Coherent change in multiyear trends of chlorophyll and bacterioplankton

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Abstract

The effects of climate variability and change on pelagic marine ecosystems are often sought as a signal propagated from primary producers to secondary producers. Yet the space and time scales of direct interaction between phytoplankton and other parts of the food web are much smaller than those of climatic drivers. A question arises whether trophic linkage can be discerned at multiyear scale. We demonstrate from regional studies in the North Atlantic that multivear concentration chlorophyll changes in are accompanied by dampened changes in bacterioplankton abundance. The coherent departure from norm, both positively and negatively, of both microbial primary and secondary producers is consistent with a directed system level change.

Introduction

The ecological coupling between phytoplankton and bacteria is a primary step in the transfer of carbon and energy through marine ecosystems. The coupling is mediated through organic substrates that include labile exudates released during photosynthesis, egesta released by grazers have consumed phytoplankters, that and cytoplasmic materials released by viral lysis and algal autolysis. These cellular processes occur within the short life span of microbes and in the close vicinity of activity microzones. Through upward hierarchical nesting of time and space, these cellular interactions may eventually become evident as ecosystem level associations spanning multiyear periods and regional ocean areas. On the other hand, complex interactions may weaken or even obscure the apparent link at large scales. Here, we explore the coherence in multiyear change of chlorophyll concentration (*Chl*) and bacterioplankton abundance (*Bac*) in large neritic and oceanic regions of the northwest Atlantic Ocean.

Study areas

The Labrador Sea AR7W ocean monitoring transect (Fig. 1) comprises 28 hydrographic stations that extend from the Labrador Shelf (LS, stations 1-10), through the central Labrador Basin (LB, stations 11-23), to the Greenland Shelf (GS, stations 24-28). These stations have been sampled once every year since 1994 in spring or early summer.

The Scotian Shelf has been sampled every year since 1997 in the spring and the fall. Three cross-shelf transects (Fig. 1) monitor downstream flow from the eastern shelf (LL, Louisbourg Line), to the central shelf (HL, Halifax Line), and to the western shelf (BBL, Browns Bank Line). Each line consists of 7 core stations.



Fig. 1. Station map showing the 6 study areas: Labrador Shelf, Labrador Basin, Greenland Shelf, Eastern Scotian Shelf, Central Scotian Shelf, and Western Scotian Shelf

Observations and anomalies

At every hydrographic station, depth profile measurements of *Chl* and *Bac* are integrated over the upper 100 m of the water column (I). Log-transformed integrated values for individual stations are averaged within each of the 6 study areas to yield area-specific observation time series (Fig. 2A,B).

For each of the 49 stations, a multiyear seasonaverage (station norm) is calculated for the logtransformed variables. The departure of each station observation from its associated norm, expressed in standard deviate units, is the normalized (standardized) anomaly. In each of the 6 study areas, the condition and variability in each year is given by the average and standard deviation of normalized anomalies for all stations within an area (Fig. 2C,D).



Fig. 2. Labrador Shelf time series . (A) Station-averaged depth-integrated chlorophyll concentration. (B) Station-averaged depth-integrated bacterioplankton abundance. (C) Station-averaged normalized anomalies of chlorophyll concentration. (D) Station-averaged normalized anomalies of bacterioplankton abundance.

Matching anomalies

Year-to-year, the degree of match between *Chl* and *Bac* anomalies varies by region and by season (Fig. 3). The match may be fairly strong, as on the Labrador Shelf (Fig. 3A, Kendall's $\tau = 0.36$, p = 0.10); or not evident at all, as on the Western

Scotian Shelf in spring (Fig. 3C, Kendall's $\tau = 0.13$, p > 0.10). This suggests that in some circumstances of place or time, the 2 trophic groups may be driven by different forces at the interannual scale.



Fig. 3. Time series of normalized anomalies for chlorophyll concentration (solid line) and bacterioplankton abundance (dashed line). (A) Labrador Shelf. (B) Greenland Shelf. (C) Western Scotian Shelf, spring. (D) Western Scotian Shelf, autumn.

Coherent change

In spite of many mismatches in anomalies from year to year, there appears to be a coherence in the direction and magnitude of change over the long term. In other words, *Chl* and *Bac* are generally both higher or both lower in recent years compared to earlier years. For example, on the Greenland Shelf (Fig. 3B), recent *Chl* is 17 times its earliest value, and recent *Bac* is over 3 times its earliest value.

With only a few exceptions, the linear rate of multiyear change in *Chl* and *Bac* anomalies (standard deviate units per year) is statistically indistinguishable from zero. However, this does not obscure the fact that large positive change in *Chl* is usually associated with large positive change in *Bac*; and vice versa, large negative change in *Chl* is usually associated with large negative change in *Bac*.

Over the entirety of the 6 ocean areas and the 2 seasons on the Scotian Shelf, the 9 study cases indicate a positive association between long term change in the 2 trophic groups (Fig. 4). This association is statistically significant (Kendall's $\tau = 0.56$, p = 0.05, n = 9), despite an apparent outlier (Eastern Scotian Shelf, autumn) indicating that the largest observed decrease in *Chl* is not accompanied by a commensurate change in *Bac* (Fig. 4).



Fig. 4. Nonparametric association between multiyear rates of change in the normalized anomalies of chlorophyll concentration and bacterioplankton abundance.

Conclusions

We have discerned an ecosystem level association between microbial primary producers and secondary producers that transcends interannual variation. Although coherent change across trophic levels is consistent with bottom-up control, we do not assign causation because the correlative approach provides only weak inference. It remains to be seen if the changes in phytoplankton and bacterioplankton are evidence of a system-level signal that propagates from the abiotic environment through lower trophic levels to higher trophic levels.

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References

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