subspecies or species of killer whale, although further samples are needed to identify whether there is monophyly of mitogenome sequences and whether nuclear DNA also indicates reproductive isolation. These findings also highlight the value of natural history museum collections and new technologies to investigate the taxonomy of rare, cryptic or difficult to access species.

Week of 9 September 2013


Abstract - Acoustic survey methods can be used to estimate density and abundance using sounds produced by cetaceans and detected using hydrophones if the probability of detection can be estimated. For passive acoustic surveys, probability of detection at zero horizontal distance from a sensor, commonly called g(0), depends on the temporal patterns of vocalizations. Methods to estimate g(0) are developed based on the assumption that a beaked whale will be detected if it is producing regular echolocation clicks directly under or above a hydrophone. Data from acoustic recording tags placed on two species of beaked whales (Cuvier’s beaked whale—Ziphius cavirostris and Blainville’s beaked whale—Mesoplodon densirostris) are used to directly estimate the percentage of time they produce echolocation clicks. A model of vocal behavior for these species as a function of their diving behavior is applied to other types of dive data (from time-depth recorders and time-depth-transmitting satellite tags) to indirectly determine g(0) in other locations for low ambient noise conditions. Estimates of g(0) for a single instant in time are 0.28 (s.d. = 0.05) for Cuvier’s beaked whale and 0.19 (s.d. = 0.01) for Blainville’s beaked whale.


Abstract - Beaked whales are diverse and species rich taxa. They spend the vast majority of their time submerged, regularly diving to depths of hundreds to thousands of meters, typically occur in small groups, and behave inconspicuously at the surface. These factors make them extremely difficult to detect using standard visual survey methods. However, recent advancements in acoustic detection capabilities have made passive acoustic monitoring (PAM) a viable alternative. Beaked whales can be discriminated from other odontocetes by the unique characteristics of their echolocation clicks. In 2009 and 2010, PAM methods using towed hydrophone arrays were tested. These methods proved highly effective for real-time detection of beaked whales in the Southern California Bight (SCB) and were subsequently implemented in 2011 to successfully detect and track beaked whales during the ongoing Southern California Behavioral Response Study. The three year field effort has resulted in (1) the successful classification and tracking of Cuvier’s (Ziphius cavirostris), Baird’s (Berardius bairdii), and unidentified Mesoplodon beaked whale species and (2) the identification of areas of previously unknown beaked whale habitat use. Identification of habitat use areas will contribute to a better understanding of the complex relationship between beaked whale distribution, occurrence, and preferred habitat characteristics on a relatively small spatial scale. These findings will also provide information that can be used to promote more effective management and conservation of beaked whales in the SCB, a heavily used Naval operation and training region.
**Week of 2 September 2013**


*Summary* - This report reviews, integrates and summarizes published literature regarding form, function and pathology in the pantropical spotted dolphin. Because the pantropical spotted dolphin is one of the primary species targeted by the tuna purse-seine fishery in the eastern tropical Pacific Ocean (ETP), the report includes discussion of spotted dolphin morphological and physiological characteristics that may be negatively affected by interaction with the ETP purse-seine fishery.

**Week of 12 August 2013**


*Abstract* - Animals are assumed to obtain/conserve energy effectively to maximise their fitness, which manifests itself in a variety of behavioral strategies. For marine animals, however, these behavioral strategies are generally unknown due to the lack of high-resolution monitoring techniques in marine habitats. As large marine herbivores, immature green turtles do not need to allocate energy to reproduction but are at risk of shark predation, although it is a rare occurrence. They are therefore assumed to select/use feeding and resting sites that maximise their fitness in terms of somatic growth, while avoiding predation. We investigated fine-scale behavioral patterns (feeding, resting and other behaviors), microhabitat use and time spent on each behavior for eight immature green turtles using data loggers including: depth, global positioning system, head acceleration, speed and video sensors. Immature green turtles at Iriomote Island, Japan, spent an average of 4.8 h feeding on seagrass each day, with two peaks, between 5:00 and 9:00, and between 17:00 and 20:00. This feeding pattern appeared to be restricted by gut capacity, and thus maximised energy acquisition. Meanwhile, most of the remaining time was spent resting at locations close to feeding grounds, which allowed turtles to conserve energy spent travelling and reduced the duration of periods exposed to predation. These behavioral patterns and time allocations allow immature green turtles to effectively obtain/conserve energy for growth, thus maximising their fitness.


*Abstract* - Recent studies have validated the use of biopsies as a minimally invasive way to identify pregnant females in several species of wild cetaceans: *Balaenoptera acutorostrata*, *Delphinus delphis*, *Lissodelphis borealis*, and *Lagenorhynchus obliquidens*. These studies found that progesterone (P4) concentrations quantified from blubber attached to biopsy samples is diagnostic of pregnancy. Here we examine a broader group of cetacean species in efforts to investigate how progesterone levels vary between species with respect to pregnancy status. We compared P4 concentrations in blubber collected from fishery bycatch and beach-stranded specimens for 40 females of known reproductive condition from *Delphinus capensis* (*n = 18*), *Stenella attenuata* (*n = 8*), *S. longirostris* (*n = 6*), and *Phocoenoides dalli* (*n = 8*). The P4 concentrations were different (*t = -7.1, p = 1.79E-08*) between pregnant and nonpregnant animals in all species, with the mean blubber P4 concentration for pregnant animals 164 times higher than that of non-pregnant animals. There was no overlap in concentration levels between sexually immature or nonpregnant sexually mature animals and pregnant animals. No significant differences (*F = 0.354, p = 0.559*) were found between mature non-pregnant and immature *D. capensis* and *P. dalli*, suggesting P4 level is not indicative of maturity state in female delphinoids. P4 concentrations in relation to reproductive state were remarkably similar across species. All samples were analyzed with two different enzyme immunoassay kits to gauge assay sensitivity to measure progesterone in small samples, such as biopsies. With the technique now validated for these cetacean species, blubber P4 is a reliable diagnostic of pregnancies across multiple species, and thus expands the utility of this method to study reproduction in free-ranging cetaceans using biopsies.
Week of 5 August 2013

Abstract - We used a combination of seabird data (both fishery-dependent and fishery-independent) and fishing-effort data to evaluate the relative fisheries risk of five west coast groundfish fisheries and one shrimp fishery to black-footed (Phoebastria nigripes), short-tailed (P. albatrus) and Laysan albatrosses(P. immutabilis). To assess risk, an overlap index was derived as the product of total fishing effort and at-sea survey density of black-footed albatross. This index was used as the primary tool to estimate overlap with the endangered, relatively rare short-tailed albatross, which show similar habitat utilization from satellite telemetry tracks. Telemetry data indicate Laysan albatross primarily occur offshore beyond observed fishing effort. Black-footed and short-tailed albatross-fishery overlap was highest at the shelf-break (201–1000 m) north of 36°N. Overlap and reported albatross mortality indicate that the sablefish (Anoplopoma fimbria) longline and Pacific hake (Merluccius productus) catch-processor fisheries pose the greatest risk to these species; the near-shore rockfish (Seabastes spp.) longline, pink shrimp (Pandalus jordani) trawl, California halibut (Paralichthys californicus) trawl, and non-hake groundfish trawl fisheries pose relatively little risk. Implementing proven seabird bycatch-reduction measures will likely minimize albatross mortality in the highest-risk fishery, sablefish longline.

Week of 29 July 2013
Edward D. Weber and Thomas J. Moore. Published Online. Corrected conversion algorithms for the CalCOFI station grid and their implementation in several computer languages. CalCOFI Reports.

Abstract - Converting between geographic coordinates in latitude and longitude and the line and station sampling pattern of the California Cooperative Fisheries Investigations (CalCOFI) program is a commonly required task for conducting research on the California Current ecosystem. This note presents several corrections and clarifications to the previously published algorithms for performing these conversions. We include computer code to implement the algorithms in Java™, Perl, Python, and R. We note that freely available code to conduct the conversions in Fortran, Matlab®, JavaScript™, and Visual Basic® has previously been published, and an online conversion tool is also available. A future version of the PROJ.4 cartographic projections library will also include support for CalCOFI conversions, thereby allowing for convenient conversions using the GRASS GIS, PostGIS, Python, Perl, R, and many other programs and programming languages.

Week of 15 July 2013

Abstract – To test the hypothesis that prey partitioning contributes to community stability in flyingfish, the gut contents of 359 flyingfish specimens (representing five genera and eight species within Exocoetidae and Hemiramphidae) were collected at 50 dip-net stations during hour-long night-time fishing in oceanic waters of the eastern tropical Pacific Ocean between August and November 2007. Analyses using multidimensional scaling, and analysis of similarity revealed significant dietary differences among species, and similarity percentages tests helped identify the specific prey taxa responsible for these differences. Six species specialized on copepods (58 · 3–96 · 9% by number), but targeted different families. Specifically, the barbel flyingfish Exocoetus monocirrhus (n = 205) focused on euchaetids (51 · 6%), the banded flyingfish Hirundichys marginatus (n = 24) fed on pontellids (21 · 8%), while the tropical two-wing flyingfish Exocoetus voltans (n = 11) and the bigwing halfbeak Oxyporhamphus micropterus (n = 34) ingested
calanoids (54 · 6 and 17 · 0%). In contrast, the whitetip flyingfish *Cheilopogon xenopterus* (*n* = 73) and the mirrorwing flyingfish *Hirundichthys speculiger* (*n* = 4) had generalized diets comprising similar proportions of amphipod, copepod, mollusc and larval fish prey. Distinct differences in mean fullness, highly digested material, per cent empty guts and mean numbers of prey per gut were also synthesized, and uncovered a pattern of asynchronous feeding. Altogether, these findings provide valuable descriptive data on the diets of an understudied group of epipelagic teleosts, and, by extension, suggest that prey partitioning (taxa and feeding times) may influence flyingfish feeding ecology by reducing interspecific competition.


*Abstract* - The difficulties associated with detecting population boundaries have long constrained the conservation and management of highly mobile, wide-ranging marine species, such as killer whales (*Orcinus orca*). In this study, we use data from 26 nuclear microsatellite loci and mitochondrial DNA sequences (988 bp) to test a priori hypotheses about population subdivisions generated from a decade of killer whale surveys across the northern North Pacific. A total of 462 remote skin biopsies were collected from wild killer whales primarily between 2001 and 2010 from the northern Gulf of Alaska to the Sea of Okhotsk, representing both the piscivorous “resident” and the mammal-eating “transient” (or Bigg’s) killer whales. Divergence of the 2 ecotypes was supported by both mtDNA and microsatellites. Geographic patterns of genetic differentiation were supported by significant regions of genetic discontinuity, providing evidence of population structuring within both ecotypes and corroborating direct observations of restricted movements of individual whales. In the Aleutian Islands (Alaska), subpopulations, or groups with significantly different mtDNA and microsatellite allele frequencies, were largely delimited by major oceanographic boundaries for resident killer whales. Although Amchitka Pass represented a major subdivision for transient killer whales between the central and western Aleutian Islands, several smaller subpopulations were evident throughout the eastern Aleutians and Bering Sea. Support for seasonally sympatric transient subpopulations around Unimak Island suggests isolating mechanisms other than geographic distance within this highly mobile top predator.


*Abstract* – The Marine Mammal Protection Act (MMPA) requires the National Oceanic and Atmospheric Administration (NOAA), National Marine Fisheries Service (NMFS), to document human-caused mortality, non-serious injury (NSI), and serious injury (SI) of marine mammals as part of assessing marine mammal stocks and to evaluate human-caused injury and mortality levels in the context of potential biological removal (PBR) levels calculated under the MMPA (Wade 1998). NMFS defines SI as “*any injury that will likely result in mortality.*” While recognizing mortality is straightforward, distinguishing NSI from SI requires reliable data on injury severity and animal condition, often in challenging environments where thorough examination of injuries is not possible. NMFS updated its SI designation and reporting process, which uses guidance from previous SI workshops (Angliss and DeMaster 1998, Andersen et al. 2008), expert opinion, and analysis of historic injury cases to develop new criteria for distinguishing SI from NSI (NOAA 2012, Moore et al. 2013).

This report contains records of human-caused injury and mortality to pinnipeds and cetaceans from 2007 to 2011, for marine mammal populations that occur in U.S. west coast waters and which are evaluated in Pacific region marine mammal stock assessment reports (SARs) (Carretta et al. 2013). Mortality records, while included, were obviously not evaluated for SI/NSI status. Subsistence and directed takes are not reported here but are reported in SARs published by NMFS.

Sources of injury data include strandings, disentanglement networks, and fishery observer programs. Stranding network data includes records of injured marine mammals at sea and ashore reported by the public, as well as researchers working in these same areas. Injury sources include, but are not limited to, *vessel*
strikes, gillnet entanglement, pot and trap gear entanglement, shootings, marine debris entanglement, research-related injuries/deaths, hook and line fishery interactions, and power plant water intake entrainment. This report covers the 5-year period of 2007 to 2011, which includes injury and mortality data used in preparation of draft 2013 Pacific marine mammal stock assessments. Most records originate from stranding networks in California, Oregon, and Washington, though a few Alaska records of Eastern North Pacific gray whales (Eschrichtius robustus) are included, because this population is assessed in the Pacific region SARs and occurs along the U.S. west coast. Other marine mammals such as Steller sea lions (Eumetopias jubatus) occur in California, Oregon, and Washington waters, but they are assessed in Alaska region SARs and not included in this report (Allen and Angliss 2013). Injury determinations for Pacific region species/stocks in the central Pacific from Hawaii westward are also included in separate reports.

Week of 8 July 2013


Overview - This report provides a step-by-step guide to constructing a modular oil-filled towed hydrophone array to be used for passive acoustic monitoring of cetaceans from ships. This report was based on a workshop hosted by SWFSC to teach acousticians from the other NMFS science centers how to construct this hardware (funding provided by NOAA’s Advanced Sampling Technologies Working Group).


Abstract - 1. The global range of Risso’s dolphin Grampus griseus is not well known, and there has been confusion in the literature as to whether the species has a broad, circumglobal range or only occurs along continental margins.
2. To clarify the species’ distribution and habitat preferences, we compiled and reviewed all available (published and unpublished) records of sightings and captures of this species for the past 62 years (1950–2012, n = 8068 records). Stranding records were not included.
3. The results showed that the species has a range that extends across ocean basins and spans at least 64°N and 46°S, and is apparently absent from high latitude polar waters. Although Risso’s dolphins occur in all habitats from coastal to oceanic, they show a strong range-wide preference for mid-temperate waters of the continental shelf and slope between 30° and 45° latitude.
4. Although a number of misconceptions about the distributional ecology of Risso’s dolphin have existed, this analysis showed that it is a widespread species. It strongly favours temperate waters and prefers continental shelf and slope waters to oceanic depths. These habitat preferences appear to hold throughout much or all of the species’ range.

Week of 1 July 2013


Abstract - The role of fishes in the global carbon cycle is poorly known and often neglected. We show that the biomass of mesopelagic fishes off the continental USA west to longitude 141°W is positively related to annual net primary productivity, and averages 17 g m⁻². We estimate the export of carbon out of the epipelagic ocean mediated by mesopelagic fishes (“fish-mediated export”; FME) with individual-based metabolic modeling using the catch from 77 mesopelagic trawls distributed over the study area. FME was 15–17% (22–24 mg C m⁻² d⁻¹) of the total carbon exported in the study area (144 mg C m⁻² d⁻¹), as estimated from satellite data. FME varies spatially in both magnitude and relative importance. Although the magnitude of FME increases with increasing total export, the ratio of FME to total export decreases. FME exceeds 40% of the total carbon export in the
oligotrophic North Pacific Subtropical Gyre, but forms <10% of the total export in the most productive waters of the California Current. Because the daytime residence depth of these fishes is below the depths where most remineralization of sinking particles occurs, FME is approximately equal to the passive transport at a depth of 400 m. The active transport of carbon by mesopelagic fishes and zooplankton is similar in magnitude to the gap between estimates of carbon export obtained with sediment traps and by other methods. FME should be considered in models of the global carbon cycle.

**Week of 24 June 2013**


*Abstract -* Identifying evolutionary divergent taxonomic units, e.g. species and subspecies, is important for conservation and evolutionary biology. The ‘type D’ killer whale, *Orcinus Orca*, is a rarely observed morphotype with a pelagic, circumpolar subantarctic distribution, making dedicated research and therefore taxonomic study extremely difficult to date. In this study, we used DNA target enrichment hybridisation capture coupled to high throughput sequencing, to obtain the first DNA sequence from the only known museum specimen of this recently described morphotype. The high coverage, complete mitogenome sequence was compared to a previously published global dataset of 139 individuals, indicating that this type is highly divergent to all previously genetically sequenced killer whale forms. The estimated divergence time (390,000 years ago) from its most recent common ancestor with other extant killer whale lineages was the second oldest split within the killer whale phylogeny. This study provides the first genetic support of type D potentially being a distinct subspecies or species of killer whale, although further samples are needed to identify whether there is monophyly of mitogenome sequences and whether nuclear DNA also indicates reproductive isolation. These findings also highlight the value of natural history museum collections and new technologies to investigate the taxonomy of rare, cryptic or difficult to access species.


*Abstract -* To test feeding selectivity, the diets of three surface-migrating myctophids [*Myctophum nitidulum* (*n*= 299), *Symbolophorus reversus* (*n*= 199), and *Gonichthys tenicusulus* (*n*= 82)] were compared to zooplankton prey collections at 32 stations in the eastern Pacific Ocean, August–November 2006. *Myctophum nitidulum* fed predominately on copepods (42.7 % by number) and ostracods (41.5 %), selected amphipods (*p*= 0.002) and ostracods (*p*= 0.014), and avoided copepods (*p* < 0.001). *Symbolophorus reversus* fed on copepods (32.5 % by number) and euphausiids (29.6 %) and selected euphausiids (*p*= 0.002) and amphipods (*p*= 0.008). *Gonichthys tenicusulus* fed on ostracods (34.6 %) and amphipods (27.3 %), but showed no significant selectivity.

**Week of 17 June 2013**


*Abstract* - Tropical cyclones are environmental disturbances that may have important effects on open-ocean ecosystem structure and function, but their overall impact has rarely been assessed. The Stenella Abundance Research Line Transect and Ecosystem (STARLITE) survey, in August–November 2007, investigated spatial and temporal ecosystem variability in the eastern tropical Pacific Ocean off southwestern Mexico. Oceanographic, plankton, flyingfish, seabird, and cetacean sampling was conducted along eight 170 km transect lines, each of which were surveyed on 2 consecutive days at ~3 wk intervals. Tropical storm Kiko passed though the study area on 15–17 October and forced changes in the physical environment and in the ecosystem, from plankton to top predators. Kiko mixed water from beneath the strong, shallow thermocline
to the surface. As a result, surface temperature decreased by 0.6°C, the thermocline and chlorophyll maximum layer shoaled by 10–20 m, stratification decreased by 27%, and chlorophyll increased by 33% at the surface and 35% over the euphotic zone. These changes persisted for at least 4 wk. Zooplankton biomass increased by 59% about 3 wk after the phyto -plankton increase. Changes in the stomach fullness and diet composition of planktivorous flyingfish were consistent with the increase in zooplankton biomass. Among top predators, the sighting rate of dolphins declined, while the response of seabirds varied by species and was confounded by seasonal migration patterns. Tropical cyclones are a recurrent disturbance in this region. They initiate a bottom-up forcing of the ecosystem, creating persistent patches of higher primary and secondary production, and may be regarded as a disturbance regime.

Available at http://www.int-res.com/articles/feature/m484p001.pdf

**Week of 10 June 2013**


**Abstract** - Echolocation signals from Baird’s beaked whales were recorded during visual and acoustic shipboard surveys of cetaceans in the California Current ecosystem and with autonomous, long-term recorders in the Southern California Bight. The preliminary measurement of the visually validated Baird’s beaked whale echolocation signals from towed array data were used as a basis for identifying Baird’s signals in the autonomous recorder data. Two distinct signal types were found, one being a beaked whale-like frequency modulated (FM) pulse, the other being a dolphin-like broadband click. The median FM inter-pulse interval was 230 ms. Both signal types showed a consistent multi-peak structure in their spectra with peaks at 9, 16, 25, and 40 kHz. Depending on signal type, as well as recording aspect and distance to the hydrophone, these peaks varied in relative amplitude. The description of Baird’s echolocation signals will allow for studies of their distribution and abundance using towed array data without associated visual sightings and from autonomous seafloor hydrophones.


**Abstract** - There is strong evidence that both the western and eastern distinct population segments (DPSs) of Steller sea lion (Eumetopias jubatus) increased in overall abundance in Alaska between 2000 and 2012. Counts of both non-pups (adults and juveniles) and pups during the breeding season in the western DPS were lowest in 2000, and increased at average rates of 1.67% per year (95% credible interval of 1.01-2.38% per year) and 1.45% per year (0.69-2.22% per year), respectively through 2012. However, there was considerable regional variability in non-pup and pup trends in 2000-2012 across the western DPS, with strong evidence of increases in three of the four regions east of Samalga Pass (eastern and western Gulf of Alaska, and eastern Aleutian Islands; ranges of 2.39% per year to 4.51% per year for non-pups and 3.03% per year to 3.97% per year for pups) being offset somewhat by both weak and strong declines in the two regions west of Samalga Pass (central and western Aleutian Islands; slow, uncertain declines in the central [-0.56% per year and -0.46% per year for non-pups and pups, respectively] and steep, certain declines in the western Aleutians [-7.23% per year and -9.36% per year for non-pups and pups, respectively]). Within the central Aleutian Islands, non-pup and pup trends varied east and west of 177°W (roughly Tanaga Pass): in the two rookery cluster areas to the east, trends were generally positive (0.51% per year and 2.25% per year for non-pups, and 2.56% per year and 0.45% per year for pups), while to the west, there was strong evidence of decline (-4.48% per year and -3.24% per year for non-pups, and -4.83% per year and -1.74% per year for pups). In southeast Alaska (eastern DPS of Steller sea lion), both non-pup and pup counts increased between 2000 and 2010, continuing the upward trend begun in the mid-1970s.

Movement of young Steller sea lions into and out of the eastern Gulf of Alaska was observed during surveys conducted ‘early’ and ‘late’ in 2008, 2009 and 2010. Analysis of the movement of sea lions branded as pups in 2000-2011 on rookeries extending from southeast Alaska through the Kodiak archipelago (including work by Jemison et al. in review) suggests a net movement from the central to the eastern Gulf of
Alaska of ~1,600 sea lions during the breeding season, as well as a smaller net movement (of ~180 sea lions) from southeast Alaska to the western DPS. Inter-regional movement of this magnitude within the western DPS could affect regional trend estimation, and therefore it may be inappropriate to treat the eastern and central Gulf of Alaska as ‘closed’ populations; non-pup counts in the combined eastern-central Gulf of Alaska increased at 2.40% per year between 2000 and 2012. Average annual inter-DPS movement represents < 0.5% of the total number of sea lions counted in the western DPS and < 1% of those counted in southeast Alaska, and likely had a negligible impact on overall trend estimates in either area.

If the overall western non-pup count in Alaska continues to increase through 2015, the western DPS appears to be on a trajectory to satisfy the first demographic criterion for down-listing from ‘endangered’ to ‘threatened’ status under the Endangered Species Act (NMFS 2008). The second demographic criterion, however, involves regional population performance, which has varied across the range. The western DPS may satisfy the first part of criterion #2 if non-pup counts in the eastern, central and western Gulf of Alaska, eastern Aleutian Islands, and Russia (overall) continue to increase through 2015. However, persistent declines in the western Aleutian Islands and the western half of the central Aleutian Islands may preclude it from satisfying the second part of criterion #2, and indicate that the western DPS is responding to meso-scale variability in factors affecting recovery.

Week of 3 June 2013


Abstract: A set of nuclear single nucleotide polymorphisms (SNPs) and microsatellite markers was used to detect genetic stock structure among 5 Pacific green turtle Chelonia mydas nesting populations. We sampled populations in the Galapagos Islands, Ecuador (n = 57), Colola, Mexico (n = 75), French Frigate Shoals, Hawaii (n = 141), Yap, Micronesia (n = 73), and Wan-an, Taiwan (n = 57), to represent eastern, central, and western Pacific regions. A combination of 29 single independent SNPs and linked SNPs combined as haplotypes were used for a total of 20 independent markers. In addition, 8 polymorphic microsatellite markers were applied to the same sample set. Both sets of nuclear markers confirmed significant differentiation between all sampled populations in the 3 Pacific regions (p < 0.001). The use of these SNPs and microsatellites resulted in sufficient power to detect small population differences not seen in previous studies using smaller numbers of nuclear markers. Our results suggest that male-mediated gene flow between regional nesting stocks is more limited than previously believed, allowing the potential to delineate stocks more clearly. Finally, we discuss the value of SNP markers as an alternative or complement to other nuclear markers such as microsatellites for the examination of stock structure.

Week of 20 May 2013


Abstract - There are three described subspecies of fin whales (Balaenoptera physalus): B. p. physalus Linnaeus, 1758 in the Northern Hemisphere, B. p. quoyi Fischer, 1829 in the Southern Hemisphere, and a recently described pygmy form, B. p. patachonica Burmeister, 1865. The discrete distribution in the North Pacific and North Atlantic raises the question of whether a single Northern Hemisphere subspecies is valid. We assess phylogenetic patterns using ~16 K base pairs of the complete mitogenome for 154 fin whales from the North Pacific, North Atlantic - including the Mediterranean Sea - and Southern Hemisphere. A Bayesian tree of the resulting 136 haplotypes revealed several well-supported clades representing each ocean basin, with no haplotypes shared among ocean basins. The North Atlantic haplotypes (n = 12) form a sister clade to those from the Southern Hemisphere (n = 42). The estimated time to most recent common ancestor (TMRCA) for this Atlantic/Southern Hemisphere clade and 81 of the 97 samples from the North Pacific was approximately 2 Ma. 14 of the remaining North Pacific samples formed a well-supported clade within the Southern Hemisphere. The TMRCA for this node suggests that at least one female from the Southern Hemisphere immigrated to the North Pacific approximately 0.37 Ma. These results provide strong evidence
that North Pacific and North Atlantic fin whales should not be considered the same subspecies, and suggest the need for revision of the global taxonomy of the species.


Summary Organic stable isotope ratios (i.e. δ²H, expressed as δ²H value in ‰) in animal tissues are related to the δ²H in diet and ingested water. Bone collagen preserves the biochemical δ²H isotopic signal in the δ²H value of collagen’s non-exchangeable hydrogen. Therefore, δ²H preserved in bone collagen has the potential to constrain environmental and trophic conditions, which is of interest to researchers studying both living and fossil vertebrates. Our data examine the relationship of δ²H values of collagen with geographic variation in δ²H of meteoric waters, with local variations in the ecology and trophic level of species, and with the transition from mother’s milk to adult diet. Based on 97 individuals from 22 marine and terrestrial vertebrates (predominately mammals), we found the relationships of collagen δ²H to both geographic variation in meteoric water δ²H (R²=0.55) and to δ¹⁵N in bone collagen (R²=0.17) statistically significant but weaker than previously reported. The second strongest control on collagen δ²H in our data is dietary, with nearly fifty percent of the variance in δ²H explained by trophic level (R²=0.47). Trophic level effects potentially confound the local meteoric signal if not held constant: herbivores tend to have the lowest δ²H values, omnivores have intermediate ones, and carnivores have the highest values. Body size (most likely related to mass-specific metabolic rates) has a strong influence on collagen δ²H (R²=0.30), by causing greater sensitivity in smaller animals to seasonal climate variations and/or high evaporative potential leading to δ³H-enrichment in tissues. In marine mammals weaning produces a dramatic effect on collagen δ²H with adult values being universally higher than pup values (R²=0.79). Interestingly, the shift in δ¹⁵N at weaning is downward, even though normally hydrogen and nitrogen isotope ratios are positively correlated with one another in respect to trophic level. Our findings suggest that in carnivores, which have an especially high variance in δ³H, large samples are needed to separate signals from precipitation, trophic level, body size, and age. For δ²H of fossil collagen to be useful as a proxy of environmental or dietary information, these confounding effects need to be understood, which means careful selection of a study species. Further, δ²H from a single fossil bone collagen is likely to be uninterpretable.

Week of 13 May 2013


Summary - Fisheries bycatch threatens populations of marine megafauna such as marine mammals, turtles, seabirds, sharks and rays, but fisheries impacts on non-target populations are often difficult to assess due to factors such as data limitation, poorly defined management objectives and lack of quantitative bycatch reduction targets. Limit reference points can be used to address these issues and thereby facilitate adoption and implementation of mitigation efforts. Reference points based on catch data and life history analysis can identify sustainability limits for bycatch with respect to defined population goals even when data are quite limited. This can expedite assessments for large numbers of species and enable prioritization of management actions based on mitigation urgency and efficacy. This paper reviews limit reference point estimators for marine megafauna bycatch, with the aim of highlighting their utility in fisheries management and promoting best practices for use. Different estimators share a common basic structure that can be flexibly applied to different contexts depending on species life history and available data types. Information on demographic vital rates and abundance is required; of these, abundance is the most data-dependent and thus most limiting factor for application. There are different approaches for handling management risk stemming from uncertainty in reference point and bycatch estimates. Risk tolerance can be incorporated explicitly into the reference point estimator itself, or probability distributions may be used to describe uncertainties in bycatch and reference point estimates, and risk tolerance may guide how those are factored into the management process. Either approach requires simulation-based performance testing such as management strategy evaluation to ensure that management objectives can be achieved. Factoring potential sources of bias into
such evaluations is critical. This paper reviews the technical, operational, and political challenges to widespread application of reference points for management of marine megafauna bycatch, while emphasizing the importance of developing assessment frameworks that can facilitate sustainable fishing practices.


Abstract - Lack of guidance for interpreting the definitions of endangered and threatened in the U.S. Endangered Species Act (ESA) has resulted in case-by-case decision making leaving the process vulnerable to being considered arbitrary or capricious. Adopting quantitative decision rules would remedy this but requires the agency to specify the relative urgency concerning extinction events over time, cutoff risk values corresponding to different levels of protection, and the importance given to different types of listing errors. We tested the performance of 3 sets of decision rules that use alternative functions for weighting the relative urgency of future extinction events: a threshold rule set, which uses a decision rule of x% probability of extinction over y years; a concave rule set, where the relative importance of future extinction events declines exponentially over time; and a shoulder rule set that uses a sigmoid shape function, where relative importance declines slowly at first and then more rapidly. We obtained decision cutoffs by interviewing several biologists and then emulated the listing process with simulations that covered a range of extinction risks typical of ESA listing decisions. We evaluated performance of the decision rules under different data quantities and qualities on the basis of the relative importance of misclassification errors. Although there was little difference between the performance of alternative decision rules for correct listings, the distribution of misclassifications differed depending on the function used. Misclassifications for the threshold and concave listing criteria resulted in more overprotection errors, particularly as uncertainty increased, whereas errors for the shoulder listing criteria were more symmetrical. We developed and tested the framework for quantitative decision rules for listing species under the U.S. ESA. If policy values can be agreed on, use of this framework would improve the implementation of the ESA by increasing transparency and consistency.


Summary - Two popular tissue preservatives, 100% ethanol and 20% salt saturated dimethyl sulfoxide (DMSO) solution were tested for the existence of amplifiable, free-floating DNA after 2 to 18 yrs of tissue storage. We found that short mtDNA fragments were consistently amplified and sequenced from DMSO preservative, while nDNA amplification was limited and inconsistent. Amplification of both mtDNA and nDNA failed most of the time for the ethanol samples.

Week of 6 May 2013

(No Abstract)


Abstract - On 9 June 2008, the UK's largest mass stranding event (MSE) of short-beaked common dolphins (Delphinus delphis) occurred in Falmouth Bay, Cornwall. At least 26 dolphins died, and a similar number was refloated/herded back to sea. On necropsy, all dolphins were in good nutritive status with empty stomachs and no evidence of known infectious disease or acute physical injury. Auditory tissues were grossly normal (26/26) but had microscopic haemorrhages (5/5) and mild otitis media (1/5) in the freshest
cases. Five lactating adult dolphins, one immature male, and one immature female tested were free of harmful algal toxins and had low chemical pollutant levels. Pathological evidence of mud/seawater inhalation (11/26), local tide cycle, and the relative lack of renal myoglobinuria (26/26) suggested MSE onset on a rising tide between 06:30 and 08:21 hrs (9 June). Potential causes excluded or considered highly unlikely included infectious disease, gas/fat embolism, boat strike, by-catch, predator attack, foraging unusually close to shore, chemical or algal toxin exposure, abnormal weather/climatic conditions, and high-intensity acoustic inputs from seismic airgun arrays or natural sources (e.g., earthquakes). International naval exercises did occur in close proximity to the MSE with the most intense part of the exercises (including mid-frequency sonars) occurring four days before the MSE and resuming with helicopter exercises on the morning of the MSE. The MSE may therefore have been a “two-stage process” where a group of normally pelagic dolphins entered Falmouth Bay and, after 3–4 days in/around the Bay, a second acoustic/disturbance event occurred causing them to strand en masse. This spatial and temporal association with the MSE, previous associations between naval activities and cetacean MSEs, and an absence of other identifiable factors known to cause cetacean MSEs, indicates naval activity to be the most probable cause of the Falmouth Bay MSE.

*Week of 30 April 2013*


*Abstract -* Currently, the acoustic detection of beaked whales during passive acoustic surveys requires trained acousticians to identify beaked whale signals with the aid of various software programs. The development of reliable automated detection and classification methods will enable passive acoustic approaches to better meet monitoring needs for real-time mitigation of industry and military impacts. During ongoing development of automated beaked whale detectors and classifiers it will be important for researchers at different institutions to utilize standardized metrics of performance. At the Southwest Fisheries Science Center (SWFSC), automated detection algorithms for Cuvier’s beaked whale (*Ziphius cavirostris*) and Baird’s beaked whale (*Berardius bairdii*) were developed using PAMGUARD software (Douglas Gillespie: www.pamguard.org). To evaluate the performance of these beaked whale detectors, 15 ten-minute recording segments were processed in PAMGUARD, and the resulting signal detections were compared to manual logs of beaked whale signals confirmed by an experienced acoustician. The comparison was conducted using three methods: precise timestamp matching between manual and automated detections, detection counts from one-minute time bins, and binary presence/absence detection classification of one-minute bins. The detections were scored as true positive, false positive, false negative or false classification. Detector efficacy was quantified using measures developed for information retrieval systems (precision, recall, and F-score) as well as the Receiver Operating Characteristic. Calculated performance scores were compared across evaluation methods. We found that the method used to evaluate detector functionality greatly influences the resulting performance scores and subsequently our perception of detector ability. Therefore, it will be important for researchers to clearly communicate methods and results of detector evaluation. To allow for greatest precision and applicability to different recording datasets, we recommend that beaked whale detectors be evaluated using timestamp matching between manual and automated detections in trial datasets and that F-scores be used to compare detectors. This approach avoids problems associated with binning datasets by eliminating the need for a measure of false negatives.


*Abstract -* Maritime forest communities on barrier islands along the Atlantic and Gulf coasts have been severely fragmented by a continuous history of human land use and natural disturbance. Isolated populations of certain tree species in maritime forest fragments may now be too small to be viable and their inability to regenerate may result in their eventual elimination from barrier islands. Using an 11-year study of a population of pignut hickory (*Carya glabra*), a common species of remnant maritime forest stands on St.
Catherine’s Island, Georgia, we present a case study of tree regeneration failure on a barrier island. We found that there has been no recruitment of new hickory individuals into the canopy of this population over the last 65 years. Field evidence of browse and a strong correlation between seedling density distributions and microsite protection from herbivory suggest that this trend in recruitment failure is related to an increased abundance of deer (Odocoileus) and pigs (Sus) on the island. Using a size class population projection model, we estimated that, if such recruitment failure and mortality rates continue, the hickory population will be extirpated from the maritime forest within 200 years. Tree species that are failing to regenerate within maritime forests represent a special challenge that is not currently being addressed in the long-term management of barrier island biodiversity.

**Week of 16 April 2013**


*Abstract* - Visual line-transect surveys are commonly used to estimate the abundance of cetaceans (whales, dolphins, and porpoises). A key parameter in this method is the probability of detecting a cetacean that is directly on the transect line or g(0). Beaked whales and dwarf & pygmy sperm whales are visually inconspicuous and dive for long periods of time. Previous studies have shown that trackline detection probability is low for these species even in the best survey conditions. Trackline detection probability has never been estimated for them in poor survey conditions. A method is developed here to estimate the relative values of trackline detection probability by comparing estimates of apparent density in different survey conditions (measured as Beaufort state) using estimated density in the best survey conditions as a reference point. Using data from line-transect surveys in the eastern tropical Pacific, this approach yields consistent estimates of trackline detection probability for beaked whales and for dwarf & pygmy sperm whales as functions of sighting conditions in two adjacent study areas. Results show that g(0) for beaked whales is similar for Beaufort 0 and 1 conditions but decreases with increasing Beaufort to less than 10% of that value in Beaufort 5. For dwarf & pygmy sperm whales g(0) decreases even faster with Beaufort state and, in Beaufort 2, is less than 10% of its value in Beaufort 0. These relative values of g(0) are used to extrapolate published estimates of g(0) for calm seas to yield values for Beaufort states 0 to 5.

**Week of 8 April 2013**


*Abstract* - We investigated the species identity and local use of cetaceans on the Gilbert Islands, Republic of Kiribati. Working with the Kiribati Ministry of Environment, Lands and Agricultural Development and Fisheries Division, we visited the islands of Tarawa, Tabiteua (North), Butaritari and Onotoa from June to July 2009, and collected 24 bones, bone fragments or teeth attributed to recent strandings. The mitochondrial DNA control region or cytochrome b was successfully amplified from 12 bones or bone fragments and used to identify four species: *Mesoplodon* sp. representing a new species or subspecies of beaked whale, the dense-beaked whale *Mesoplodon densirostris*, Cuvier’s beaked whale *Ziphius cavirostris* and the pygmy sperm whale *Kogia breviceps*. This is the first confirmed identification of the dense-beaked, Cuvier’s and pygmy sperm whales from the Gilbert Islands. All specimens were reportedly used for human consumption.


*Summary* - Since Archie Carr’s seminal work in the 1960s and 1970s and efforts by Karen Bjorndal and others in the 1980s and 1990s, feeding biology has been a relatively well-studied facet of sea turtle biology. This is opportune for the science of sea turtles considering that nutrient acquisition strategies are among the most important components of a sea turtle’s life history, influencing key demographic parameters such as
somatic growth, age-at-maturity, and timing of reproductive migrations. Over the past two decades, however, the advent of new research fields such as physiological monitoring, biologging, and stable isotope analysis (SIA) have helped strengthen this understanding even further. These tools have provided insights that have in some cases confirmed earlier wisdom about how a sea turtle makes a living, and in other cases have redefined long-standing biological paradigms. Considering the new information that has come available, it is clear that the ecological strategies of some species are much more diverse than originally considered. For example, green turtles (*Chelonia mydas*), long-considered obligate neritic herbivores instead eat large amounts of animal matter in many places, and at least in the Pacific are commonly high-seas dwellers, even as adults. Hawksbill turtles (*Eretmochelys imbricata*), the “coral reef dwelling” turtle, are turning up in the strangest of places. In the eastern Pacific, for example, adult hawksbills inhabit mangrove estuaries during non-breeding periods, a huge departure from our belief that the species was tied to coral reefs. In the Caribbean and Indian Ocean, hawksbills are now known to depend on seagrass pastures for foraging and residence. Leatherbacks (*Dermochelys coriacea*), historically defined as “high-seas inhabitants,” are now seen in coastal habitats more than ever before. These and other novel revelations about feeding biology are at least partly due to the globalization of sea turtle research and an everexpanding toolbox at the disposal of field and laboratory scientists. Indeed, more research with both traditional and novel tools is conducted in more parts of the world than ever before, and we are now gaining an appreciation of just how complex and adaptive sea turtles can be. Much new biological information has emerged in the published literature since The Biology of the Sea Turtles (Volume 1) was first published and a thorough update is warranted, particularly for aspects relating to feeding biology. In this chapter we present new information for all seven sea turtle species, building on Karen Bjorndal’s chapter on Feeding Biology in Volume 1 that summarized what was known at that time. In Section 9.2 we present the latest information about sea turtle diet and feeding biology. Here we describe new diet items and novel foraging tactics that are reshaping our perceptions about the types of prey consumed and methods by which sea turtles access food resources. In Section 9.3 we focus on the feeding physiology of sea turtles (e.g., specific dynamic action (SDA), digestive efficiency, and passage rates of digesta), a still-understudied area of sea turtle feeding biology, but one that is expanding thanks to additional field and lab-based scientific research. Understanding how sea turtle energy acquisition is constrained by physiological and environmental factors is important as these data factor into growth rates, residency times, population demographics, bioenergetics and energy budgets, and reproductive output. In Sections 9.4 (stable isotopes) and 9.5 (fatty acids and trace elements) we explore the “molecular-based” techniques that are showing great promise for estab- ling diet, trophic status, and foraging movements of sea turtles. Clearly, the advent of these approaches allows us to learn much about the types of foods consumed by turtles based on the analysis of their own body tissues. As described earlier, the feeding biology of sea turtles is a broad topic with many nuisances. Together the established (e.g., stomach content analysis, esophageal lavage) and emerging (e.g., SIA, fatty acids) techniques give greater insight and understanding into the unique foraging strategies of sea turtles both intra- and interspecifically and through life-history stages. Studies of feeding physiology then begin to tie together what, when, and where sea turtles eat with why and how they eat to meet daily and yearly energy demands of maintenance, growth, and reproduction. In the end, our goal is to provide an update on the current knowledge of sea turtle feeding biology and share a perspective of how our understanding has evolved in the past decades.


**Abstract** - Protection of endangered species requires an understanding of their spatial ecology in relation to human activities. Recent improvements in monitoring technologies, such as automated acoustic telemetry, have enabled the collection of these data for mobile marine organisms such as sea turtles. The east Pacific green sea turtle *Chelonia mydas* uses San Diego Bay, CA, a heavily developed ecosystem, as a year-round foraging ground. We used a combination of manual and automated acoustic telemetry from 2009 to 2011 to elucidate the distribution of green turtles throughout South San Diego Bay and to understand their diel behavior. Tracked turtles (n = 20) ranged in size from 54.9 to 102.5 cm straight carapace length and had fidelity to two sites: the warm-water effluent channel of a waterfront power plant and an eelgrass meadow. Turtles tracked manually during the night were more sedentary (mean swimming speed ± SE: 0.38 ± 0.03 km
h−1) and generally restricted their activity to waters near the power plant. During the day, turtles swam at higher speeds (0.67 ± 0.07 km h−1) and were mainly found in eelgrass meadows where they are known to forage. Turtles were occasionally found near a shipping terminal, which occurred almost exclusively during the daytime. Turtles in areas of increased boat traffic are at risk of vessel strikes, and future monitoring should investigate the potential for turtle–human interactions in other heavily-used areas of San Diego Bay. Future monitoring should also characterize how turtle behavior may change following the decommissioning of the power plant, which occurred six months before the end of this study.

*Week of 1 April 2013*


*Abstract* - We use data from six ship-based cetacean and ecosystem assessment surveys in the California Current Ecosystem (CCE) to update habitat-based density models for 11 species and one small-beaked-whale guild. We previously had modeled cetacean density as a function of oceanic variables for the same 12 species/guild using data collected during four line-transect ship surveys conducted in the CCE in summer and fall of 1991, 1993, 1996, and 2001. An independent set of survey data collected in the summer and fall of 2005 was used to validate the models. These estimates were incorporated into a web-based system that allows users to estimate cetacean density within any user-defined region within the CCE study area. In this study, data from an additional line-transect survey conducted in 2008 were pooled with the 1991-2005 data and used to re-build the habitat-based density models. We also refit the 1991-2008 data to the previous “best” models to compare model performance. The additional year of data provided increased sample sizes and a greater range of oceanic conditions for robust model development. Predicted densities for each year were smoothed and then averaged to produce a composite grid that represents our best estimate of CCE cetacean density over the past 20 years. The final model predictions were used to update the web-based system and also provided to the U.S. Navy to help assess potential impacts from their at-sea training and testing activities.


Available at [http://swfsc.noaa.gov/prd-sars/](http://swfsc.noaa.gov/prd-sars/)


*Abstract* - Within the Hawaiian archipelago, green turtle nesting has occurred almost exclusively in the northwestern Hawaiian Islands, mainly at French Frigate Shoals (FFS), however an increase in occasional nesting has recently been observed on the main Hawaiian Islands (MHI). Due to logistical constraints, monitoring the nesting activity on the MHI has been limited to nest documentation. Without systematic tagging of the nesting females it is not clear how many are nesting here. We used mitochondrial (mt) DNA sequencing combined with nuclear (n) DNA analysis based on 14 microsatellite markers to infer the number of individual nesters. Genotypes were determined for 181 dead embryos and hatchlings salvaged from 71 nests laid on Maui, Molokai, Kauai, Lanai, and Oahu, along with those of 81 nesting females that were sampled on FFS. MtDNA results showed that 58% of the MHI clutches were laid by females with a relatively rare haplotype only reported in 16% of the FFS nesting population. Nuclear DNA results showed that nesting in the MHI might be attributed to a relatively small number of females that appear to be related to each other. We were able to reconstruct genotypes for nesting females from hatchling profiles and we estimate that 15 different females were responsible for clutches laid on the MHI. Taken together, the mtDNA and nDNA results suggest that the nesting population at the MHI may be the result of a few founders that
originated from the FFS breeding population, possibly facilitated by captive rearing and release of FFS juveniles locally from Oahu. We suggest that this regional range expansion may buffer against the loss of current nesting sites at FFS due to sea level rise. Our results demonstrate the potential for genetic tools to be incorporated into population assessment, particularly in areas where access to reproductive females is difficult and population size is unknown.

Abstract - Coincident with climate shifts and anthropogenic perturbations, the highly voracious jumbo squid Dosidicus gigas reached unprecedented northern latitudes along the NE Pacific margin post 1997–98. The physical or biological drivers of this expansion, as well as its ecological consequences remain unknown. Here, novel analysis from both bulk tissues and individual amino acids (Phenylalanine; Phe and Glutamic acid; Glu) in both gladius and muscle of D. gigas captured in the Northern California Current System (NCCS) documents for the first time multiple geographic origins and migration. Phe δ15N values, a proxy for habitat baseline δ15N values, confirm at least three different geographic origins that were initially detected by highly variable bulk δ15N values in gladius for squid at small sizes (<30 cm gladius length). In contrast, bulk δ15N values from gladius of large squid (>60 cm) converged, indicating feeding in a common ecosystem. The strong latitudinal gradient in Phe δ15N values from composite muscle samples further confirmed residency at a point in time for large squid in the NCCS. These results contrast with previous ideas, and indicate that small squid are highly migratory, move into the NCCS from two or more distinct geographic origins, and use this ecosystem mainly for feeding. These results represent the first direct information on the origins, immigration and habitat use of this key “invasive” predator in the NCCS, with wide implications for understanding both the mechanisms of periodic D. gigas population range expansions, and effects on ecosystem trophic structure.

Summary - A single population stock of gray whales (Eschrichtius robustus), referred to as the eastern North Pacific (ENP) stock, is presently recognized in U.S. waters. New information, however, suggests the possibility of recognizing two additional stocks of gray whales in U.S. waters: the Pacific Coast Feeding Group (PCFG) and the western North Pacific (WNP) stock. To evaluate the currently recognized and potentially emerging characterization of gray whale stock structure, NMFS established a scientific Task Force (TF). The overarching objective of this TF was to provide an objective scientific evaluation of gray whale stock structure as defined under the MMPA and implemented through the NMFS Guidelines for Assessing Marine Mammal Stocks (GAMMS; NMFS 2005). More specifically, the TF was convened to provide advice on the primary question – “Is the PCFG a “population stock” under the MMPA and GAMMS guidelines”? In addition, the TF was asked to provide advice on a question of developing importance – “Is the WNP stock a “population stock” under the MMPA and GAMMS guidelines”?

Week of 25 March 2013

Abstract - Marine spatial planning provides a comprehensive framework for managing multiple uses of the marine environment and has the potential to minimize environmental impacts and reduce conflicts among users. Spatially explicit assessments of the risks to key marine species from human activities are a requirement of marine spatial planning. We assessed the risk of ships striking humpback (Megaptera novaeangliae), blue (Balaenoptera musculus), and fin (Balaenoptera physalus) whales in alternative shipping routes derived from patterns of shipping traffic off Southern California (U.S.A.). Specifically, we developed whale-habitat models and assumed ship-strike risk for the alternative shipping routes was proportional to the number of whales predicted by the models to occur within each route. This definition of risk assumes all ships travel within a single route. We also calculated risk assuming ships travel via multiple routes. We estimated the potential for conflict between shipping and other uses (military training and fishing) due to
overlap with the routes. We also estimated the overlap between shipping routes and protected areas. The route with the lowest risk for humpback whales had the highest risk for fin whales and vice versa. Risk to both species may be ameliorated by creating a new route south of the northern Channel Islands and spreading traffic between this new route and the existing route in the Santa Barbara Channel. Creating a longer route may reduce the overlap between shipping and other uses by concentrating shipping traffic. Blue whales are distributed more evenly across our study area than humpback and fin whales; thus, risk could not be ameliorated by concentrating shipping traffic in any of the routes we considered. Reducing ship-strike risk for blue whales may be necessary because our estimate of the potential number of strikes suggests that they are likely to exceed allowable levels of anthropogenic impacts established under U.S. laws.


**Week of 11 March 2013**


**Summary**

1. Investigating migratory connectivity between breeding and foraging areas is critical to effective management and conservation of highly mobile marine taxa, particularly threatened, endangered, or economically important species that cross through regional, national and international boundaries.
2. The leatherback turtle (*Dermochelys coriacea*, Vandelli 1761) is one such transboundary species that spends time at breeding areas at low latitudes in the northwest Atlantic during spring and summer. From there, they migrate widely throughout the North Atlantic, but many show fidelity to one region off eastern Canada, where critical foraging habitat has been proposed. Our goal was to identify nesting beach origins for turtles foraging here.
3. Using genetics, we identified natal beaches for 288 turtles that were live-captured off the coast of Nova Scotia, Canada. Turtles were sampled (skin or blood) and genotyped using 17 polymorphic microsatellite markers. Results from three assignment testing programs (ONCOR, GeneClass2 and Structure) were compared. Our nesting population reference data set included 1417 individuals from nine Atlantic nesting assemblages. A supplementary data set for 83 foraging turtles traced to nesting beaches using flipper tags and/or PIT tags (n = 72), or inferred from satellite telemetry (n = 11), enabled ground-truthing of the assignments.
4. We first assigned turtles using only genetic information and then used the supplementary recapture information to verify assignments. ONCOR performed best, assigning 64 of the 83 recaptured turtles to natal beaches (77.1%). Turtles assigned to Trinidad (164), French Guiana (72), Costa Rica (44), St. Croix (7), and Florida (1) reflect the relative size of those nesting populations, although none of the turtles were assigned to four other potential source nesting assemblages.
5. Our results demonstrate the utility of genetic approaches for determining source populations of foraging marine animals and include the first identification of natal rookeries of male leatherbacks, identified through satellite telemetry and verified with genetics. This work highlights the importance of long-term monitoring and tagging programmes in nesting and highuse foraging areas. Moreover, it provides a scientific basis for evaluating stock-specific effects of fisheries on migratory marine species, thus identifying where coordinated international recovery efforts may be most effective.

**Week of 3 March 2013**

Kathleen E. Hunt, Michael J. Moore, Rosalind M. Rolland, Nicholas M. Kellar, Ailsa J. Hall, Joanna Kershaw, Stephen A. Raverty, Cristina E. Davis, Laura C. Yeates, Teresa K. Rowles, and Scott D. Kraus. *In Review*. Opening
the biggest black box: New approaches to the study of conservation physiology of large whales. Conservation Physiology.

Abstract- Large whales are subjected to a variety of conservation pressures that could be better monitored and managed if physiological information could be gathered readily from free-swimming whales. However, traditional approaches to studying physiology have been impractical for large whales, since there is no routine method for capture of the largest species and there is presently no practical method of obtaining blood samples from free-swimming whales. We review novel techniques for gathering physiological information on large whales using a variety of nonlethal and minimally invasive (or noninvasive) sample matrices. We focus on methods that should produce information relevant to conservation physiology, e.g. measures relevant to stress physiology, reproductive status, nutritional status, immune response, health, and disease. Four types of samples are discussed: fecal samples, respiratory samples ("blow"), skin/blubber samples, and photographic imaging. Fecal samples have historically been used for diet analysis but increasingly are also used for hormonal analyses, as well as for assessment of exposure to toxins, pollutants, and parasites. Blow samples contain many hormones as well as respiratory microbes, metabolites, and a variety of immune-related measures. Biopsy dart samples are widely used for genetic and contaminant analyses and are now being used for endocrine studies along with proteomic and transcriptomic approaches. Photographic analyses have benefited from recently developed quantitative techniques allowing assessment of skin condition, ectoparasite load, and nutritional status, along with wounds and scars from ship strike and fishing gear entanglement. Field application of these novel techniques has the potential to greatly improve our understanding of the physiology of large whales, better enabling assessment of the relative impacts of many anthropogenic and ecological pressures.

Week of 25 February 2013


Abstract - This study presents a comprehensive genetic analysis of stock structure for leatherback turtles (Dermochelys coriacea), combining 17 microsatellite loci and 763 bp of the mtDNA control region. Recently discovered eastern Atlantic nesting populations of this critically endangered species were absent in a previous survey that found little ocean-wide mtDNA variation. We added rookeries in West Africa and Brazil and generated longer sequences for previously analyzed samples. A total of 1,417 individuals were sampled from 9 nesting sites in the Atlantic and SW Indian Ocean. We detected additional mtDNA variation with the longer sequences, identifying ten polymorphic sites that resolved a total of ten haplotypes, including three new variants of haplotypes previously described by shorter sequences. Population differentiation was substantial between all but two adjacent rookery pairs, and FST values ranged from 0.034 to 0.676 and 0.004 to 0.205 for mtDNA and microsatellite data respectively, suggesting that male-mediated gene flow is not as widespread as previously assumed. We detected weak (FST = 0.008 and 0.006) but significant differentiation with microsatellites between the two population pairs that were indistinguishable with mtDNA data. POWSIM analysis showed that our mtDNA marker had very low statistical power to detect weak structure (FST < 0.005), while our microsatellite marker array had high power. We conclude that the weak differentiation detected with microsatellites reflects a fine scale level of demographic independence that warrants recognition, and that all 9 of the nesting colonies should be considered as Demographically Independent Populations (DIPs) for conservation. Our findings illustrate the importance of evaluating the power of specific genetic markers to detect structure in order to correctly identify the appropriate population units to conserve.


Abstract - Strandings of marine megafauna can provide valuable information on cause of death at sea. However, as stranding probabilities are usually very low and highly variable in space and time, interpreting the results can be challenging. We evaluated the magnitude and distribution of at-sea mortality of marine turtles along the Pacific coast of Baja California Sur, Mexico during 2010–11, using a combination of
counting stranded animals and drifter experiments. A total of 594 carcasses were found during the study period, with loggerhead (62%) and green turtles (31%) being the most common species. 87% of the strandings occurred in the southern Gulf of Ulloa, a known hotspot of loggerhead distribution in the Eastern Pacific. While only 1.8% of the deaths could be definitively attributed to bycatch (net marks, hooks), seasonal variation in stranding frequencies closely corresponded to the main fishing seasons. Estimated stranding probabilities from drifter experiments varied among sites and trials (0.05–0.8), implying that only a fraction of dead sea turtles can be observed at beaches. Total mortality estimates for 15-day periods around the floater trials were highest for PSL, a beach in the southern Gulf of Ulloa, ranging between 11 sea turtles in October 2011 to 107 in August 2010. Loggerhead turtles were the most numerous, followed by green and olive ridley turtles. Our study showed that drifter trials combined with beach monitoring can provide estimates for death at sea to measure the impact of small-scale fisheries that are notoriously difficult to monitor for by-catch. We also provided recommendations to improve the precision of the mortality estimates for future studies and highlight the importance of estimating impacts of small–scale fisheries on marine megafauna.

**Week of 18 February 2013**


*Abstract* - Adjustments in body composition over the annual cycle have been documented in many organs and muscle groups. Here we consider the nature and significance of intra-organ variation in the eared grebe *Podiceps nigricollis* stomach, a large and variable organ that can weigh 30 g when birds are staging, drop to 8–11 g before setting off, or to as little as 6.6 g after a several-day migration. Weight reduction in association with migration is conventionally regarded as an adaptation to reduce wing loading and flight costs. This interpretation applies to the premigratory reduction of the entire stomach. However, it does not fit the differential in-flight reduction of the proventriculus, because grebes require a large proventriculus to initiate digestion, and its smaller size when they need to rebuild the entire stomach and resume feeding quickly is opposite that expected in a functional context. We view the reduction of the proventriculus as a non-adaptive response, or spandrel, stemming from its intrinsically higher turnover rate. Starving birds, like migrants, also need to digest food quickly. In their case, the proventriculus is maintained as body weight declines and the gizzard is sacrificed. Mechanisms by which individual organisms achieve different responses to similar challenges, including starvation, merit further investigation.

**Week of 11 February 2013**


*Abstract* - Habitat-based density models were developed for cetaceans in the Central North Pacific based on cetacean survey data collected by the Southwest Fisheries Science Center in 1997-2006. Cetacean sighting data were collected on systematic line-transect surveys in the temperate eastern Pacific, around Hawaii and other Pacific Islands, and in the eastern tropical Pacific west of 120 degrees longitude. Habitat variables, derived from satellite data, included sea surface temperature, sea surface chlorophyll, sea surface height root-mean-square, primary productivity, distance to land, latitude, and longitude. Models were developed for the pantropical spotted dolphin, spinner dolphin, striped dolphin, rough-toothed dolphin, common bottlenose dolphin, false killer whale, short-finned pilot whale, sperm whale, Bryde’s whale, and an “other dolphins”
group that included the short-beaked common and Pacific white-sided dolphin. Uniform densities were estimated for species/guilds that had insufficient sightings for modeling, including pygmy killer whale, Risso’s dolphin, killer whale, a small beaked whale guild (including Cuvier’s beaked whale and beaked whales of the genus *Mesoplodon*), and pygmy/dwarf sperm whale. Although validation using an independent survey was not possible, modeled density estimates for the 10 species/species group were compared to previously published line-transect density estimates derived within the U.S. Exclusive Economic Zone around Hawaii. The model-based estimates of abundance fall within the 95% confidence limits of the standard line-transect analyses, and they provide greater spatial resolution of the density estimates based on habitat associations. These new models are intended as baseline density estimates for Navy planning and environmental impact statements, to be updated and improved as additional survey data become available in the future.


*Executive Summary* - Recent observations of gray whales (*Eschrichtius robustus*) identified in the western North Pacific (WNP) migrating to areas off the coast of North America (Alaska to Mexico) raise concern about the possibility of the small western population being subjected to the gray whale hunt proposed by the Makah Indian Tribe in northern Washington, USA. To address this concern, we estimated the probability of striking (i.e. killing or seriously injuring) a WNP whale during the Makah hunt using six models from 4 model sets that varied based on the assumptions and types of data used for estimation. Model set 1 used WNP and ENP abundance estimates. Model set 2 used these abundance estimates, as well as sightings data from the proposed hunt area. Model sets 3 and 4 used only the sightings data. Within model sets 1 and 2, two models (A and B) differed based upon whether migrating ENP and WNP whales were assumed to be equally available to the hunt per capita (A) or whether this assumption is relaxed (B). We consider Model 2B the most plausible of all models because model set 2 makes use of all available information and 2B contains fewer assumptions than 2A. Based on model 2B, the probability of striking ≥1 WNP whale in a single season ranges from 0.007 to 0.036, depending on if the median or upper 95th percentile estimate is used and on which maximum is used for the total number of whales struck. The probability of striking ≥1 WNP whale out of 5 seasons ranges from 0.036 to 0.170 across the same scenarios. The expected number to be struck in a single year ranges from 0.01 to 0.04 and from 0.04 to 0.19 across 5 years. For context, these strike estimates were compared to different possible values of Potential Biological Removal (PBR). We also summarized analogous estimates for the number of WNP whales that would be “taken” non-lethally, in terms of the number of attempted but unsuccessful strikes as well as the number of animals approached and pursued during the hunt.

*Week of 4 February 2013*


*Abstract* - Because of the precarious condition of small cetacean species and subpopulations listed as Endangered or Critically Endangered by the IUCN, use of captive breeding for conservation has been suggested for some of them, and will likely be suggested for others. A successful captive breeding program for a new species cannot be implemented until reliable capture and husbandry techniques have been developed. Techniques for assisted reproduction and reintroduction may also be needed. We review attempts to capture, maintain, and breed poorly known small cetaceans and discuss assisted reproductive technologies (ART) that have been used to enhance captive breeding efforts for other small cetaceans. We conclude that the techniques required for successful captive breeding of most Endangered or Critically Endangered small cetacean species have not been sufficiently developed. Development of these techniques should begin before a species or population is Critically Endangered. In particular, ARTs tend to be species specific, necessitating considerable time, money, and research to develop for each species of concern. Critically Endangered populations cannot afford to lose the individuals needed for technique development. The fairly large captive
population sizes necessary (to avoid loss of genetic diversity, inbreeding, and genetic adaptation to captivity), limited space available in aquariums, and high costs of captive breeding and reintroduction programs make it unlikely that captive breeding will play a major role in the conservation of most small cetaceans. The substantive conservation measures needed to prevent extinction of Critically Endangered small cetaceans is reduction or elimination of their primary threats, which are usually by-catch and habitat loss.


*Abstract* - Climatic variability of the pycnocline in the eastern tropical and North Pacific has oceanographic and ecological implications. Gridded monthly profiles of temperature and salinity from the Simple Ocean Data Assimilation (SODA) reanalysis, 1958–2008, were used to derive estimates of four variables related to the density structure of the upper-ocean water column: surface temperature, pycnocline depth, mixed layer depth, and stratification (potential energy anomaly). The pycnocline is primarily a thermal gradient in this region, except in subarctic waters at the northern extreme of the study area, where salinity becomes more important than temperature in determining stratification. Spatial patterns of mean and standard deviation of the four pycnocline variables are presented. Partitioning of variance between seasonal and interannual scales shows the predominance of interannual variability in the tropics and seasonal variability at higher latitudes. Low-frequency variations (trends) in the pycnocline variables were derived by state-space analysis of time series averaged in 5° squares. Regionally coherent trends were either monotonic over 50 years or had decadal-scale changes in sign (+5–10 m depth, ±5%–10% of stratification). For example, in the eastern equatorial Pacific, the pycnocline shoaled by 10 m and weakened by 5% over the 50 years, while in the California Current the pycnocline deepened by ~5 m but showed little net change in stratification, which weakened by 5% to the mid-1970s, strengthened by 8% to the mid-1990s, and then weakened by 4% to 2008. These observed changes in the pycnocline, and future changes resulting from global climate change, may have important biological and ecosystem effects.


*Abstract* - Next-generation sequencing (NGS) is emerging as an efficient and cost-effective tool in population genomic analyses of nonmodel organisms, allowing simultaneous resequencing of many regions of multi-genomic DNA from multiplexed samples. Here, we detail our synthesis of protocols for targeted resequencing of mitochondrial and nuclear loci by generating indexed genomic libraries for multiplexing up to 100 individuals in a single sequencing pool, and then enriching the pooled library using custom DNA capture arrays. Our use of DNA sequence from one species to capture and enrich the sequencing libraries of another species (i.e. cross-species DNA capture) indicates that efficient enrichment occurs when sequences are up to about 12% divergent, allowing us to take advantage of genomic information in one species to sequence orthologous regions in related species. In addition to a complete mitochondrial genome on each array, we have included between 43 and 118 nuclear loci for low-coverage sequencing of between 18 kb and 87 kb of DNA sequence per individual for single nucleotide polymorphisms discovery from 50 to 100 individuals in a single sequencing lane. Using this method, we have generated a total of over 500 whole mitochondrial genomes from seven cetacean species and green sea turtles. The greater variation detected in mitogenomes relative to short mtDNA sequences is helping to resolve genetic structure ranging from geographic to species-level differences. These NGS and analysis techniques have allowed for simultaneous population genomic studies of mtDNA and nDNA with greater genomic coverage and phylogeographic resolution than has previously been possible in marine mammals and turtles.

**Week of 28 January 2013**


**Week of 22 January 2013**

Abstract - The Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis) is a highly threatened cetacean endemic to the middle and lower reaches of the Yangtze River that has suffered a dramatic decline in recent decades. We characterize and quantify recent distribution patterns of porpoises in the Yangtze River in order to facilitate strategic management of existing in situ cetacean reserves and maximize effective utilization of limited conservation resources. We calculated porpoise relative abundance (encounter rate) using a 1-km moving average along the Yangtze main stem based on a combined visual and acoustic survey conducted in 2006. We then evaluated conservation priority areas based on encounter rates along the river. High-porpoise density areas (> 0.20 porpoises km-1) cover approximately one-third (33.9%, 599 km) of the survey area and contain approximately two-thirds of the porpoise population, making them priority areas for porpoise conservation. In contrast, low-porpoise density areas (0.05 porpoises km-1) cover 28.8% (509 km) of the survey area but contain only 4.5% of the porpoise population, and may already be of little value for porpoise conservation. Five high-priority porpoise conservation sites and five sections that now contain few or no surviving porpoises are identified. Proposed spatial modifications to existing reserves and associated conservation recommendations are made for five existing protected areas along the Yangtze main stem, and we emphasize that some additional river sections should urgently be designated as new protected areas given their high porpoise density. Our approach for identifying conservation priorities may provide lessons for reserve design and management in other protected area networks.

Week of 14 January 2013


Abstract - Loggerhead turtles Caretta caretta in the North Pacific are listed as Endangered under the US Endangered Species Act and the IUCN Red List. Due partly to their imperiled status, the US National Marine Fisheries Service established a time-area closure in 2003 for the California drift gillnet (CDGN) fishery operating within the Southern California Bight (SCB) to avoid incidental captures. This closure is triggered when sea surface temperatures are above normal, generally caused by El Niño-derived warm-water conditions, which is the time when loggerheads are thought to enter the SCB. Knowledge of the previous foraging grounds of loggerheads incidentally captured by the CDGN fishery in the SCB will help elucidate the oceanographic mechanisms that may influence turtle movement into this region and can assist in optimizing the environmental triggers for implementation of the SCB fishing closure. Stable carbon (δ13C) and nitrogen (δ15N) isotope analysis was used to determine the previous foraging grounds of loggerheads encountered in the SCB. Skin samples from loggerheads captured in the CDGN fishery were compared with skin from loggerheads in the central North Pacific, incidentally caught in the Hawaii-based longline fishery, as well as skin from turtles sampled during in-water research along the Baja California Peninsula, Mexico. The stable isotope values of CDGN-caught turtles were more similar to those from the central North Pacific than to those from Baja, indicating movements from the central North Pacific to the SCB. We elaborate on potential oceanographic mechanisms by which turtles access the SCB and provide insights that can inform future management decisions for the time-area closure.


Abstract - 1. Human-caused mortality threatens many marine turtle populations worldwide, with fisheries interactions being a primary cause for population declines. National and international management of fisheries interactions with marine turtles are rarely tied to turtle population biology. Quantitative tools tied to population-based objectives can provide insight into the effectiveness and urgency of bycatch mitigation. 2. A management approach is proposed based on a bycatch control rule called Reproductive Value Loss Limit (RVLL), generalized from the Potential Biological Removal management model for marine mammal populations. For RVLL, population size is scaled by reproductive value to account for strongly age-structured population dynamics and age-dependent fisheries mortality rates in marine turtle populations. 3. RVLL is an estimate of maximum sustainable mortality for a population, calculated from estimates of maximum population growth rate, total reproductive value in the population, and an uncertainty factor. RVLL estimates correspond to specified management goals and risk tolerances. For demonstration, simultaneous goals of maintaining populations above the maximum net productivity level (analogous to the population size that produces maximum sustainable yield) and preventing a decrease in adults are assumed, both with 95% probability. A management-strategy-evaluation-like process was used to explore parameterization of the RVLL equation for robust performance over a range of plausible life history characteristics and uncertainties in abundance and bycatch mortality estimates for marine turtle populations. 4. The RVLL-based management approach presented here proved robust to several important sources of uncertainty and to violation of several key underlying assumptions, and can be adapted to account for important sources of bias. The architecture presented, including tailored management strategy evaluation, provides a useful basis for further development of reference-point-based management of human-added mortality in populations that experience large changes with age in reproductive value and human-caused mortality rates, as is the case for marine turtles.

Week of 7 January 2013


Abstract—Jumbo squid (Dosidicus gigas) and purpleback squid (Sthenoteuthis oualaniensis) (Teuthida: Ommastrephidae) are thought to spawn in the eastern tropical Pacific. We used 10 years of plankton tow and oceanographic data collected in this region to examine the reproductive habits of these 2 ecologically important squid. Paralarvae of jumbo squid and purpleback squid were found in 781 of 1438 plankton samples from surface and oblique tows conducted by the Southwest Fisheries Science Center (NOAA) in the eastern tropical Pacific over the 8-year period of 1998–2006. Paralarvae were far more abundant in surface tows (maximum: 1588 individuals) than in oblique tows (maximum: 64 individuals). A generalized linear model analysis revealed sea-surface temperature as the strongest environmental predictor of paralarval presence in both surface and oblique tows; the likelihood of paralarval presence increases with increasing temperature. We used molecular techniques to identify paralarvae from 37 oblique tows to species level and found that the purpleback squid was more abundant than the jumbo squid (81 versus 16 individuals).


Abstract - Local ecological knowledge constitutes a potentially useful source of information for conservation, but the quality, limitations and biases of this body of knowledge remain largely untested. The Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis) is a highly threatened freshwater cetacean found in one of the world’s most densely populated human environments. The dynamics of porpoise decline remain poorly understood, and local ecological knowledge from fishing communities across its range may represent an important conservation tool for monitoring porpoise population status and quantifying levels of human-caused mortality. We used interview data from an extensive survey of fishing communities across the middle-lower Yangtze drainage to investigate spatial and temporal patterns of
porpoise abundance, mortality and population change. Interview data on porpoise relative abundance and
decline, especially weekly sighting frequencies, show congruent spatial patterns with data collected from
boat-based Yangtze cetacean surveys, demonstrating that informant data can provide accurate quantitative
information on these two key parameters of species conservation status. Interview-based collection of local
ecological knowledge therefore represents a useful monitoring method for assessing population trends in
freshwater cetaceans and other charismatic or distinctive aquatic species, and may be particularly appropriate
in regions where resources for regular boat-based surveys are limited. Using local ecological knowledge to
identify primary threats to the porpoise population is less straightforward due to probable biases in interview
data on porpoise mortality. However, interview data are able to demonstrate that the number of porpoises
killed annually in the Yangtze mainstem may have doubled, and that annually mortality rate may have
quadrupled, over the past two decades, with mortality due to vessel strikes and other factors having increased
more in recent years than by-catch mortality. It seems unlikely that fisheries mortality has been the dominant
driver of porpoise decline in the Yangtze mainstem, suggesting that regulating regional fisheries may not be
sufficient for porpoise conservation.