MICROBIAL LOOP : ITS SIGNIFICANCE IN OCEANIC PRODUCTIVITY AND GLOBAL CHANGE

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Abstract

This paper discusses the need to integrate the microbial loop into models of pelagic ecosystems functioning. We emphasize the role of the microbial loop in ecosystem response to stress. An hypothesis is examined that small scale structure of the organic matter field can create hot spots of microbial activity. Microbial activity and interactions at such microscale features have important implications for the fundamental issues of nutrient and metal cycling and food web structure and dynamics. These ideas could provide mechanistic insights for modeling marine ecosystems subject to stresses such as eutrophication and pollution.

Key-words : bacteria, organic matter, pollution, eutrophication, models

"... men are still under the strong influence of the medieval concept of an endless ocean". Ward and Dubos, [1]

Society wants oceanographers to predict how human activities will affect the health of the ocean. But the "health of the ocean" is not a well defined concept. Broadly, it has been thought of in terms of maintenance of ecosystem homeostasis. In practice, the focus has been on studying the consequences of specific and localized human-induced perturbation such as pollutant or nutrient discharges into coastal waters. Generally, the emphasis has not been so much to predict the effects but to ameliorate present and obvious ecological damage. For example, we are asked to monitor and suggest ways to control eutrophication, contamination of edible fish by harmful chemicals and microbes or declines of local fishery. Clearly, the goal should be to predict, before-hand, the consequences of altering the ocean's chemistry and biology, but we lack sufficient knowledge of ecosystem structure and functioning to make reliable predictions. Ecosystem management at present amounts to trial and error because of our lack of understanding of underlying mechanisms.

This approach is untenable as concerns global change, due to the probable scale of the problem. Human-induced alteration of atmospheric chemistry can profoundly change the structure and functioning of the entire global ecosystem, with significant implications for human environment. This raises a number of urgent questions. What role will the ocean's biota play in various global change scenarios? Will it help purify the atmosphere of the greenhouse gases? Can we safely manipulate the ocean's biota to cause it to absorb additional carbon dioxide? Will global warming adversely affect marine fisheries and biodiversity? Will global change affect the aesthetic attributes of the oceans and their beaches? We do not know the answers to these questions. We do know, however, that trial and error is not a prudent option. We must acquire the ability to *predict* how the ocean's ecosystem will respond to global change. Ideally, one would want to develop a framework which enables one to predict the outcomes of global as well as local ecosystem perturbations. This will require elucidating the mechanistic bases of ecosystem functioning and response to stress.

A unifying theme is how biological forces determine the fate and spatial-temporal patterns of distribution of organic matter. This framework enables one to conceptually integrate the fate of organic matter from all sources, for example whether derived from *in situ* photosynthesis or from river or sewage outfalls. Also, one can develop an integrative approach for conceptualizing the response of the biota to variations in organic matter inputs. For example, eutrophication-enhanced organic matter production and increased photosynthesis due to global change could both be treated within the same framework. Pollutants introduced into the sea tend to associate with the biota and organic matter. Their pathways of transformation and transfer could also be studied within the general context of the consequences of the interactions of the biota with organic matter.

The microbial loop is a major biological force in oceanic carbon flux.

Our views of the ocean's biota as well as organic matter have changed dramatically. For the first hundred years of oceanography it was believed that the grazing food chain was mainly responsible for organic matter dynamics. Microbial abundances were considered too small to warrant their inclusion into ecosystem models. As a result, models of fisheries, productivity, nutrient recycling and pollutant transfer pathways were exclusively conceptualized in the context of the grazing food chain [2] and this trend has not ceased [3]. Older methods had failed to detect most microorganisms and their metabolism. Modern studies have established that bacteria account for a major fraction of the oceanic biomass and particulate carbon pool [4, 5] and use about one-half of the photosynthetically produced organic matter [6]. Bacterial use of dissolved organic matter (DOM) thus mediates large-scale organic matter fluxes through the pathway: DOM -> Bacteria -> Protozoa (or viruses) (the microbial loop [7]. Indeed, marine bacteria use about one-quarter of the total carbon fixed on earth. Organic matter flux into bacteria is highly variable and this could affect flux partitioning between major pathways: microbial loop, sinking and grazing food chain. We proposed that variability is due to bacterial interaction with a patchy organic matter field ([8] and below).

Organic matter is a continuum which creates microbial hot spots.

Recent discoveries are changing our view of the organic matter with which bacteria interact. The distinction between particulate organic matter (POM) and DOM is being replaced by the idea of an organic matter continuum — a gel-like matrix of polymers, replete with colloids and criss-crossed by "transparent" polymer strings, sheets and bundles, few to 100s of μm [9, 10, 11, 12] — the oceanic "dark matter" [13]. Chin *et al.* [14] used several physical techniques to demonstrate that the sea is a thin gel. The traditional particles, including living organisms would be encountered by bacteria as "hot spots" in the gel. The critical questions with respect to bacteria-organic matter interaction are: Do bacteria "care" about the structure of organic matter field in their microenvironments? Do they respond to the patchiness of the distribution of organic matter? It had been assumed that bacteria solely depend on DOM released from the grazing food chain [15]. However, recent studies show that bacteria do exhibit behavior towards organic matter [16, 17]. Five to 60% of bacteria in coastal assemblages were motile and could congregate in response to organic matter. Thus, bacteria do respond to the patchy structure of the organic matter field creating hot spots of abundance and activity.

Action of bacteria on patchy organic matter has microscale as well as ocean-basin-scale biogeochemical consequences.

A main adaptation for bacteria-organic matter interaction in pelagic bacteria is the expression of diverse ectohydrolytic enzymes (protease, glucosidase, phosphatase, lipase, nuclease [18, 19]). Cell-specific activities vary [20], so, shifts in species composition [21, 22] change the hydrolytic enzyme activities which pelagic bacteria exert on the organic matter field. Since bacteria attack the organic matter field, including living organisms, to generate DOM, they profoundly alter the behavior of organic matter (even when their own carbon demand is low; "modification interactions" [13]). Consequently, bacteria can influence all carbon flux pathways, not only DOM -> Bacteria. For instance, they can inhibit diatom aggregation by hydrolyzing diatom surface mucus [23], decreasing the downward flux of organic matter while increasing the intensity and the duration of the phytoplankton bloom. They can also solubilize marine snow, releasing most of the liberated DOM [24] – all these are small scale interactions with ocean-basin-scale consequences for carbon flux and energy transfer. Pollutants and radionuclides associated with