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We compared the spatial structure across the North Atlantic Ocean of the genetic variation in the mitochondrial and nuclear genome in minke, fin, blue and humpback whales. Across all four species we found a qualitatively similar spatial distribution of genetic diversity where the major break in genetic homogeneity follows the edge of the sea ice cover during the last glacial maximum (LGM). Populations in areas that were covered with ice (and hence inaccessible to rorquals) during the LGM contain comparatively lower genetic diversity, genetically homogenous (F_{st} values at ~ 0) and have increased dramatically in abundance since the LGM. In contrast, populations situated outside the area covered with sea ice during the LGM (main in the eastern part of the North Atlantic) are genetically distinct from the aforementioned populations (F_{st} values in the range of 0.10 across most species) and show no signs of recent expansion or even in some cases signs of population decreases. This genetic break also coincides with ocean currents system following the eastern arm of Gulf Stream to a large extent. Our comparative analysis suggests that evolution and population structure of rorquals in the North Atlantic are shaped by the same fundamental oceanographic and geological processes.

Examining persistent organic pollutant concentrations and expression of a biomarker (CYP1A1) in stranded cetaceans from the Pacific Islands region

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Persistent organic pollutants (POPs) are toxic man-made chemicals that bioaccumulate and biomagnify in food webs, making them a ubiquitous threat to the marine environment. Although many studies have determined concentrations of POPs in top predators, no studies have quantified POPs in stranded cetaceans within the last 30 years around the Hawaiian Islands. A suite of POPs were measured in the blubber of 16 cetacean species that stranded in the central Pacific from 1997 to 2011. The sample set includes odontocetes (n=39) and mysticetes (n=3). Detectable

contaminants from highest to lowest concentration with medians (standard deviation) in ng/g lipid are: 8,150 (30,300) for Σ DDTs (dichlorodiphenyltrichloroethanes), 5,120 (17,200) for Σ PCBs (polychlorinated biphenyls), 821 (2,730) for Σ chlordanes, 864 (1,720) for Σ toxaphenes, 185 (1,600) for Σ PBDEs (polybrominated diphenyl ethers), 159 (206) for Σ chlorobenzenes (hexachlorobenzene and pentachlorobenzene), 152 (1,160) for mirex, 47.8 (122) for Σ HCHs (hexachlorocyclohexanes), 31.7 (167) for Σ HBDCs (hexabromocyclododecanes) and 1.93 (2.61) for octachlorostyrene. POP concentrations in these Pacific Island cetaceans approach and sometimes exceed proposed toxic threshold values. Backward stepwise multiple regressions indicated life history effects on contaminant concentrations when performed with three independent variables (species, year of stranding, and sex/age class). No temporal trends were noted ($p > 0.100$), but species differences were evident for all compound classes ($p \leq 0.0004$) as well as sex/age class influences with adult males displaying higher contaminant loads than adult females and juvenile animals for Σ DDT, Σ PCBs and Σ CHLs ($p \leq 0.013$). POP concentrations were lower in mysticetes than odontocetes for most compound classes ($p \leq 0.023$). p,p' -DDE / Σ DDT ratios were lower than those found in other marine mammals from tropical environments, perhaps indicating greater exposure to the parent DDT pesticide for this central Pacific region. This presentation will also explore organismal health effects by examining POP concentrations in relation to expression of a cytochrome P450 protein biomarker in the liver (CYP1A1).

Paleogenomics of Spitsbergen Bowhead Whales (*Balaena mysticetus*)

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The Spitsbergen stock of bowhead whales, distributed in the Greenland, Norwegian, Barents, and Kara Seas, was once the largest stock but was heavily depleted by whaling. Today, the stock is considered "critically endangered" by the IUCN. Previous studies have documented excellent DNA survival in ancient bowhead whale bones collected from the elevated beaches throughout the Svalbard archipelago. We developed a rapid experimental strategy for testing the suitability of ancient DNA extracts from such bones for next-generation sequencing of total genomic DNA. Promising DNA extracts were subjected to multiplexed high-throughput sequencing on an Illumina HiSeq 2000™ instrument (2 x 100 bp paired-end). Complete mitochondrial genomes with relatively high coverage (ca 10-120 x) were assembled for 15 samples ranging in age between ca 20 and 9300 years. We assess mutation rates for different genes in the mitochondrial genome of bowhead whales by directly assessing mutational changes in temporally spaced samples. We discuss the implications of the results for the demography of the Spitsbergen stock of bowhead whales throughout the Holocene.

Behavior and group characteristics differ in mixed-species associations of cetaceans in the Southern California Bight

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Effects of mixed-species associations (MSA [at least two different species swimming together and/or interacting]) on cetacean behavior rarely have been quantified, but are important for identifying and differentiating potential anthropogenic impacts. Baseline marine mammal behavior was assessed during 77,390 km of U.S. Navy supported aerial line-transect surveys in the Southern California Bight during 2008-2013. Multinomial logistic regression was used to assess effects of MSA on group size, maximum nearest neighbor distance (a "cohesion" index, in body lengths), behavior state, and heading. Two percent (43) of 2,330 sightings were MSA involving 13 species (5 baleen whales, 7 toothed whales, 1 pinniped). Behavior and group size of some species differed significantly in MSA vs. non-MSA. MSA were predominated by Risso's dolphins (44%; 19 of 43 MSA). Risso's dolphins were most frequently associated with bottlenose dolphins (37% of 19 Risso's MSA groups) followed by northern right whale dolphins (NRWD; 3% of 19). Risso's dolphins tended to change headings more often in MSA ($p < 0.10$), socially interacting by moving/orienting toward or away from other species. Notable MSA included a Risso's dolphin chasing/charging a lone minke whale, a Risso's dolphin repeatedly charging the heads of sperm whales that reacted by opening their mouths, and a mother/calf fin whale closely following/interacting with ~1,000 NRWD. Risso's dolphin mean group size was significantly higher in MSA (26) vs. non-MSA (15). Group cohesion generally decreased in MSA vs. non-MSA but not significantly. Speculated explanations for the observed MSA include kleptoparasitism, feeding, defense of conspecifics, "floating maritories," play, harassment, and social interest. Increased group sizes and tighter cohesion in MSA may indicate elevated defensiveness and/or facilitate social interactions. Interspecific interactions have remained historically uncommon in the SCB, but similar proportionally based on similar spatial/temporal effort (2-6%). MSA likely involve both benefits and risks to members, depending on species and motivations.

Marine mammals in the future ecosystems: individual-based models from current observations can help conservation policy to deal with the unknown.

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Global climate change is frequently considered a major threat for conservation of marine ecosystems. Impacts on the demography of animal populations, on shifts in geographic range of species and on changes in the structure and functioning of ecosystems are already observed. However, what can be expected if the changes accelerate and amplify in the future as it is predicted remains unclear. This work promotes the use of individual-based models (IBM) developed from field observations to help understanding current interactions of marine mammals with their environment and to develop realistic scenarios on their future. We used bio-logging technology to track the foraging behavior of three different species - Arctic beluga whales, Antarctic fur seals and Southern elephant seals - within their marine environment. From these data, we developed an IBM to explore the impact of directional changes in food spatial structuring on life-history components of the three species. The model first showed that the level of food resources aggregation in summer impacts the annual prey capture and the timing of migration to the winter grounds of beluga whales. Second the model showed that an increasing distance of resources from the colony impacts the survival and the fitness of adult female fur seals. Moreover, we observed that longer females were better able to respond to simulated changes in resources distance than smaller females. Third the model

determined physiological limits of elephant seals face to an increasing depth of resources. The overall aim of such a model, which might be generalized to many other species, is to identify potential changes in phenotype distribution of populations and to define the limiting conditions beyond which marine mammals would be unable to adjust and therefore their sensitivity to the potential future changes.

Combining association and movement analyses of short-finned pilot whales in the Hawaiian Islands: evidence for multiple populations within the Hawaiian Archipelago

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Currently a single stock of short-finned pilot whales is recognized in Hawaiian waters, with an estimated abundance of over 12,000 individuals in the EEZ. However, preliminary genetic results suggest that pilot whales around the main Hawaiian Islands are reproductively isolated from those elsewhere in the tropical Pacific. Since the type and extent of anthropogenic interactions varies both among the main Hawaiian Islands and offshore, we test the hypothesis that there is only a single stock of this species in Hawai'i using a combination of association analyses of photo-identification data and movement/habitat use analyses from satellite tags. Photographs over 13 years included over 6,500 identifications of 868 distinctive individuals. Satellite tag data from 64 deployments averaged 37 days (max=228 days). Combining tag and association analyses indicate individuals do not mix freely among the islands and suggest the existence of three socially isolated but partially overlapping insular communities and an offshore population. The ranges of the three insular communities are from Ni'ihau to western O'ahu, from O'ahu to Lana'i, and primarily off Hawai'i Island. Tagged individuals from these insular communities (n=61 deployments) remained an average of 57.5 km from their tagging location, with a grand mean of depth used and distance from shore of 1,564 m and 15.2 km, respectively. Evidence for an offshore population comes from three individuals tagged in two isolated social clusters with mean distances from their tagging locations of 249 km, with a grand mean of depth used and distance from shore of 4,336 m and 81.1 km (max=381 km) respectively. Anthropogenic interactions vary among the population ranges, with long-line fishing in offshore waters, Navy activities primarily off Ni'ihau, Kaua'i and O'ahu, and vessel-based whale watching and swim-with operations primarily off Hawai'i Island. As each community is exposed to different anthropogenic threats they should be managed independently.

Wiggle me this: How do elephant seals forage?

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Wiggles at the bottom of marine predator dive profiles are usually believed to be associated with feeding. Quantifying these in space and time can provide insights into how cryptic marine predators, such as southern elephant seals (*Mirounga leonina*), acquire energy. Using custom built multi-channel dive