CHAPTER 6

MONITORING IMPACTS OF OFFSHORE WIND FARMS ON HYPERBENTHOS: A FEASIBILITY STUDY

LEFAIBLE Nene, BRAECKMAN Ulrike & MOENS Tom

Ghent University, Biology Department, Marine Biology Research Group, Krijgslaan 281, Campus Sterre – S8, 9000 Ghent, Belgium

Corresponding author: Nene.Lefaible@UGent.be

Abstract

Despite their important role in bentho-pelagic coupling and analogies with macrobenthic communities in terms of distribution patterns and seafloor dependency, hyperbenthos is often not included in current monitoring programs. It is proposed that turbine-related habitat changes such as altered hydrodynamics and organic enrichment could create more favourable conditions for the settlement of pelagic species and attract mobile species, resulting in richer hyperbenthic communities within the offshore wind farms (OWFs). Therefore, the 2019 monitoring campaign was used to perform a feasibility study concerning sampling effort (design/strategy, processing time) and to explore the obtained data (inside *vs.* outside tracks) within two OFWs (C-power and Belwind). The unsuccessful initial sampling showed that efficient sampling strongly depends on appropriate weather conditions and local topography. Eventually, an adjusted sampling strategy (tracks parallel to sand ridges and shorter towing distance) resulted in two representative samples (reference – and impact tracks) at C-power, which were processed within a reasonable time frame. While no actual conclusions can be made from the obtained dataset, this study did reveal some results that show the relevance of including this group within future monitoring to allow a more comprehensive view of turbine-related impacts on seafloor associated communities within the Belgian part of the North Sea (BPNS).

1. Introduction

Hyperbenthos can be described as the group of animals that occur in the lower part of the water column and are dependent on their association with the seafloor (Dewicke 2001; Hamerlynck *et al.* 1991). These communities are usually divided into two groups: the holohyperbenthos, which contains animals that are permanently present, and a temporary group, the merohyperbenthos, which only spend a part of their life cycle in the hyperbenthic zone. Comparable to the infaunal macrobenthos, hyperbenthic communities are believed to play a major role in bentho-pelagic coupling (Dewicke 2001). Being characterised by good swimming capacities and vertical migrations, these species contribute to the modification and transport of organic matter within the water column (Dewicke 2001). In addition, the mobility of the hyperbenthos at the seafloor-water

Table 1. Overview of hyperbenthos sampling campaigns and sample status (NR = non-representative)

Date of sampling	Vessel	Location	Impact / reference	Track name	Sample status
22-26/10/2018	RV Belgica	BB	Impact	WBB06a	Not sampled
		BB	Reference	WBB02	Not sampled
		TB	Impact	ftTrack2	Sampled but NR
		TB	Reference	ftwT2triss	Sampled but NR
06/02/2019	Simon Stevin	TB	Impact	ftTrack2	Sampled and processed
		TB	Reference	ftHyper	Sampled and processed

column interface could influence important processes such as bioturbation and bioresuspension, thereby changing overall particle fluxes (Dewicke 2001). At last, hyperbenthic communities are considered an important food source for higher trophic levels such as juvenile demersal fish (Dewicke 2001).

Large-scale studies on the distribution of hyperbenthic communities were performed throughout the 90's and revealed two gradients in community structure which consisted of a principal onshore-offshore gradient (abundance and biomass) perpendicular to the coastline and a less pronounced east-west gradient parallel to the coastline reflecting differences in species richness and diversity (Vincx *et al.* 2004). The latter gradient seems to be most pronounced in the onshore area, with more diverse communities at the western Coastal banks compared to the eastern Coastal banks (Vincx *et al.* 2004). In general, hyperbenthic abundance and diversity were significantly lower at the offshore Hinder Banks compared to the Flemish and Zeeland Banks closer to the coast (Vincx *et al.* 2004; Dewicke 2001). These findings are in accordance with described distribution patterns of macrobenthic communities, indicating that scarcer food supply and stronger water flow at offshore locations provide a less favourable environment for bottom-dwelling animals (Vincx *et al.* 2004). Due to these analogies with macrobenthic communities in terms of

distribution patterns and seafloor dependency, it is very likely that the permanent presence of wind turbines would also affect this part of the bentho-pelagic community within the Belgian part of the North Sea (BPNS). Alteration of hydrodynamics around the turbines and the creation of sheltered areas with lower current velocities might promote the settlement of planktonic species with passive transport mechanisms that comprise a substantial portion of the hyperbenthic community (Hamerlynck & Mees 1991). In addition, the proposed organic enrichment around the turbines due to the combined effects of sediment fining and the deposition of organic matter from the epifouling communities (Lefaible *et al.* 2018) may also influence the occurrence of mobile organisms such as mysids which can actively migrate to areas with higher food availability (Hamerlynck & Mees 1991). A potential hypothesis could therefore be that wind turbines within the offshore areas create more favourable conditions for the settlement of several species and attract mobile species, resulting in richer hyperbenthic communities.

Therefore, the main objectives of this feasibility study were to i) assess the suitability of the sampled tracks for hyperbenthos research, ii) estimate the time needed to process the obtained samples, and iii) explore the abundance and diversity data of the sampled hyperbenthos inside versus outside of offshore wind farms.

2. Material and methods

The sampling of the hyperbenthos was done at two sandbanks, the Bligh Bank (BB) and the Thornton Bank (TB). The proposed sampling sites consisted of one track within each offshore wind farm (Belwind at the BB, C-power at the TB), together with a reference track. The locations of the tracks were based on existing tracks that are sampled during the epifauna research (fig. 1, table 1).

Due to adverse weather conditions, hyperbenthos sampling at BB had to be cancelled. The two remaining sites at TB were sampled through the use of a hyperbenthic sledge containing 4 nets: two pairs of nets were mounted next to each other with mesh sizes of 0.5 and 1 mm of the two superimposed (upper and lower) nets on the left and right side of the sledge. Collectors were placed at an angle of 45° and a flowmeter was installed to calculate the volume of water filtered during each sampling event. Tows were made during daytime conditions for 1 km against the current at a speed

of 1.5 knots. Sampling at TB resulted in a non-representative (NR) reference sample due to the high accumulation of sediment within the collectors and the near absence of organisms.

One potential explanation for the lack of successful sampling at the reference site could be a combination of the position of the track relative to the sandbank ridges and the long towing distance. Therefore, an alternative sampling strategy was proposed with shorter (150 m) tracks that run parallel to the ridges. During a one-day sampling cruise (06/02/2019) on board the Simon Stevin, this new sampling method was tested in C-power where two tracks were performed during daytime conditions: one impact track and one adjusted reference track just outside the offshore wind farm (fig. 1, table 1). The hyperbenthic sledge on the Simon Stevin only consists of two nets: the lower-net samples from 0.2 to 0.5 m, and the upper-net from 0.5 to 1 m above the bottom; both nets have a 1 mm mesh size. Comparable to the sledge
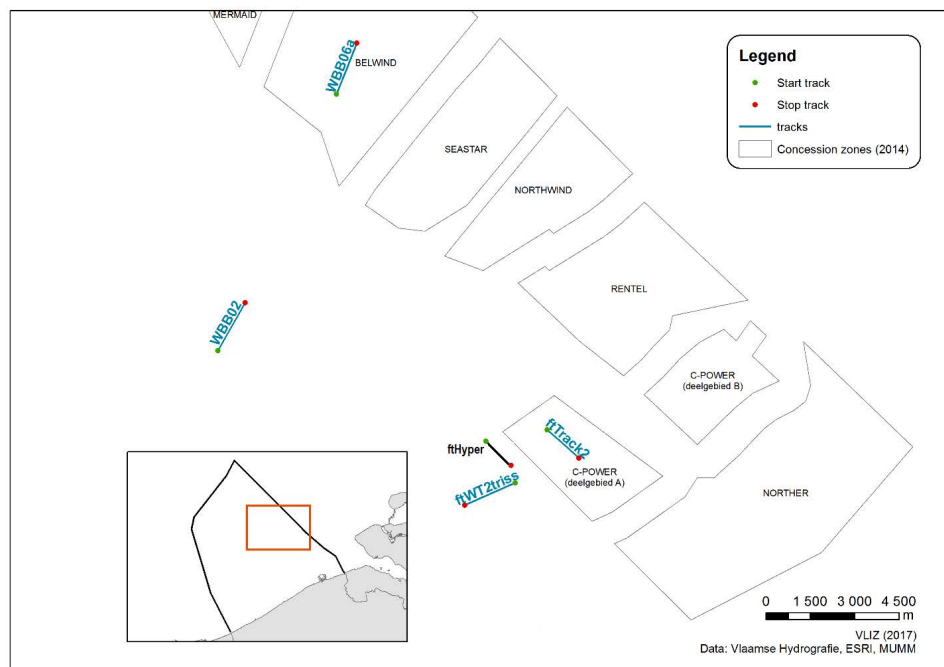

Figure 1. Wind farm concession areas in the Belgian part of the North Sea and the hyperbenthos sampling tracks (blue lines). The black line represents the newly proposed hyperbenthos track for the reference site at C-power.

of the RV Belgica, collectors were placed at an angle of 45° and a flowmeter was installed within the lower-net. Sampling proved to be successful and catches were rinsed separately (upper- and lower-nets) over a 1 mm sieve on board and preserved in an 8% formaldehyde solution.

Organisms were sorted, counted and identified to the lowest possible taxonomic level. In case of uncertainty, organisms were identified to a higher taxonomic level (genus, family or order) and typical macrobenthic species were removed from the dataset. Structural community characteristics within TB were explored by calculating total densities and diversity indices (species richness and Shannon-Wiener diversity) within each sample (REF upper, REF lower, IMPACT upper and IMPACT lower). Diversity indices were calculated using raw count data. Species reported on a higher taxonomic level were considered as "unique" if no other representative of the same taxon level was present or if they were distinctly different (morphospecies). Densities were obtained by standardising the data to individuals per 100 m³ through the following formula:

ind/100 m³ = number individuals / (surface net * amount of turns flowmeter) * 100. In addition, the Bottom Association (BA) index was also calculated to assess the vertical distribution of the animals in the hyperbenthic layer. The BA index was calculated by the total numbers caught in the lower net divided by the total number of individuals caught in both nets. Finally, differences in community structure were analysed through CLUSTER analysis (based on the Bray-Curtis dissimilarity index) and SIMPER analysis was performed both on untransformed and transformed (fourth root) data to specify the contributions of individual species to the distinction between groups of samples and/ or to the similarity of samples within a group (Clarke & Gorley 2006).

3. Results

Total densities (upper- and lower-nets combined) were higher at the REF site (91 ind. 100 m⁻³) compared to the impact site (66 ind. 100 m⁻³), but strongest differences were found within each site between both nets, with higher total densities in the
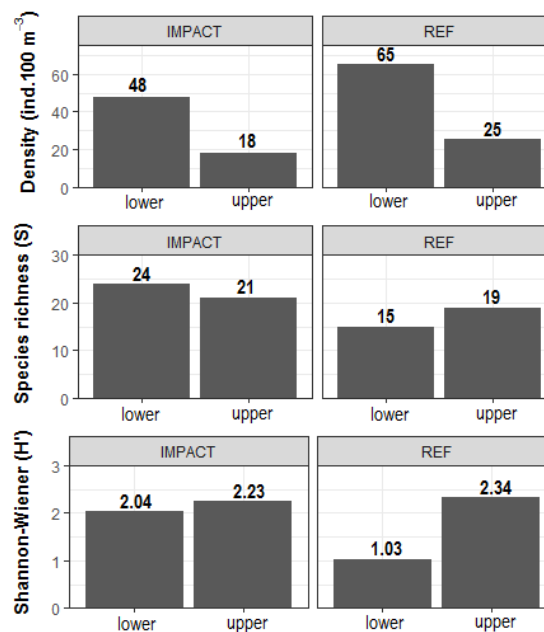

Figure 2. Overview barplots for calculated structural indices: total density (ind. 100 m⁻³), species richness (S) and Shannon-Wiener diversity (H') per sample (upper- and lower-nets) within the impact and reference site at C-power. Total values were added per sample above the corresponding barplot.

lower-net samples (fig. 2). It must be mentioned, however, that in the impact sample a significant amount of hydromedusae (upper sample) and mysids (lower sample) were too damaged for identification and were thus excluded from all analyses. Therefore, total densities in this sample might be underestimated. Total densities were highest for the sample Cref_lower (65 ind. 100 m^{-3}), which could be attributed to the high abundances of hydromedusae (48 ind.) and the amphipod *Atylus swammerdamei* (10 ind.). This finding of higher densities in the lower samples was also confirmed by the Bottom Association index, which revealed that about 70% of all individuals were caught in the lower-nets, indicating a vertical segregation within the hyperbenthic zone at both sites. In contrast, Cref_lower had the lowest diversity (S, H'), while these values were rather comparable among the other samples (fig. 2). In general, it can be concluded that for the structural indices, the most pronounced differences were found between both nets within the two sites in terms of total densities, while diversity differed mostly between the lower-net samples of the reference and impact site.

Hyperbenthic communities were mainly composed of hydromedusae (47%), Amphipoda (12%), fish larvae (11%), Chaetognatha (10%) and Mysida (8%). A total of 33 species were recorded and mysids proved to be the most species-rich order. Almost 1/3 of these species were unique for the impact site, and most of them represented smaller crustaceans such as mysids (*Siriella* sp., *Praunus inermis* and three mysid morphospecies), amphipods (*Corophium volutator*, *Orchomene* sp.) and cumaceans (*Bodotria* sp., *Pseudocuma* sp.). Species that were only found at the reference site included: *Gastrosaccus spinifer*, *Schistomysis kervillei*, *Ammodytes* larvae and two morphospecies of the orders Ctenophora and hydromedusae.

Comparable to the univariate results, CLUSTER analysis on untransformed density data revealed a clear separation between the lower and upper net samples in terms of community composition (fig. 3), and SIMPER results showed that average dissimilarity between nets was higher at the reference site (85%) compared to the impact site (66%). Lower samples were
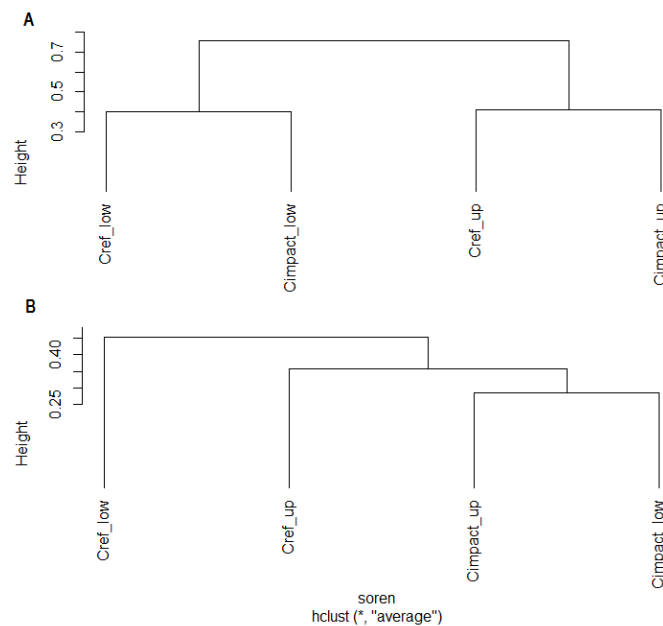

Figure 3. CLUSTER dendrograms based on untransformed density data (top) and fourth root transformed density data (bottom) per samples (upper- and lower-nets) within the reference and impact site at C-power.

dominated by hydromedusae (74%), *Atylus swammerdamei* (10%) and *Syngnathus rostellatus* (3%). The most important species contributing to about 90% of total densities for the upper samples included: *Sagitta elegans* (40%), *Atylus swammerdamei* (16%), *Mesodopsis slabberi* (15%), *Beroe cucumis* (6%), *Jassa* sp. (4%) and *Calanoida* sp. (3%).

A similar cluster analysis on fourth-root transformed density data showed a different trend in which the sample Cref_low was distinguished from the other samples (fig. 3). Despite the high total densities, this sample was dominated by hydromedusae and had the lowest diversity (S, H'). SIMPER analysis showed that strongest dissimilarities were found between Cref_low – Cref_up (46%) and Cref_low – Cimpact_low (40%). Differences between both nets at the reference site were mainly due to the higher average abundances of hydromedusae, Ctenophora and *Gastrosaccus spinifer* in the lower-net sample, while average abundances of *Mesodopsis slabberi*, *Neomysis integer* and *Jassa* sp. were higher within the upper-net sample. Shared species between the lower-net samples at the reference and impact site included: Hydromedusae, *Atylus swammerdamei* and *Sagittus elegans* where only the latter had higher average abundances at the impact site. Strongest between-site differences were, however, due to the unique presence of Ctenophora, *Gastrosaccus spinifer* and *Ammodytes* larvae at the reference site, while a high species richness (12) was only found at the impact site. Most of these unique species were representatives of mysids such as *Praunus inermis*, amphipods (*Corophium volutator*, *Jassa* sp.) or cumaceans such as *Bodotria* sp. and *Pseudocuma* sp.

4. Conclusions and future perspectives

The unsuccessful initial sampling showed that efficient hyperbenthos sampling strongly depends on favourable weather conditions and local topography, leading to potential practical difficulties in terms of sample collection. It appears that the relative position of the sampled tracks to the sandbank ridges is of great importance. Implementation of this prerequisite of tracks that run parallel to the sandbank ridges, together with a shorter towing distance (150 m), resulted in representative hyperbenthos samples. The obtained samples were processed in a reasonable time frame (one week), but it must be stated that there are no baseline studies for hyperbenthos communities within these areas of the wind farms, so it is not clear whether the processed samples can be considered as poor/rich in terms of abundance and diversity. As a result, future samples with higher abundances and the occurrence of many rare species might substantially prolong the sample processing.

Due to the small dataset (4 samples within C-power), it is difficult to draw firm conclusions with regard to turbine-related impacts on hyperbenthic communities. Nevertheless, this feasibility study did reveal some results that show the relevance of including this group of the bentho-pelagic community in future monitoring. Firstly, the strong association with the seafloor and the differences (densities, species composition) between upper- and lower-net samples indicate a vertical segregation within the hyperbenthic zone at both sites. The sediment-bound species that comprise an important component of total hyperbenthos densities could therefore be influenced by the altered sediment characteristics that are created by the presence of wind turbines. Secondly, the high amount of unique species at the impact site and the tendency of a higher diversity (S, H') at Cimpact_low compared to Cref_low suggest that structural differences might be established between the reference and impact site, but a more elaborate sampling design is necessary to confirm or discard this idea.

We therefore propose to perform several (2-3 replicates) shorter (150 m) reference and impact tracks for each wind farm.

When tracks are chosen, the position of the sand ridges should be taken into account and lower- and upper-net samples should be separated during sampling. In order to validate the proposed hypothesis of enriched hyperbenthic communities due to turbine-related habitat changes like decreased current velocities (improved settlement) and organic enrichment (attraction mobile fauna), environmental variables (grain size, bottom-current flow and food availability) should also be incorporated within the sampling strategy. If done correctly, the study of hyperbenthos may provide new insights and result in a more comprehensive view of wind turbine-related impacts on seafloor associated communities.

References

Clarke, K.R. & Gorley, R.N. 2006. PRIMER v6: user manual/tutorial PRIMER-E. Plymouth: Plymouth Marine Laboratory, 190 p.

Dewicke, A. 2001. *Hyperbenthic Communities of the North Sea*. Ghent: Ghent University, 219 p.

Hamerlynck, O. & Mees, J. 1991. Temporal and spatial structure in the hyperbenthic community of a shallow coastal area and its relation to environmental variables. *Oceanologica Acta* 11: 205-212.

Lefaible, N., Braeckman, U. & Moens, T. 2018. Effects of wind turbine foundations on surrounding macrobenthic communities. In . Degraer, R. Brabant, B. Rumes & L. Vigin (eds), *Environmental Impacts of Offshore Wind Farms in the Belgian Part of the North Sea: Assessing and Managing Effect Spheres of Influence. Memoirs on the Marine Environment.* Brussels: Royal Belgian Institute of Natural Sciences, OD Natural Environment, Marine Ecology and Management Section, pp. 57-77.

Mees, J. & Jones, M.B. 1997. The Hyperbenthos. *Oceanography and Marine Biology: an Annual Review 1997* 35: 221-255.

Vincx, M., Bonne, W., Cattrijsse, A., Degraer, S., Dewicke, A., Steyaert, M., Vanaverbeke, J., Van Hoey, G., Stienen, E., Van Waeyenberghe, J., Kuijken, E., Meire, P., Offringa, H., Seys, J., Volckaert, F.A.M., Gysels, E., Hellemans, B., Huyse, T. & Pampoulie, C. 2004. Structural and functional biodiversity of North Sea ecosystems: species and their habitats as indicators for a sustainable development of the Belgian continental shelf. *Belgian Science Policy: scientific support plan for a sustainable development policy (SPSD-I)*, 94 p.