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The microbial engine behind whale-driven iron fertilization

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The International Monetary Fund has identified whales as a natural solution for enhancing oceanic carbon storage. The "whale pump" describes the process by which whales release nutrients such as iron (Fe) through defecation, stimulating primary production and enhancing carbon export to the deep ocean. However, the role of whale gut microbiota in regulating the elemental composition of faeces remains unknown. Here, we examined, through total element concentrations, labile fractions and metagenomics, faecal samples from both humpback (*Megaptera novaeangliae)* and southern right (*Eubalaena australis*) whale species along the West African coast (Southern Benguela Upwelling system). This study is the first profiling of southern right whale gut microbiota. Analysis revealed marked interspecies differences, with Fe concentrations being between 2- and 3-fold higher in southern right whale faeces, where Fe was also more labile. Taxonomic composition was dominated by Bacillota in both whale species yet bacteria phylum Bacteroidota and archaea phylum Thermoplasmatota showed whale species specific differences. Functional roles of gut microbiota towards ocean fertilisation was evaluated through known Fe-related genes. Preliminary analysis indicate that the whale gut microbiome cycles Fe with whale species microbiomes showing differences in siderophore-mediated Fe acquisition and Fe reduction-based strategies. Together, these findings suggest that both the quantity and speciation of Fe in faeces are tightly linked to gut microbial community dynamics. Consequently, the fertilization potential of whale-derived Fe in surface waters depends not only on the characteristics of the marine region where defecation occurs, but also on species-specific faeces shaped by metabolism and feeding grounds of whales.