

## The interaction between the gut microbiome and environmental pollutants and its impact on the health of wild harbour porpoises

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Anthropogenic PCB (polychlorinated biphenyl) pollutants pose a major threat to populations of marine mammals worldwide [1,2]. More than 90% percent of adult male harbour porpoises from the southern North Sea are exposed to PCB levels associated with severe negative health consequences [3]. Although, PCBs have been banned since 2001 by the Stockholm Convention on POPs (persistent organic pollutants), they still pose a major threat to marine mammals such as porpoises due to their environmental persistence, bioaccumulating and -magnifying nature and efficient mother-offspring transfer [1]. Porpoises get exposed to PCBs by consumption of polluted prey or contaminated mother milk, through which these pollutants enter the gastrointestinal tract and eventually accumulate in the blubber layer [3,4]. From there, they lead to immunosuppression and reproductive impairment, which increases susceptibility to infectious disease and compromises recruitment of offspring, eventually negatively affecting population viability [4,5]. As a means to monitor the health of wild porpoise populations, many researchers have collected blubber samples from stranded individuals to quantify PCB levels [3,4]. Thanks to this endeavor, it has become clear that especially male porpoises are exposed to levels well above safety thresholds, which results in immune system and reproductive impairment [3,4]. In investigating the health consequences from pollution on porpoises, the gut microbial community has never been considered before. However, as porpoises are exposed to PCBs through trophic transfer or lactation, the gastro-intestinal tract with its microbial community is the first site of potential metabolization. As such, it's interesting to study the interaction between pollution and the gut microbiome as it will give us a more elaborate insight into the effects of PCBs on the health of porpoises and how the gut microbiota interact with pollutants to affect bioavailability and eventual accumulation in fat tissue. Pollutants are known to disrupt the balance of the gut microbial community (i.e. gut dysbiosis) in numerous vertebrate species, evoking loss of beneficial members and expansion of pathogenic ones resulting in negative health consequences, such as metabolic disorders and chronic infections [6]. As porpoises are exposed to very high PCB concentrations through biomagnification, it is conceivable that pollution-induced gut dysbiosis develops in heavily polluted individuals. Moreover, the gut microbial community is known to be involved in the metabolism of environmental pollutants such as PCBs [7]. They alter the bioavailability of pollutants either by activation leading to increased accumulation in fat tissue or detoxification leading to increased excretion out of the body. This opens up the question if we can find bacterial strains or genes in the gut microbiome of porpoises involved in pollutant metabolization.

The objective of this study is three-fold, I will characterize the gut microbiome of porpoises, study the impact of PCB exposure on gut microbial health and screen the microbial community for members or genes involved in PCB metabolization. To that end, I will jointly collect fecal and blubber samples from porpoise individuals stranded along the Belgian and Dutch coast. First, by running gas chromatography analyses on blubber samples, the PCB burden will be quantified for each porpoise individual. Secondly, as a novel practice in porpoise monitoring, the gut microbiome composition will be determined by a metagenomics approach. By integrating this data, I can test for an effect of PCB burden on gut microbiome composition to seek evidence of pollution-induced gut dysbiosis. Moreover, by screening the metagenome of the gut microbial community for genes and pathways involved in pollutant metabolization, I can expand our knowledge on the potential of the microbiome from a wild marine mammal to metabolize environmental pollutants.

### References

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**Keywords**

Harbour Porpoise; Gut Microbiome; Gut Dysbiosis; PCB; Environmental Pollution; PCB Metabolization