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ON THE MESOSCALE HETEROGENEITY OF THE BALTIC SEA PELAGIC ENVIRONMENT: SOME METHODOLOGICAL INFERENCES OF THE JOINT STUDY PEX'86

Abstract. During the Patchiness Experiment (PEX '86) very complicated mesoscale patterns of the biological and chemical parameters in the upper layer of the Baltic Proper were described, but so far only a few attempts have been made to explain them. The available explanations can be grouped into two main types — structural and genetic. The structural explanation refers to the occurrence, 'development, and interactions of several mesoscale planktonic ecosystems. The concrete processes accounting for the formation and development lines of particular mesoscale patterns in terms of "cause-effect" chains are the object of the genetic explanation. There is still no adequate genetic explanation of the biological-chemical patterns recorded in PEX.

Key words: Patchiness, mesoscale variability, pelagic ecosystem, explanation, Baltic Sea.

Introduction

The mesoscale patterns (patchiness) of pelagic environmental and biological (plankton) parameters have largely been beyond the scope of traditional research strategies. An international joint study — the Patchiness Experiment (PEX '86), conducted in 1986 — was aimed at investigating this phenomenon during the spring phytoplankton bloom in the central Baltic Sea. Almost all countries around the Baltic with altogether 14 ships and the scientific personnel of about 150, were engaged in the project. The two main objects of the study had been formulated as follows:

(1) to observe the spatial and temporal scales of the biological and chemical fields in the Baltic Proper;

(2) to understand the processes generating the observed patchiness in terms of physical and biological processes (Dybern and Hansen, 1989).

In short, they can be reformulated into (1) description and (2) explanation; the terms indicating different steps of the scientific procedure.

By now the PEX endeavour is coming to an end. The results have been presented in General Report, Vols. 1 & 2 (Dybern and Hansen, 1989) and in several scientific papers (Fonselius et al., 1989; Passow, 1990; Kahru et al., 1990; Kahru and Nõmmann, 1990; Nõmmann and Kaasik, 1990; Kononen et al., 1990; Nõmmann, 1990), to mention but those on chemistry and biology.

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An analysis of the PEX'86 results from the standpoint of the abovementioned description-explanation ratio reveals an enormous disbalance: in General Report Vol. 1 (text) less than 20 from the 100 pages are devoted to explanation, and most of these 20 pages deal with physical events. Some more attention has been paid to the explanation of biological-chemical patterns by Passow (1990) and Nommann (1990); nevertheless, the descriptive approach is overwhelming. In this paper I attempt to analyse the manner and limits of available explanations of chemical-biological patterns recorded in PEX '86.

Description

A striking spatial heterogeneity in the distribution of several biological, chemical and physical parameters in the PEX area was recorded at the very beginning of the study, on April 25. Therefore below I will refer to the situation on this day. Figs. 1 and 2 demonstrate that the variability of the parameters occurred over the whole PEX window. The correspondence between the distribution patterns of various parameters varied from clear coincidence to only more or less detectable overlapping or even no visible correlations. Both sharp gradients and smooth continuum-like changes are represented.

According to the methodology of science the available explanations of the picture described above can be grouped into two main classes: structural and genetic.



Salinity



 $NO_2 + NO_3$



PO4

Chlorophyll a

Fig. 1. Spatial distribution of salinity, NO_2+NO_3 (µmol/l), PO₄ (µmol/l) at 10 db level, and chlorophyll *a* concentration (µg/l) in 0–10 m layer in the PEX area (20×40 n.mi.) on April 25.

The shaded area in the left side of the window denotes the low salinity water mass, on the right side — the high salinity water mass. The dotted line circles in the medium salinity area mark the anticyclonic eddy (left) and cyclonic eddy (right) domains. The salinity panel is provided by J. Elken, nutrients are redrawn from Fonselius et al. (1989), chlorophyll a from Dybern and Hansen (1989).



T. levanderi







< 5 · 10⁴ 5 - 10 · 10⁴ 10 - 15 · 10⁴

> 15 · 10⁴ cells /dm³

Chaetoceros spp.



A. taeniata



S. costatum



Structural Explanation

In case of structural explanation the heterogeneity of variables is explained by treating it as consisting of several qualitatively different compartments. This approach involves a threat of tautology. It arises if in the first step the study area has been divided into several domains on the basis of the patterns of the variables investigated, and in the next step, vice versa, the occurrence of the distribution patterns of variables is rationaled through the existence of different domains. Nikitin (Никитин, 1970) and Harvey (Харвей, 1974) showed that the tautology can be avoided by including into explanation theoretical generalizations, independent of the phenomena to be explained.

Physical oceanographers distinguish several structural entities within the PEX area: on the basis of salinity data it is divided into three independent water masses; thereafter, from the analysis of hydrodynamic characteristics is deduced the occurrence of two substructures — eddies — in one of them (see Fig. 1, salinity) (Elken and Kõuts, 1989). The theoretical foundation for the distinction of these structures is derived from the theory of physical oceanography. This enables to avoid tautology and give a structural explanation to the variability of physical parameters.

Among marine chemists and biologists the mesoscale differentiation of the pelagic environment has been largely limited to identifying "patches" of various parameters investigated (Dybern and Hansen, 1989), although one feels intuitively that in the case of coincidence of several patches there should be from ecological standpoint something more than merely "multipatch" (the term provided by Aitsam, 1989). Being neutral to any theory the term "patch" is just a descriptive one, it does not have any explanatory value itself. Using it for explanation one faces tautology as mentioned above.

Since Passow (1990), biologists have based their approaches on the division of the PEX area into four domains: low and high salinity areas and two eddies in the water mass of medium salinity. Thus, the biological-chemical differentiation of the study area is based on some of the most striking physical structures. Certainly, physical oceanography alone is not able to give exhaustive explanations to the chemical and biological patterns even if they coincide with physical ones, and the theory of these disciplines is to be applied. The key for this is provided in Passow's (1990) inference about the occurrence of several independent mesoscale blooms in the study area - perhaps the most significant generalization drawn from PEX'86. The idea of phytoplankton bloom is grounded on the generalization of different studies like experiments with enclosed ecosystems, upwelling events, and of course, previous studies of vernal blooms, including the vernal blooms in the sea. Strictly speaking, the explanatory power of generalizations based on the vernal blooms in the sea is somewhat limited in this case, because the idea of independent mesoscale blooms itself contradicts the previous concept of vernal bloom. As pointed out by Passow (1990), some of the present notions about the vernal phytoplankton bloom in the sea may have resulted from the misleading compilation of data from different mesoscale blooms. In any case, by including the concept of bloom into the explanation, tautology can be logically avoided.

The explanation of the patterns of chemical and biological variables is not exhausted by the conclusion about the occurrence of separated water compartments with independently developing blooms within them in the study area. The question arises: what is a relatively isolated water compartment (mass, body, eddy or whatever) with independently developing plankton community in it from the general viewpoint of the theory of ecology? The answer is: an ecosystem.

The idea of mesoscale pelagic (transit) ecosystems was probably first presented by Koblentz-Mishke (Кобленц-Мишке, 1983) and related to local upwellings. The analogy between upwelling events and vernal phytoplankton bloom was pointed out by Denman and Powell (1984), but until PEX '86 no data were available for evaluating the correspondence between their spatial scales.

Thus, the structural explanation of the mesoscale spatial variability of biological-chemical parameters recorded in the PEX area is referred to the occurrence, development, and interactions of several mesoscale planktonic ecosystems within it. Some of them (eddies) may be of transit type, having moved into the PEX area from outside (Elken, personal communication).

The structural explanation raises several questions, first of all about the criteria for treating the study area as a continuum or as consisting of discrete entities. Questions arise also about the meaning of the identified entities within the frame of the theory. These questions are fundamental and directly connected with the ways and possibilities of ex-plaining the phenomena observed. The term "ecosystem" gives the possibility to identify these mesoscale units only in a very general sense. Both in terms of spatial-temporal scales and functions they are particular subsystems occurring in the pelagic ecosystem during the transient period from a relatively homogeneous winter situation to a likewise homogeneous summer situation. Thus, we are facing the question about the relations of these subsystems to a system of a higher hierarchical level, particularly their roles in the matter and energy flows. It is evident that differences in the meaning of variables applied at different scales result from the hierarchical structure of the pelagic environment. For instance, the average nutrient concentration in the mesoscale pelagic ecosystem (like eddy domains in PEX) characterizes both the nutrient supply of the system and phytoplankton growth conditions, but the average nutrient concentration in the larger scale (like PEX window) characterizes the nutrient supply only.

As mentioned above, so far the mesoscale biological-chemical differentiation of the PEX area has been carried out on the basis of four physical structures. This approach is effective if attention is focused on particular entities and on studying the dynamics within them, but it does not work as the general principle for the spatial differentiation of the study area. According to the logic of classification, the division should be based on one single criterion at every step. It is easy to see that in dividing the PEX area into two water masses and two eddies this logic is ignored: these physical structures belong to different steps of classification. As a result the water mass of medium salinity outside eddies is excluded of the scope (see Fig. 1, salinity).

Being conceptual, the structural explanation does not comprise the concrete processes and causal mechanisms accounting for the formation and development lines of particular mesoscale ecosystems. This is the object of the genetic explanation.

Genetic Explanation

The formation of mesoscale pelagic ecosystems is first and foremost determined by the formation of physical structures providing convenient biotopes. Here I focus on the genetic explanation of the development of the plankton community within some of them.

According to the generally accepted concept, the onset of the vernal bloom is explained by the appearance of favourable light (PAR) conditions. This may be due to a favourable combination of solar irradiance entering the sea surface and the amplitude of phytoplankton's vertical excursion by turbulent mixing. Usually the importance of the latter is stressed. Kaiser et al. (1981) argued that in the Baltic the vernal phytoplankton bloom is triggered off first in areas with salinity-induced density stratification or bottom-limited vertical mixing, in other areas only after the formation of seasonal thermocline. This statement can be seen as a reduced version of the verbal model, consisting of a chain of "cause — effect" links: "salinity stratification \rightarrow density stratification \rightarrow shortening of mixed layer \rightarrow elevated mean PAR level in the upper mixed layer \rightarrow enhanced phytoplankton growth rate \rightarrow rapid increase of phytoplankton biomass (=bloom)". For the representation of this idea in a formalized fashion Sverdrup's (1953) critical depth model is suggested (e.g., Sambrotto et al., 1986; Perry et al., 1989).

Both these approaches to genetic explanations have been proposed for the explanation of the mesoscale blooms described in PEX, too (Kahru and Nõmmann, 1990; Nõmmann, 1990).

There are two restrictions to the explanation of the genesis of mesoscale patterns on the basis of Sverdrup's model. One is technical. As a precondition for the initiation of bloom Svedrup's model states the ratio $Z_m:Z_{cr} < 1$, where Z_m is the thickness of the upper mixed layer and Z_{dr} is the critical depth, defined as the depth whereby the daily average net production (excl. extracellular excretion) for the water column from the surface to depth Z is zero. Z_m is commonly defined as the shallowest depth at a $0.02\sigma_t$ change from the top 3-5 m values. Mixing is assumed to be uniform and intensive enough to provide an equal daily mean PAR for all cells and prevent the formation of vertical biomass gradients within the mixed layer.

Usually (e. g., Sambrotto et al., 1986; Perry et al., 1989), Z_{cr} is derived from the formula

 $I_z = (I_0/k \cdot Z) \cdot (1 - e^{-kZ}),$

or from its simplified version

 $I_z = I_0 / k \cdot Z$

where I_z is the mean daily PAR for the layer with the thickness Z, I_0 is the PAR just below the water surface, k is the average extinction coefficient, Z_{cr} is calculated as Z if $I_z = I_c$, where I_c is defined as compensation point PAR.

It is easy to notice that the ratio $Z_m:Z_{cr}$ is equal to the ratio $I_c:I_m$, where I_m is the average PAR for the mixed layer Z_m . Thus, the idea of Sverdrup's model is to find out whether there is enough solar energy in the given layer to maintain a positive energy budget (net production) of plankton within it.

The I_m values for the four water compartments under study (water masses of low salinity and high salinity and two eddies) can be found from Z_m , I_0 , and k available for April 25. Problems arise in connection with estimating I_c (Z_{cr}). The estimation might be based on the data about I_c for some single species (e. g. Sambrotto et al., 1986; Nommann, 1990) or on abstract "plankton", derived from the studies of various communities (e. g. Perry et al., 1989). From four species dominating in the vernal phytoplankton of the Baltic Sea (see Fig. 2), I_c is available only for *S. costatum*: 0.025 E/m²·h (Falkowski and Owens, 1978, cit. in Sambrotto et al., 1986). Depending on wave length, 0.025 E/m²·h correspondends approximately to 1—2 W/m²; Perry et al. (1989) have set I_c to 19 W/m². Thus, the difference between the I_c -s used in different approaches is about an order of magnitude. Keeping in mind that the species-related differences up to four orders of magnitude have been documented in I_c (Falkowski and Owens, 1978, cit. in Rhee, 1982), this result is not surprising. It is obvious that because of so weakly defined I_c (Z_{cr}) Sverdrup's model can be a matter of speculations and not fulfil the expected function in the explanation.

The other restriction is logical. Sverdrup's model is deductive and relates the possibility of the bloom to the energy (matter) budget of phytoplankton community. It does not say anything about the real onset of bloom, showing only under which conditions the possibility of bloom is excluded. Thus, it is futile to try to explain the genesis of phytoplankton bloom on the basis of $Z_m:Z_{cr}$ ($I_c:I_m$) ratio in terms of causal links, i. e. there is no character of intrinsic necessity.

Some attempts have been made to improve Sverdrup's model by more precise setting of the ratio $Z_m:Z_{cr}$ (Sambrotto et al., 1986; Nõmmann, 1990), or substitute Z_{cr} by euphotic depth (Kaiser et al., 1981). In both cases the clear theoretical meaning of Sverdrup's model (zero point of energy budget) gets lost, but the limits analysed above still persist.

The validity of the verbal model mentioned above is testable on the basis of the available information. As shown, on April 25 we could detect four relatively independent subareas in the PEX window. According to Lass (1989), at this moment the depth of the mixed layer in the low-salinity area and in the domain of the anticyclonic eddy was about 20 m, in the cyclonic eddy and the high-salinity area about 40-50 m. If we assume that the onset of bloom is determined by the depth of the mixed layer, we can hypothesise the occurrence of similar phytoplankton communities in areas with a close depth of the mixed layer, and vice versa, different ones in areas with different mixing depth. (It is to be kept in mind that we have no information to assume, and neither does the model, that there was any other reason for differences in light condition besides the depth of the mixed layer some days before April 25. So, we have no information to assume that the ratio of mixed layer depths documented on April 25 was invalid at the moment the bloom started in some areas under study.)

The real situation observed on April 25 refutes this hypothesis the plankton communities (species structure and biomass) were identical in eddy domains having a different thickness of the mixed layer. At the same time, there were dramatic differences between the communities of the domains with close mixed layer depth (see Figs. 1 and 2). So, the verbal model "salinity-induced density stratification \rightarrow $\rightarrow \dots \rightarrow$ mesoscale bloom" does not work as a causal explanation for mesoscale blooms, documented in PEX. This does not mean that it is false, it is just insufficient. Of course, it can be improved by including additional information in it, but one has to keep in mind that if this is done by *ad hoc* hypotheses, the explanation as a particular logical construction will get lost. It will be changed to a different thing — hypothetical explanation, which is a kind of hypothesis.

Summary and Conclusions

The data collected during the PEX demonstrate in a very expressive manner the occurrence of a complicated mesoscale structure of several important biological, chemical, and physical variables. The huge data set obtained provides almost unlimited possibilities for the description of their spatial heterogeneity. Unfortunately, so far there are no exhaustive explanations of the biological-chemical patterns observed. The domination of descriptive approach is not a peculiarity of PEX '86 alone. Most likely the situation symptomatic to marine ecology in a much wider extent is here revealed in a particularly clear manner. Keeping in mind that explanation is inherently a theoretical procedure, there arises a question about the theoretical status of marine ecology, or at least, about the possible gap between empirical and theoretical approaches.

The problems faced in the structural explanation of the heterogeneity of the pelagic environment have visible analogies with those in geography where the coincidence of spatial patterns of several parameters is the common base for identifying structural entities of higher rank (complexes), which have fundamental notion in the theory of this discipline. Links to the theoretical controversy between plant ecologists several decades ago can also be observed. It can be expected that the theories of these disciplines can provide fruitful ideas to marine ecology dealing with the mesoscale spatial patterns.

Salinity-induced stratification as the explanation of the onset of phytoplankton bloom may be adequate at a larger scale (e.g. region). Applied at the mesoscale level it indicates only an important condition, not relation of intrinsic necessity. Beside Sverdrup's model there exists a more adequate way for the formalized approach to blooms in terms of cause-result relationship - all the theory dealing with the dependence of growth rate on evironmental conditions, incl. PAR, e.g., Platt et al. (1977), Rhee (1982), Niemi (1986). It is astonishing that so far no attempts have been made to interpret PEX data in this frame. Moreover, even the question whether the set of variables, measured during PEX is sufficient for such an explanation, is still open. Thus, PEX gave rise to many more questions than it has been able to answer so far.

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