

VIRUS AND HETEROTROPHIC MICROPLANKTON

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Summary

This article highlights the specific features of viruses, prokaryotes and the heterotrophic protists present in the pelagic realm of the oceans and the interspecific interactions regulating the composition of these microbial communities. Viruses are numerically the most abundant forms of life in the ocean and are believed to be species- or even strain-specific in their infectivity. Due to this specificity, viruses are probably playing a role in regulating species successions. Their diversity might be higher than those of the prokaryotes, although this has not been firmly established yet. Prokaryotes are divided into two major groups, *Bacteria* and *Archaea*. Most of the oceanic prokaryotes are not yet culturable, thus their metabolic pathways are largely unknown. Phylogenetic analysis revealed that most of the marine *Bacteria* belong to the γ -Proteobacteria, to the Cytophaga-Flavobacter-Bacterioides group and to the α -Proteobacteria while β -Proteobacteria are clearly not playing a major role in marine systems. The planktonic *Archaea* are dominant in the mesopelagic layer and the deep waters where they constitute probably about half of the prokaryotic biomass. No representatives of these planktonic *Archaea* have been cultured yet. Molecular characterization of oceanic bacterial communities revealed that the communities are highly variable over space and time despite the fact that some groups like the SAR 11 cluster are ubiquitously present. Protists exert grazing pressure on prokaryotes and this bacterivory is probably to a larger extent species-dependent than assumed hitherto. Thus, all these biotic compartments of the microbial food web show a differentiation and niche separation similar to the better understood macrobial food web. The major challenge for the near future is to characterize the microhabitat of these microorganisms and their specific requirements. Only with this knowledge it will be possible to fully understand their role in the marine realm and to use specific microorganisms for biotechnological applications.

1. Introduction

Until the late 1970s the pelagic food web was seen as a more or less linear food chain with phytoplankton at the base and zooplankton preying on phytoplankton and fish grazing on zooplankton or smaller fish. Heterotrophic bacteria were considered as terminal members of this food chain acting as decomposers of dead organic matter. This classical view was revolutionized in the late 1970s and early 1980s when it has been realized that the number of bacteria present in the euphotic layer of the water column had been grossly underestimated with the traditional (plate-counting) methods. Using epifluorescence microscopy and direct counting of the bacteria it has been found that bacteria are 2 to 3 orders of magnitude more abundant than assumed hitherto. This finding prompted research on measuring bacterial growth rates under near-natural conditions. Using radio-labeled substrates it was shown in the early 1980s that bacteria are not only numerous but also that they are growing at turnover times of 0.5 to 10 days depending on nutrient availability and temperature. Consequently, the question arose of the nature of the main predators of this bacterial production. Protists (mainly flagellates but also ciliates) have been identified as the main biotic control agent of bacterioplankton.

In 1983, a seminal paper on the ‘microbial loop hypothesis’ was published. In this paper it was hypothesized that bacteria are the principal consumers of the large pool of dissolved organic matter (DOM) in the ocean converting DOM into bacterial biomass which is then available for other consumer organisms. This ‘loop’ via bacteria makes the pool of DOM available for higher organisms (see Figure 1).

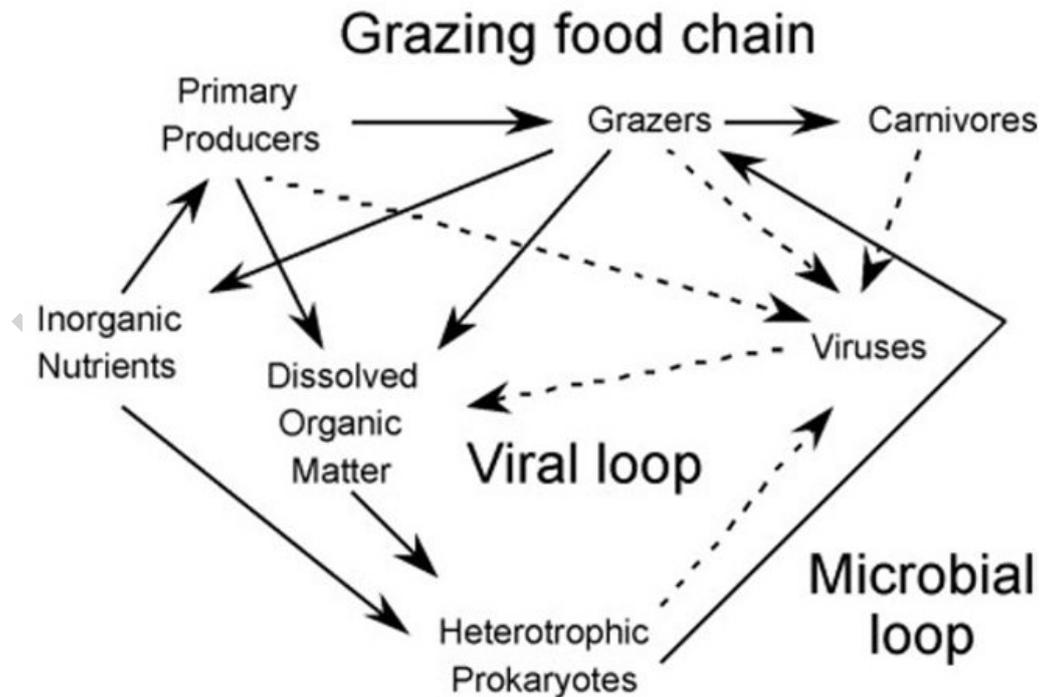


Figure 1. The main living and non-living compartments of the oceanic food web and their interactions

The microbial loop concept has served as the frame and nucleus of modern aquatic microbial ecology and has been refined over the past two decades. It is now clear that viruses also play a significant role in controlling bacterial biomass and that overall, about 50% of the primary production is channeled through the microbial food web. This microbial food web has been shown to be more complex than originally assumed involving several trophic levels within the microbial food web including a wide range of hetero- and mixotrophic protists of varying size (from 0.5 μm to $\approx 50\mu\text{m}$). Moreover, very recently aerobic photoheterotrophic prokaryotes have been found capable of photosynthetic light utilization when organic carbon sources are scarce. Their importance in the biogeochemical cycles of the ocean still needs to be evaluated.

In recent years, due to the wider use of molecular biology techniques, fundamental ecological questions other than carbon and energy transfers between different levels of the microbial food web can be addressed now in microbial ecology, i.e., the phylogenetic composition of microbial communities and synergistic and antagonistic interactions between different members of the microbial community. Since most of the microbes are lacking distinct morphological features and are not culturable, knowledge on the community structure relies on the information provided by the nucleic acid sequences (DNA and RNA) of the individual species. Despite the recent progress made using molecular tools in microbial ecology our understanding of the composition and dynamics of microbial communities is still in its infancy.

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