

How do faecal pellets from fouling fauna contribute to the marine organic matter pool in offshore wind farms?

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Nowadays, the demand for renewable energy is increasing. One option to respond to this demand is to build Offshore Wind Farms (OWFs). However, the presence of the turbines changes the marine habitat. The hard structures provide new habitat that is rapidly colonized by epifaunal marine organisms. This fauna consists mainly of suspension feeders, organisms feeding on organic particles in the water column. In the shallow subtidal zone, the communities are dominated by the blue mussel (*Mytilus edulis*). Deeper down, there are high numbers of tube building amphipods (*Jassa herdmani*), and closer to the seafloor, anemones (*Metridium senile*) can be found. They filter suspended particles as well as phyto- and zooplankton and produce faecal pellets (FP), which are thought to play a crucial role in the local organic matter (OM) dynamics and possibly also in carbon sequestration in the sediment surrounding the turbines.

Within this scope, the general objective of the OUTFLOW (Quantifying the cONtribUTION of Fouling fauna to the Local carbon budget of an Offshore Windfarm) project is to assess the importance of FP within the OWFs ecosystems by estimating their contribution to the pelagic and benthic organic matter pools. To reach this goal, tracers of FP of the dominant organisms (*M. edulis*, *J. herdmani*, and *M. senile*) will be developed. This will be done by applying stable isotope analysis of amino acids (AA) in the FPs.

This is done because as the AA transfer from primary producers to consumers, they follow different pathways. These possible changes can be observed on the $\delta^{15}\text{N}$ of the AA. Some AAs suffer little change (defined as “Source” amino acids), and others undergo significant metabolic alterations (defined as “Trophic” amino acids). This change is not only associated with a specific AA, but also depends on the possible alteration due to passage through the metazoan gut. Based on previous research (Doherty et al., 2021)¹, specific AA ratios will be selected together with the determination of the trophic position, to produce a multivariate fingerprint to apply in a Bayesian Mixing Model.

Together with the analysis of the ^{15}N signals in the AA of other OM sources (phytoplankton, zooplankton, and bacteria-degraded OM), the developed fingerprints will be used to differentiate between the contributors to the OM pool and provide the means to estimate the contribution of FP to the OM pool both in the water column and the sediment from the OWFs, model the potential spatial dimensions of FP enrichment of sediments, determine the fate of FP in the sediment, estimate the carbon sequestration potential of altered OWF sediments, and investigate the effect of OWFs on OM dynamics at a larger geographical scale.

Reference

¹ Doherty, S. C., Maas, A. E., Steinberg, D. K., Popp, B. N., & Close, H. G. (2021). Distinguishing zooplankton fecal pellets as a component of the biological pump using compound-specific isotope analysis of amino acids. *Limnology and Oceanography*.

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