Changes in Arctic Benthos

Objectives

The shift towards a seasonally ice-free Arctic Ocean raises questions related to the future of productivity and function of Arctic ecosystems.

We use biological trait analysis (BTA) to study benthic functions and responses in the Eurasian part of the Arctic Ocean along a gradient of depth and latitude and compare the results between the years 1991 and 2012.

Fig. 1 Study area and dataset. The data from the Barents Sea were published in Kendall (1996), data from Nansen and Amundsen Basin and Lomonosov Ridge in Kröncke (1994, 1998), data from 2012 (sampled on the Polarstern cruise ANR-XXIV/3) are included in Degen et al. [in press].

Method

The BTA uses a series of life history, morphological and behavioral characteristics of species present in assemblages to indicate ecological functioning (Bremner et al. 2006). Traits for every taxon were fuzzy coded (i.e. scored a number between 0 – 3, where 3 indicates high affinity and 0 indicates no affinity for a certain trait).

Here we used 11 traits and 39 trait modalities:

1. Size < 5 mm
2. L > 5 – 20 mm
3. Larval Development Settlement
4. Body Form Flattened
5. Body Form Mounded
6. Morphology Eel
7. My
8. Exaration
9. Ctenophora
10. Ctenophora
11. Ctenophora
12. Ctenophora
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As we consider benthic secondary production (P) the most important factor, all fuzzy coded traits were P weighted. P was estimated with an ANN model (see Brey 2012).

Functional diversity was estimated with Rao’s quadratic entropy index (QEI) (Champely and Chessel 2002). Similarity between P weighted trait distributions was assessed via cluster dendrograms constructed from Bray-Curtis similarity values.

Results

Highest secondary production occurs on the Barents Sea shelf (> 6 g C m-2 y-1), second highest on the Lomonosov Ridge and lowest in the Arctic basins (Fig. 2). This pattern is also visible in the functional diversity index (FDI) which is significantly higher for the Barents Sea and the Lomonosov Ridge compared to the deep Amundsen Basin stations from 1991 (Fig. 3), depicting the strong correlation of P and functional diversity. Cluster analysis of P weighted biological traits clearly separates the 1991 Amundsen Basin stations from the higher productive stations of the Barents shelf (cluster 1) and Lomonosov Ridge (cluster 2) (Fig. 5).

1991 vs 2012

Nansen Basin stations show high heterogeneity and seem not much different between 1991 and 2012 (Fig. 2, 4, 5). Stations from Amundsen Basin 2012 showed a higher number of species (Fig. 4) and functional diversity (Fig. 3) compared to 1991. Also P was higher in Amundsen Basin 2012 and four stations cluster together with the intermediate-production stations from 1991 in Cluster 2 (Fig 5). Fig. 6 shows the sea ice minimum in 2012 and indicates that the stations from Amundsen Basin 2012 showing higher P might be influenced by processes related to sea ice reduction.

Fig. 2 Secondary production of the 26 stations sampled in 1991 (yellow) and the 14 stations sampled in 2012 (green) (note the difference in scale in the legend between 1991 and 2012).

Fig. 3 Functional Diversity Index (FDI) and standard deviation between regions and years (the letters above the bar chart indicate significant differences between regional groups as identified with ANOVA and a Post Hoc test).

Conclusions

Demand for a ‘Functional Trait Atlas’

By analyzing biological traits we can show that macrobenthic communities in the Arctic have changed in the last twenty years. The regions prone to change seem to be the regions under direct influence of a changing sea ice cover (Fig. 6). An arctic-wide atlas of functional traits in combination with a pan-arctic benthos database (see PANABIO project) would enable us to analyze the ongoing changes on a large scale and predict future scenarios.

Fig. 6 The sample stations in relation to the sea ice minimum in 2012. The red line indicates sea ice extent in the year 1991.

Fig. 4 Number of species in Nansen and Amundsen Basin 1991 (yellow) and 2012 (green).

Fig. 5 Results of the cluster analysis based on Bray-Curtis similarity of production weighted traits per station (left) and MDS plot (right). The analysis clearly groups the high (cluster 1), intermediate (cluster 2), low and very low (clusters 3, 4, and 5) production stations together.