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Dwarf (*Kogia sima*) and pygmy (*Kogia breviceps*) sperm whales are small toothed whales that employ narrow band high frequency (NBHF) clicks for echolocation. Such NBHF clicks are normally found in small, shallow-water toothed whales, such as porpoises, that produce clicks at ~125 kHz. These high frequency clicks are subject to high levels of acoustic absorption and are in keeping with porpoises' short-range echolocation. Here we sought to address the problem of how the little studied *Kogia*, as deep-diving toothed whales, can find food with NBHF clicks in the deep. Specifically, we tested the hypotheses that *Kogia* use NBHF clicks with longer inter-click intervals (ICIs), higher directionality, and higher source levels (SLs) compared to shallow water NBHF species. We did this by deploying an autonomous deep-water vertical hydrophone array of 7 synchronized SoundTraps at 576 kHz, for 74.6 hours over 18 deployments in May-June 2018 in the Bahamas, where no other NBHF species are present. Depth/tilt sensors (Star-Oddi) next to the peripheral hydrophones measured array straightness and allowed for calculations of localisation errors arising from tilt. NBHF clicks were detected, classified, and localised (n=828), with 276 clicks deemed on-axis. Based on the calculated locations of clicking *Kogia* and known positions of each hydrophone, the apparent SL and half-power beamwidth were quantified. Apparent SLs (up to 197 dB re 1 μ Pa_{r-p}) with a peak frequency of 129 kHz mean that *Kogia* could use their biosonar to inspect out to twice as far as porpoises, assuming the same prey target strength. This range agrees with the mode of their ICIs (245 ms). Their half-power (-3 dB) beamwidth of <10° confirmed our hypothesis of their narrow acoustic field of view. Thus, *Kogia* use a directional long-range echolocation system with high SLs to compensate for the considerable absorption losses of their NBHF clicks while hunting.

Epigenetic effects of environmental contaminants on the skin of the fin whale (*Balenoptera physalus*) in the Mediterranean basin.

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The phenotypic plasticity of many organisms is mediated in part by epigenetics, the heritable changes in gene activity that occur without any alterations to DNA sequence. A major mechanism is the DNA methylation (DNAm). Hypo- and hypermethylation are generalized responses to control gene expression but recent studies have demonstrated that classes of contaminants could mark specific DNAm signatures, therefore be used to assess prior environmental exposure.

We sampled skin and blubber from 6 fin whale (*Balenoptera physalus*) individuals living in the northern Mediterranean Sea. Blubber was analyzed for Organochlorines levels while genomic DNA extracted from the skin of the animals with the lowest (mean value = 19 μ g/g lipid basis, l.b.) (group 1, n=3) and the highest (mean value = 53 μ g/g l.b.) (group 2, n=3) levels of contaminants were used for DNAm profiling through reduced representation bisulfite sequencing (RRBS).

We tested the hypothesis that the differences in the methylation patterns observed comparing the 2 groups are linked to environmental contaminant exposure and load in the whale tissues.

While pronounced variations in CHH and CHG methylation (where H is any base except G) were not observed, the CpGs showed 32683 differentially methylated Cs in promoters and/or exon/intron regions of genes (p < 0.05, mean coverage = 8.5), accounting for 13% of the whole set.

Gene Ontology indicated that DNAm affected genes dealt with cell differentiation and function in nervous, endocrine, immune, circulatory and muscular systems.

qPCR on a larger set of skin samples with known contamination loads correlated differential expression of selected genes with DNAm changes.

Eco-epigenetics have extraordinary potential to advance our understanding of biological responses to environmental challenges, and yield sensitive tools for pollution biomonitoring and ecotoxicity assessment.

Introducing the Risso's dolphins of the Isle of Man

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