# D1.5c: Option for integrating pelagic indicators with other ecosystem components.

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#### List of abbreviations

COMP: Common Procedure FW: Food Web ENA: Ecological Network Analysis GES: Good Environmental Status LCBD: Local Contribution to Beta Diversity MSFD: Marine Strategy Framework Directive OSPAR: Oslo Paris Convention PH: Pelagic Habitats

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## 1. Introduction

The goal of the Marine Strategy Framework Directive (MSFD; 2008/56/EC) was to achieve and maintain Good Environmental Status (GES) of all European marine waters through the assessment of 11 Descriptors. The most recent assessment of GES in the North-East Atlantic was carried out using a suite of indicators through their single metric approach. However, current best practices in the field of environmental policy management involves applying the ecosystem approach, to better inform Ecological Status. This ecosystem approach can be carried out through synthetising several linked indicators into combined multi-metric indices which can provide additional meaning. Furthermore, for OSPAR there is a need for better integration within and across ecosystem components, as the establishment of the quality status in OSPAR relies on a large variety of indicators to assess MSFD criteria across multiple descriptors.

The ecosystem approach can be carried out by cross-linking relevant indicators within and across MSFD Descriptors. This approach is fundamental to the MSFD because it provides a holistic view of current environmental quality status. For the descriptor D1 Biological Diversity, work carried out previously for the EcApRHA project (Applying an Ecosystem Approach to (sub) Regional Habitat Assessment) established methods for integrating results from the Benthic Habitat indicators and the Food Webs FW4 'Mean Trophic Level' indicator (Eliott et al. 2017). More recently, a working group dedicated to the integration proposed different methods for integrating across D1C1 to D1C5 Marine Strategy Framework directive biodiversity assessments (Dierschke et al. 2021). However, the D1C6 assessment (Pelagic Habitats) remains to be integrated with other relevant indicators. Until now, the ecosystem approach for D1C6 has strictly focused on the integration of biological quality elements (plankton diversity, phytoplankton biomass, plankton lifeforms abundance and total zooplankton abundance) within Pelagic Habitats (Budria et al. 2017) and applied to the OSPAR convention (Holland et al. 2023). The integration of the Pelagic Habitat indicators assumes an understanding of the factors defining and mechanisms affecting plankton communities at multiple levels (species, lifeforms, biomass), including mechanisms which generate direct top-down and bottom-up effects on the plankton community. For the NEA-PANACEA project, we started the integration of the Pelagic Habitats with relevant pressure indicators (eutrophication) through MSFD descriptor D1.5b (Louchart et al. 2023a). At present, the integration between pelagic habitats with other biodiversity and food web components remains undeveloped.

The marine food web represents a network of complex prey-predator interactions among benthic, and pelagic organisms, fish, birds, and mammals. The marine food web begins with primary producers. Subsequently, food energy is transmitted up the food web until it reaches the top-predators. Therefore, the links between plankton with fish and mammals are well known. The relationship with the benthic habitats directly concerns only meroplankton, organisms which spend the first part of their life as plankton and the rest of their life as benthic organisms (e.g., echinoderms, decapods). Linkages between Pelagic Habitats and birds are more indirect and less obvious (through consuming benthic organisms and fish). These disparate components of the food webs are complex and support diverse ecosystems. Usually, the length of the food web and the number of nodes is used to describe this complexity. A short path from primary producers to the higher trophic levels implies more efficient transfer of energy when compared to longer food chains. In the latter case there are many trophic transfers where energy is lost. Regarding the interactions described above, it is obvious that any alteration of one level of the food web will have repercussions on the other levels. These changes can be induced by humans either through direct or indirect pressures on one or more levels of the food web (see Schückel et al. 2022). For these reasons, it is crucial to assess each ecosystem component, but also to conduct a full integration assessment to gain a more holistic view of GES for the complete marine food web.

This report provides a guide for the integration of Pelagic Habitats with Food Web, Mammals, Marine Birds and benthic habitats indicators. Indeed, the pelagic habitat diversity, lifeforms and biomass indicators (PH3, PH1/FW5 and PH2, respectively) from MSFD Descriptor 1 are linked to other Biological components through the Descriptor 4 (Food Web) of the MSFD, such as primary production indicators (FW2), biomass, species composition and spatial distribution of zooplankton (FW6), size composition in fish communities (FW3) and "Mean Trophic Level" (FW4) indicators. In order to get the best picture of the biodiversity and food webs descriptors, it is coherent to incorporate the Pelagic Habitat indicators with the other indicators of D1 and D4. Since OSPAR QSR 2023, the integration of biodiversity and food web indicators in OSPAR is done through the Ecological Network Analysis indicator (FW9; Schückel et al. 2022). Briefly, the FW9 is an ecosystem-based approach providing a holistic view of marine ecosystems by looking at all direct and indirect carbon fluxes from primary producers to top predators. Nevertheless, the integration across MSFD Descriptors remains challenging for several reasons. First, it is crucial to understand the relations and the mechanisms acting between the elements. This aspect is currently studied in the present report under the section Synergy between Pelagic Habitat and Food Web indicators. Then, these indicators may not be directly comparable because each descriptor has its own methodology to assess quality status. This report investigates first the synergies between Pelagic Habitat and Food Web indicators and then conceptualises the integration of Pelagic Habitat indicators with Benthic Habitat, Food Web, Marine Birds and Mammals indicators under the FW9 indicator.

# 2. Description of the indicators

## PH1/FW5 indicator

This indicator focuses on ecosystem function by measuring changes in the abundance of plankton lifeforms. Changes are identified based on whether trends in lifeform abundance are likely to be associated with parallel trends in pressures. Significant changes in the abundance of planktonic lifeforms represent important changes in ecosystem functioning and have consequences for food webs and trophic interactions.

Eight lifeforms were assessed, due to their ecological relevance and ease of identification (McQuatters-Gollop et al. 2019). Long-term lifeform abundance trends are assessed by calculating the nonparametric Kendall rank correlation coefficient for each time-series within each assessment unit. This test generates a statistic which is derived by comparing each value in a time-series with each of the values preceding it. The sign of the statistic test (i.e., positive or negative) reveals the direction of the trend, with a positive statistic indicating an increasing trend and a negative statistic indicating a decreasing trend.

To determine whether any changes in lifeform abundance are associated with parallel changes in the environmental pressure, first monthly time-series for both are smoothed to remove seasonal variation by calculating mean values for each time-series with a 12-month moving window. Then, a random forest algorithm is applied to assess the ability of environmental parameter time-series to predict the lifeform abundance time-series. Pressures are ranked in order of their predictive ability. This indicator is currently a common indicator in OSPAR Regions II, III and IV. Further information can be found in the OSPAR PH1/FW5 indicator assessment (Holland et al. 2023).

#### PH2 indicator

This indicator is based on the identification of phytoplankton biomass and zooplankton abundance trends within plankton time-series. Anomalies represent deviations from the assumed natural variability of a time-series. Thus, the greater the magnitude of the anomaly (in terms of absolute value, since anomalies can be positive or negative), the greater the change. An anomaly value of zero indicates no difference from the time-series mean (which must be de-seasonalised). To understand the changes presented (i.e., annual anomalies) and to be most useful for decision makers, annual anomalies are best interpreted with information provided by anomalies on monthly timescales.

Once the data are at monthly timescales, the time-series analysis can be run. The analysis uses an Rscript for both discrete-station data and non-station data, after the pre-analysis steps have been followed. The first step consists in identifying the mean seasonal cycle (which is called seasonality in this assessment) during the whole study period. Removing the seasonality is required to analyse the variations of each plankton compartment (i.e., phytoplankton biomass or zooplankton abundance) beyond their natural cycle. The second step consists in obtaining anomalies by subtracting this seasonality from the original time series. The method used is the seasonal differentiation by the seasonal deviation methods. Finally, the cumulative sum of these anomalies was produced to detect regime shifts in the time-series for the assessment and comparison periods. A Spearman rank correlation test is now implemented to test the trend of the cumulative sum of the anomalies of the assessment and comparison periods. The correlation can move towards a significant ( $p \le 0.05$ ) increase in phytoplankton biomass/zooplankton abundance (0 to 1), no changes (=0) or decrease in phytoplankton biomass/zooplankton abundance (-1 to 0). The results of the Spearman rank correlation provides an indication of change. A t-test against the cumulative sum of the anomalies of the comparison period and the assessment period provide information whether the trends are significantly different or not. This indicator is currently a common indicator in OSPAR Regions II, III and IV. Further information can be in the OSPAR PH2 indicator assessment (Louchart et al. 2022a).

#### PH3 indicator

PH3 is a complex multi-metric indicator which focuses on plankton diversity. The method focuses on  $\alpha$ -diversity (i.e., the diversity within a site or sample) and  $\beta$ -diversity, which focuses on the rate of change, or turnover, in species composition (Rombouts et al., 2019). For the QSR 2023, we used the  $\alpha$ - and  $\beta$ -diversity as consecutive steps to detect the temporal changes in community composition (through the  $\beta$ -diversity) and then to report the state of the community while changes were seen (through the  $\alpha$ -diversity). First, the beta diversity was computed and significant deviation from the overall composition was flagged. More specifically, the Local Contribution to Beta Diversity (LCBD) shows how much each observation in a time-series contributes to  $\beta$ -diversity; for example, a site with an average species composition would have an LCBD value of 0. Large LCBD values may indicate sampling units (in time) characterised by high conservation values, or degraded and species-poor sites that need restoration (Legendre and De Cáceres, 2013). High values may also correspond to special ecological conditions or may result from the disturbance effect of invasive species (i.e., differing from normal conditions in a positive or a negative way). When significant community composition was detected, the alpha diversity was investigated to observe whether the richness and/or the dominance were responsible. Assessment of richness was processed by the Menhinick index. The dominance of phytoplankton was assessed by the Hulburt index while the dominance of zooplankton was assessed by the Patten index. For the OSPAR QSR 2023, the plankton diversity is at the stage of candidate indicator in OSPAR Regions II and IV while it is a common indicator in OSPAR Region II. Further information can be in the OSPAR PH3 indicator assessment (Louchart et al. 2022b).

#### FW2 indicator

This indicator is based on the identification of trends in anomalies of primary production within timeseries. As primary production is closely related to phytoplankton biomass, we used the same methodology as for the Pelagic Habitat indicator PH2: 'Changes in phytoplankton biomass/zooplankton abundance'. Anomalies represent deviations from the assumed natural variability of a time-series. Thus, the greater the magnitude of the anomaly (in terms of absolute value, since anomalies can be positive or negative), the greater the change. An anomaly value of zero indicates no difference from the time-series mean trend (which must be de-seasonalised). To understand the changes presented (i.e., annual anomalies) and to be useful for decision makers, the annual anomalies must be considered using details given by the monthly anomalies (since an early warning indicator should be assessed at the highest temporal resolution possible). For the OSPAR QSR 2023, FW2 is at the stage of candidate indicator. Further information can be in the OSPAR FW2 indicator assessment (Louchart et al. 2022c).

#### FW6 indicator

In OSPAR regions, the "biomass, species composition and spatial distribution of zooplankton" indicator is at the stage of candidate indicator. Because this indicator is at an early stage of development no assessment for the OSPAR QSR 2023 was produced. In parallel to the present document, the deliverable D1.5a provides the first steps in the development of the FW6 indicator (Louchart et al. 2023b). Due to its obvious link with Pelagic Habitat and Food Webs indicators, FW6 is mentioned in this document but is not included in the exploratory statistical analysis prior to the integration.

#### FW9 indicator

The FW9 'Ecological Network Analysis' (ENA) indicator is an integrated indicator providing a holistic view of the food web. It focuses on the trophic interactions between biological elements of ecosystems by investigating the fluxes of carbon following a strict methodology. Prior the calculation, the ENA needs 3 types of information's per ecosystem (Schückel et al. 2022):

- A community table of biomass for planktonic, benthic organisms, fish, invertebrates, birds and mammals;
- (II) A table of energetic ratios containing physiological parameters;
- (III) A diet matrix.

Once these 3 tables are obtained per ecosystem, a flux matrix can be calculated giving the carbon transfer possible between the biological elements. While most of the carbon energy is transferred to an upper level, some carbon is lost. Therefore, the steady-state model includes respiration and detritus. The flux matrix represents the input matrix for the calculation of different ENA indices that

can be used to analyse the structure, diversity, functioning and robustness against pressures on the food web. Focusing on plankton, the FW9 indicator currently uses shared data products with the PH2 (phytoplankton biomass), FW6 (zooplankton biomass) and FW2 (primary production). In this report, we present the conceptualisation of the integration for pelagic habitat indicators into FW9 to establish the connectivity of Pelagic Habitats with Benthic Habitats, Food Web, Birds and Mammal indicators. For the OSPAR QSR 2023, a pilot assessment of the ENA indicator was produced for three assessment units within OSPAR Region II and one assessment unit within OSPAR Region V.

# **3.** Identification of synergy between Pelagic Habitat and Food web indicators

One sub-task within NEA-PANACEA activity 1 concerned synergies between the Pelagic Habitats and Food Webs indicators. This sub-task represents an important step because understanding the relation between the biological elements (related to the PH and FW indicators here) is fundamental in understanding the role of biodiversity and ecosystem functioning. Therefore, we have decided to include this task to NEA-PANACEA D1.5c as it defines the base of the network between Pelagic Habitats, Food Webs, Benthic Habitats and Birds. Consequently, any changes in one indicator should be related directly or indirectly to the other indicators. **Figure 1** displays the connections between the 5 OSPAR Pelagic Habitats and Food Web indicators. On this figure, we represent the links between the indicators as bidirectional except for between PH1/FW5 and FW6. Considering the example between PH1/FW5 and PH2, this bidirectional relationship means that the abundance of a lifeform can be a cause or a consequence of a biomass change. The generalisation of this example states that all the plankton indicators are dependant, directly or indirectly connected.



*Figure 1: Conceptualization of the network between Pelagic Habitats and Food Webs indicators and the direction of interactions.* 

# 4. Methodology

For this section, we focused on two assessment units where PH1/FW5, PH2, PH3 and FW2 have been produced to support the OSPAR QSR 2023 assessment. The decision to focus on only two assessment units was necessary for simplicity and the choice of assessment units was arbitrary. The prerequisite is to have usable results for the four indicators mentioned above. Finally, for the reason described in Section 2, FW6 'biomass, species composition and spatial distribution of zooplankton' is not included in this section. The link between two biological elements of the indicators is evaluated by modelling their relationship. Both linear and second order polynomial models are tested simultaneously. Each model is associated with a Root Mean Squared Error (RMSE) which is a measure of the average magnitude of the predictions. The choice of the best model is based on the smallest RMSE. In addition, the strength between two biological elements in each model is expressed by the R-squared (note R<sup>2</sup>). So, the higher the R-squared, the stronger the relation. Finally, a 3D scatter plot is used to integrate the relationship between three indicators.

# 5. Modelling between the biological quality elements of the indicators

## 5.1. Phytoplankton

## 5.1.1. Relationship between PH3 and PH1/FW5

The relationship between diversity (richness) and the abundance of diatom lifeform followed a unimodal pattern for the two assessment units presented here (**Figure 2**). While the relationship between the richness and the abundance of diatoms showed a concave down curve in the Channel Well Mixed assessment unit, the curve was concave up in the Northern North Sea assessment units. The points of inflexion were also obtained for different values, revealing ecological heterogeneity between the two areas. The R-square of both was low even if only evidence of a relationship between the two parameters exists in the Northern North Sea (p<0.05). This suggests that both parameters are linked but additional parameters may influence the relation such as abiotic and biotic parameters.



Figure 2: Polynomial model (order 2) of phytoplankton richness (given by Menhinick index) and the abundance of diatoms within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

In both assessment units, the dominance (Hulburt index) and diatoms abundance followed a unimodal pattern (Figure 3). A convex curve characterised both dominance models. The R-square was low and only significant for the Channel Well Mixed assessment unit. The low R-square suggests that additional abiotic or biotic parameters may influence the relationship.



PH1/FW5 - PH3 relationship

Figure 3: Polynomial model (order 2) of phytoplankton dominance (given by Hulburt index) and the abundance of diatoms within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

#### 5.1.2. Relationship between PH1/FW5 and PH2

Similar to PH1/FW5-PH3 models, the relationship between PH1/FW5 and PH2 followed a unimodal pattern for diatoms (**Figure 4**) and dinoflagellates (**Figure 5**). While the relation was insignificant for the Northern North Sea between the two variables, the model did not strongly explain the relation in the Channel Well Mixed area. The shape of the model was also different. The curve of the model in the Channel Well Mixed area was convex (hump-shaped) while it was concave in the Northern North Sea (U-shaped). The different shape of the curve revealed the heterogeneity of the biomass-diatom abundance relationship across assessment units. The low R-square value provided evidence that additional parameters may influence the relationship, such as abiotic and biotic parameters.



Figure 4: Polynomial model (order 2) of the abundance of diatoms and phytoplankton biomass within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.



Figure 5: Polynomial model (order 2) of the abundance of dinoflagellates and phytoplankton biomass within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

#### 5.1.3. Relationship between PH1/FW5 and FW2

The polynomial models between the abundance of diatoms and primary production showed a positive and significant relation for both assessment units (**Figure 6**). The models were similar across space. While the diatoms abundance accounted for 42% of the primary production variability in the Channel Well Mixed area, it accounted for 34% of the primary production variability in the Northern North Sea. The large dispersion relates the large variability of diatoms in their contribution to primary production. Similar to the PH1/FW5 and PH2 relationship and the PH1/FW5 and PH3 relationships, the curve followed a hump-shaped pattern.



*Figure 6: Polynomial model (order 2) of the abundance of diatoms and phytoplankton productivity within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.* 

Similar to diatoms abundance, the polynomial models between the abundance of dinoflagellates and primary production showed a positive relation for both assessment units (**Figure 7**). The models were similar across space. The relation obtained followed a unimodal distribution. The model revealed that maximum productivity was obtained at intermediate levels of diatom abundance. While dinoflagellates abundance accounted for 46% of the primary production variability in the Channel well mixed area, it accounted for only 22% of the primary production variability in the Northern North Sea.



Figure 7: Polynomial model (order 2) of the abundance of dinoflagellates and phytoplankton productivity within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

#### 5.1.4. Relationship between PH2 and FW2

The polynomial models between phytoplankton biomass and primary production showed opposite relationship, depending on the assessment units investigated (**Figure 8**). While the biomass could potentially explain an important amount of the variability of primary production in the Channel well mixed assessment unit, there was no relation in the Northern North Sea. Phytoplankton biomass explained roughly 50% of the primary production variability in the Channel well mixed area.



*Figure 8: Polynomial model (order 2) of phytoplankton biomass and phytoplankton productivity within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.* 

#### 5.1.5. Integration between three biological quality elements

We found contrasting relationship between diatom abundance (PH1/FW5), phytoplankton biomass (PH2) and primary production (FW2) between the two assessment units. The best fitting model was the additive polynomial model (RMSE = 0.28) for CWM and multiplicative polynomial model (RMSE = 0.20) for NNS. Both models explained 43% of variance. The results showed that the ecosystem was more productive for intermediate values of biomass and abundance (**Figure 9**). The results were consistent with the observations made in sub-section 5.1. which examined two-variable models. These results are supported by the intermediate disturbance hypothesis theory (IDH; Connell, 1978) which states the maximum productivity was obtained at intermediate levels of abundance or biomass.



*Figure 9: 3D scatter plot between diatoms abundance (PH1/FW5), phytoplankton biomass (PH2) and primary production (FW2) for CWM (A) and NNS (B) assessment units. The grid represented the best fitting model explaining primary production.* 

There are single and linear relationships between the PH3 (richness and dominance), the PH1/FW5 (diatoms and dinoflagellates) and phytoplankton biomass. The maximum phytoplankton richness (PH3 indicator) is obtained at high diatom abundance (PH1/FW5) and for high phytoplankton biomass. The relationship presented in figure 10 is very different to the unimodal distribution observed in figure 9.



Figure 10: 3D scatter plot between diatoms abundance (PH1/FW5), phytoplankton richness (PH3 and phytoplankton biomass (PH2) for the CWM assessment unit. The grid represented the best fitting model explaining phytoplankton biomass. The NNS area is not displayed as the R-squared is less than 0.01, thus no relation existed between the variables.

## 5.2. Zooplankton

## 5.2.1. Relationship between PH3 and PH1/FW5

**Figure 11** showed an overall pattern in which the highest species richness is obtained for the lowest abundances for each lifeform. Most models showed a strong relationship between the biological elements of PH1/FW5 and PH3 except for small copepods, large copepods and meroplankton in the Channel Well Mixed assessment unit, however, all these relationships were statistically significant.



Figure 11: Polynomial model (order 2) of zooplankton richness and zooplankton lifeforms (small copepods, large copepods, holoplankton and meroplankton) within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

**Figure 12** displays the relationship between the zooplankton dominance index (PH3 indicator) and zooplankton lifeforms (PH1/FW5 indicator). Unlike the PH1/FW5 and species richness relationship, the relationships vary according to the evaluation unit considered and by lifeform. While the highest dominance was reached for the lowest abundance for each lifeform in Channel Well Mixed, the pattern was different in the Northern North Sea. A weak but significantly decreasing relationship was found for small copepods and holoplankton versus zooplankton dominance. No significant relationship between large copepods and meroplankton with zooplankton dominance.



Figure 12: Polynomial model (order 2) of zooplankton dominance and zooplankton lifeforms (small copepods, large copepods, holoplankton and meroplankton) within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

#### 5.2.2. Relationship between PH1/FW5 and PH2

**Figure 13** showed an overall pattern in which the largest zooplankton abundance was obtained for the largest abundance for each lifeform. Most models showed a strong relationship between the biological elements of PH1/FW5 and PH2 except the meroplankton in the Channel Well Mixed assessment unit. However, all these relations were significant. This positive relation was expected between the zooplankton total abundance and small and large copepods and holoplankton while the relationship between meroplankton and zooplankton total abundance was expected to be weak or even insignificant.



Figure 13: Polynomial model (order 2) of zooplankton total abundance and zooplankton lifeforms (small copepods, large copepods, holoplankton and meroplankton) within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

#### 5.2.3. Relationship between PH3 and PH2

In both assessment units, the relationship between the zooplankton diversity indices (richness and dominance, PH3 indicator) and zooplankton total abundance (PH2) was significant. The strength of the relationship was higher between the zooplankton total abundance and richness ( $R^2_{CWM} = 0.44$  and  $R^2_{NNS} = 0.64$ ) than between the zooplankton total abundance and dominance ( $R^2_{CWM} = 0.28$  and  $R^2_{NNS} = 0.10$ ). The highest values of dominance and richness were obtained for the lowest abundance of zooplankton. The shape of the relationship between total zooplankton abundance and richness was concave while the shape of the relationship between total zooplankton abundance and dominance

was convex. This means that richness decreased less rapidly than dominance at low total zooplankton abundance while richness decreased more rapidly than dominance at high total zooplankton abundance.



log10 Abundance

Figure 14: Polynomial model (order 2) of zooplankton diversity (top: richness; and bottom: dominance) and zooplankton total abundance within the Channel well mixed (CWM) and the Northern North Sea (NNS) assessment units.

## 5.3. Relationship between phytoplankton and zooplankton

The integration between three biological quality elements within the pelagic food web showed that the best models were multiplicative polynomial model in the CWM and NNS assessment units. In the Northern North Sea assessment unit (**Figure 15**), the best biodiversity models included large copepods abundance for the PH1/FW5, primary production (FW2) and phytoplankton richness (PH3) and

holoplankton abundance (PH1/FW5), primary production (FW2) and phytoplankton richness (PH3). The relationships were weak despite being significant ( $R^2 = 0.24$  and  $R^2 = 0.27$  considering holoplankton and large copepods abundance, respectively).



Figure 15: Biodiversity pattern of phytoplankton in the Northern North Sea assessment units. Left panel: Phytoplankton richness, as expressed by the Menhinick index plotted as a function of primary production and large copepods (> 2  $\mu$ m) abundance. Right panel: Phytoplankton richness as expressed by the Menhinick index plotted as a function of primary production and holoplankton abundance.

In the Channel Well Mixed assessment unit (**Figure 16**), the best models included large copepods abundance for the PH1/FW5, primary production (FW2) and phytoplankton dominance (PH3) and holoplankton abundance (PH1/FW5), primary production (FW2) and phytoplankton dominance (PH3). The relationships were weak despite being significant ( $R^2 = 0.20$  and  $R^2 = 0.19$  considering holoplankton and large copepods abundance, respectively).



Figure 16: Biodiversity pattern of phytoplankton in the Channel Well Mixed assessment units. Left panel: Phytoplankton dominance, as expressed by the Hurlburt index plotted as a function of primary production and large copepods (> 2  $\mu$ m) abundance. Right panel: Phytoplankton dominance as expressed by the Hurlburt index plotted as a function of primary production and holoplankton abundance.

# 6. Integration of Pelagic Habitat indicators with Benthic Habitat, Birds, Mammals and Food Web within the FW9 indicator

## 6.1. Conceptualisation of the integration across the different biological elements

. It is widely recognised that plankton dynamics is highly variable in space and time. Plankton dynamics depend on combined interaction of "bottom-up" processes where the physico-chemical properties of the environment are the cause of the changes, and on the so-called "top-down" relationships where the action comes from the higher trophic levels. Therefore, plankton integration within the marine ecosystems is complex because of its connexion to many different levels. It represents the connection between several descriptors of the MSFD (D1: Biodiversity; D4: Food webs and D5: Eutrophication). Some biological elements and their connection are investigated in NEA-PANACEA D1.5b (Louchart et al., 2023b).



Figure 17: Conceptualization of the integration of the Pelagic Habitats with Eutrophication, Food webs, Benthic Habitats and Birds.

At present, the OSPAR food web thematic assessment provides a holistic picture of the biodiversity indicators within the FW9 indicator (**Figure 17**). In **Figure 17**, we resume the ecological network of the indicators integrated in the D1.5b of NEA-PANACEA to the indicators integrated in NEA-PANACEA D2.2 (FW9 indicator; Schückel et al., 2022). The connection between most indicators is a two-way path (e.g. PH2 acting on FW6 and FW6 acting on PH2) even if some of them are one-way (e.g. FW6 to benthos).



Figure 18: Integration flow between D1 (Biological diversity) and especially the D1C6 (Pelagic Habitats), D4C1 (diversity of trophic guild), D4C2 (Balance of total abundance between the trophic guilds) and D4C4 (Productivity of trophic guild). Adapted from Magliozzi et al. (2021).

The first level of consideration for a good integration across MSFD descriptors starts by applying consistent 'Elements' and 'Scales and areas' (Figure 18). According to Magliozzi et al. (2021), the term 'Elements' refers to the 'essential characteristics of the criterion to be evaluated'. The 'Elements' are common and defined as the four types of habitats, i.e. variable salinity, coastal, shelf, and oceanic/beyond shelf habitats. The term 'Scales and Areas' refers to the 'subdivision of the region or subregion to assess'. We added the temporal resolution to 'Scales and Areas'. This step is mixed because the assessment of the FW9 and the Pelagic Habitats indicators is assessed at the COMP4 scale while the temporal resolution is assessed at monthly scale for the Pelagic Habitats indicators and the annual scale for the FW9. More precision can be found in the related OSPAR indicators. The FW9 indicator processed the integration of Benthic Habitat, Birds, Mammals and Food Webs at a unique scale of "elements" and "scales and areas" (Schückel et al. 2022) despite different 'Elements' and 'Scales and Areas' of assessment between these themes. This includes the grouping of all species in the food web into different trophic guilds. The 'Element' step is achieved at the scale of the habitats as described earlier while the 'scales and areas' step is defined by the OSPAR common procedure (COMP). The COMP aims to define the OSPAR maritime area by a set of ecologically and physically distinct areas or spatial units. For the current version of COMP (COMP4), the parameters used to differentiate these areas include physical, chemical, and biological factors: depth, salinity,

stratification, suspended particulate matter and primary production. Consult Enserink et al. (2019) for a more detailed description of the procedure used to define assessment units.

# 6.2. Connectivity of Pelagic Habitats indicators with components of FW9

The incorporation of Pelagic Habitats (PH1/FW5, PH2 and PH3) and Food Web pelagic indicators (FW2 and FW6) within the FW9 "Ecological Network Analysis" indicator can occur at different levels:

- Zooplankton:
  - Meroplankton lifeform (PH1/FW5) and Benthic Habitats: Meroplankton represent organisms that are planktonic only during the larval (and in some cases juvenile) phase of their life cycle. The other phase of their life cycle is spent on the seafloor.
  - Zooplankton abundance (PH2), zooplankton diversity (PH3) and biomass, species composition and spatial distribution of zooplankton (FW6).
- Phytoplankton:
  - Diatom and dinoflagellate lifeforms (PH1/FW5) with primary production (FW2) and phytoplankton biomass (PH2)
  - Phytoplankton diversity (PH3) with primary production (FW2) and phytoplankton biomass (PH2)

# 7. Discussion

# 7.1. Synergies between indicators

The unimodal pattern is commonly observed in the aquatic ecosystems especially for marine phytoplankton and zooplankton (e.g. Irigoien et al. 2004) and described as the Intermediate Disturbance Hypothesis (IDH; Connell, 1978). This type of relation has been used as evidence for describing richness-biomass, richness-production and abundance-biomass relationships. In general, at low levels of productivity (biomass and/or primary production), the balance is controlled by bottom-up effects. Under food limited environment only the slow-growing specialists with high affinity for the available food can grow, resulting in a limited richness. Thus, the low richness at low levels of productivity is the consequence of an unproductive environment. At intermediate levels of nutrient availability, richness is at its highest level because slow-growing specialists and fast-growing opportunists can grow and coexist. At higher values of nutrient supply, the observations of low diversity of phytoplankton and high productivity are inconsistent with the theory of enrichment. This last pattern is often explained by increasing competition of some species for resource acquisition. In such cases, the reduction of richness at high levels of productivity is consistent with an increase in dominance. This observation is typically observed during massive phytoplankton blooms that escape predation.

Although nutrient concentrations shape phytoplankton biomass which in turn affect higher trophic levels, nutrients stoichiometry in the environment also impacts diversity and biomass (Gerhard et al. 2022). This is known by the Resource-supply ratio hypothesis (Tilman, 1982). This hypothesis suggests that the replacement and/or coexistence of species is a function of the ratio of limiting nutrients (Tilman, 1982). In addition, water transparency can impact diversity. Water transparency can be affected by plankton, through higher biomass or abundance or larger cells or by the concentration of suspended particulate matter in the water column.

An additional explanation to the reduction of richness at high levels of productivity (biomass and/or primary production) is marked by a substantial pressure of predation of zooplankton on phytoplankton (Irigoien et al. 2004). However, zooplankton grazing on phytoplankton is a complex behavioural phenomenon. Prey-size, morphology, abundance and nutritional quality determine the preference for particular prey types. Thus, at high levels of productivity (biomass and/or primary production), the balance is in favour of selective predation (Wirtz 2012) which in turn may drive habitat-specific patterns of diversity change (Irigoien et al. 2004). The unimodal pattern in zooplankton diversity can be interpreted similarly to the unimodal pattern in phytoplankton diversity, resulting as a balance between food limitation at low population levels and selective predation at high population levels (Irigoien et al. 2004, Hillebrand and Lehmpful, 2011). However, this model is less evident and does not fully support the IDH of Connell (1978).

Despite the unimodal pattern is very common, some pairs of biological elements and some integration between three biological elements do not follow this theory. While we found a positive relationship between richness and phytoplankton biomass (**Figure 10**), Irigoien et al. (2004) found that the minimum of diversity is found for maximum values of phytoplankton biomass. This is even more striking for zooplankton, which only followed the unimodal relationship for the link between diversity and total zooplankton abundance. This can be explained by the fact that the relationships between biological elements are habitat-specific since the study of Irigoien et al. (2004) is not restricted to one habitat type but includes several habitats at global scale model while our study only concerns a subdivision of habitats at the scale of the North-East Atlantic. This assumption is largely supported by the diversity theory of Whittaker et al. (2001) which states that the increasing spatial scale can bias the relationship between diversity and productivity and to some extend to abundance. It is also possible that high plankton biomass is never reached because it is consumed too quickly by predators thus our model never reached the equilibrium. This latter hypothesis is even stronger as we are focusing on planktonic organisms which live in a permanently moving environment, from the micro to the macroscale.

## 7.2. Integration of Pelagic Habitats and Food Web indicators within the FW9

The FW9 is a holistic and powerful indicator providing a status of biodiversity and food webs descriptors of the MSFD through an ecosystem-based approach. The FW9 is currently integrating (phytoplankton) primary production, zooplankton (production and biomass), fish, birds and mammals through food web indicators. Nevertheless, plankton functionality and diversity and phytoplankton biomass are not currently implemented. Therefore, the FW9 can link the pelagic habitat indicators and pelagic food web indicators in a qualitative and quantitative way.

#### Knowledge gaps:

There are still challenges to overcome prior integrating the Pelagic Habitats indicators within the FW9. This section discusses the various aspects to consider running the most effective and accurate integration possible as seen by the pelagic indicators perspective and considering the existing methodology of the FW9.

- Identification of end-to-end datasets. To perform reliable and accurate integration within the FW9, there is a need to identify areas with the most complete data sets to obtain a picture of the whole food web (from plankton to mammals and birds). An inventory of data should be realised by OSPAR region, within each habitat of each OSPAR region or for each assessment unit.
- Defining an appropriate temporal scale. The ENA model is built at the annual scale. Although it is quite easy to incorporate the plankton bulk and fluxes measurements (PH2, FW2 and FW6) as they can be assessed at annual scale, lifeforms (PH1/FW5) and species composition (PH3) indicators represent a thorny issue to the network because both plankton lifeform and species are highly dynamic in space and time justifying the monthly computation. In order to match to scale of the FW9, additional development of PH1/FW5 and PH3 towards an annual index could significantly improve the integration. One possibility could be the use of the Ecological Quality Ratio. The definition of the appropriate temporal scale depends also on the data available which sometimes are lower than the annual resolution.
- Spatio-temporal resolution of the datasets. Most of the time winter months are not sampled or used in assessments. Considering only the productive period may miss early initiation of phytoplankton blooms. In addition, in some habitats (such as the shelf and oceanic/beyond shelf habitats) the major size class during the productive period is picophytoplankton which is not yet considered in PH1/FW5 and PH3 (Holland et al. 2023). Finally, one species which might have a strong ecological importance at one place might not have the same ecological importance in another place. This interaction is already set up as the first step of the ENA

model for many organisms, but it is important to recall it for plankton organisms as Pelagic Habitats indicators are not yet implemented in the integration. This important knowledge gap is closely related to the third knowledge gap on lifeform consideration.

- Consideration of sub-trophic guilds in the FW9 for Pelagic Habitat integration. The FW9 indicator is based on trophic guilds. The PH1/FW5 indicator is based on lifeforms. However, a lifeforms are not strictly associated to one trophic guild. There may be several guilds within a lifeform (i.e., dinoflagellates). For the purpose of the integration, sub-trophic guilds should be defined, considering the methodological criteria of the PH1/FW5 and FW9 indicators.
- Inadequacy of lifeform consideration. Typical assessments of Pelagic Habitats consider diatom and dinoflagellates species. Nevertheless, some lifeforms of important ecological interests in some assessment units are not yet considered. For example, *Phaeocysits globosa* which represents up to 80% of the total phytoplankton biomass of the spring blooms in the Southern North Sea and Eastern English Channel (e.g. Louchart et al. 2020) is not considered by the PH1/FW5 indicator as a distinct entity for assessment, while it is currently assessed by the PH3 indicator. Another example concerns the lack of consideration of pico- and nanoplankton size fractions which usually dominate abundance biomass and diversity, and perform a significant trophic role (De Vargas et al., 2015) relevant to marine food webs and carbon export (Leblanc et al., 2018). Small plankton is neither considered by the PH1/FW5 nor the PH3 indicator (Holland et al. 2023). We must be particularly attentive to this point because the plankton communities of the Northeast Atlantic are changing from microplankton dominated to nano- and picoplankton size classes due to lower river runoff degrading the food webs (Schmidt et al., 2020). This change disrupts marine food webs.
- Methodological development for lifeform inclusion within the FW9. Information on biomass, trophic interactions (food and predators) and carbon content estimation of the eight existing plankton lifeforms (holoplankton, meroplankton, small and large copepods, diatoms, dinoflagellates, gelatinous plankton, fish larvae/eggs).
- Specificity of interactions between indicators within and in between the four habitat types (variable salinity, coastal, shelf, oceanic/beyond shelf habitats). Based on the results highlighted by the section *Identification of Synergy between pelagic habitat and food web indicators*, the interaction of Pelagic Habitats and Food Web indicators is further complicated by the fact that relationships between indicators are both habitat and scale-specific. There is no single ecological theory to explain the relationships between the biological elements of the indicators, but the relationships result from the combination of several ecological theories.

- Lack of knowledge about the traits for many planktonic species. diet, carbon content, trophic interactions.

# 8. Conclusion

Integrating across MSFD descriptors provides a holistic view of marine ecosystems for the purpose of marine management. Recent improvement within the NEA-PANACEA project have now made it possible to integrate within and across Pelagic Habitats indicators, within and across Food Webs indicators through the Ecological Network Analysis model (the FW9 indicator). This report focused on an integration approach centred on plankton. First, we identified the connections between existing plankton indicators and already integrated biological elements (e.g. Benthic Habitats, Mammals, Birds and Food Web indicators). Then, we identified critical knowledge gaps that need to be addressed prior running the integration of Pelagic Habitats indicators within the ENA model.

Additionally, we explored synergies and antagonisms between pelagic indicators (including Pelagic Habitats per se and pelagic Food Web indicators). The case study demonstrated that the relationships between plankton indicators are habitat type-specific and that variation in relationships also exists between assessment units within the same habitat type. No single ecological theory can explain the origin of variation, but rather a combination of several theories can be useful. The identification of the type of interaction between indicators within and between the four pelagic habitat types has been identified as a priority for improving reliability for the integration of plankton into the Food Web. It is hoped that this collaboration between working groups will enhance the relevance of the integration between plankton indicators under Descriptors 1 and 4.

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