STEADY STATE MODELS OF THE MICROBIAL FOOD WEB. A USEFUL TOOL IN EXPLORATION AND MANAGEMENT OF MEDITERRANEAN SURFACE WATERS ?

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Abstract

Characteristic time scales for division of micro-organisms are potentially short compared to those of larger animals and those of water exchange processes. An approximate description may therefore be obtained assuming steady state within the microbial part of the food web. Particular properties of the Mediterranean ecosystem (P-limitation of both phytoplankton and heterotrophic bacteria, relatively high levels of silicate), makes the mathematical solutions particularly simple. If such descriptions can be verified experimentally, fairly elaborate representations of the microbial food web could be included in large scale ecosystem models without excessibe demands for computing power.

Key-words : geochemical cycles, models, food webs, bacteria.

Why model the microbial food web ?

Basic research

The latest two decades has brought us a lot of knowledge on individual trophic interactions in the microbial food web, but few tools to link this knowledge into a unifying concept of food web and how its structure and function is regulated. We therefore still need models to explore how the system of unicellular phytoplankton, protozoa, bacteria, and viruses really works.

Applications

The microbial food web is the system that transforms dissolved substances into particulate form and small particles into larger ones, eventually producing food for organisms large enough to be of commercial value. This system links the ocean's uptake of atmospheric CO_2 to the downwards transport of organic matter and it links the C-cycle to those of N, P, and Si, as well as all other elements that are natural components of microbial biomass. As the organic-C:N:P:Si ratio is highly variable with the source of runoff-water and its contamination with farmland drainage or urban sewage, the fate and effect of such discharges is closely linked to the mechanisms regulating structure and function in the microbial food web. Since most of the particle surface area is associated with the smallest particles, while sinking particles are large, the fate and effect of surface-active pollutants originating from industrial waste, transport of crude oil or anti-fouling ship paints, will also be associated with functions of the microbial food web. As in any ecosystem, the success of any microbe in the pelagic ecosystem depends on a successful strategy for obtaining a share in the flux of energy and matter through the food web. Diversity and food web functioning are thus just two aspects of the same reality, and have ultimately to be understood from the same description of the food web. To get a description of the integrated type needed to approach such problems, there seems to be few alternatives to some kind of mathematical model of the microbial food web.

How to model the microbial food web

Most mathematical models of the microbial food web are based on sets of coupled differential equations linking the rate of change in one microbial population to its trophic neighbours in the food web. Such models have, however, at least two problems.

- It is difficult to get a good insight into how assumptions concerning interactions and parameter values influence the model's behaviour.
- Due to rapid dynamics, numerical solutions may require the use of short time steps. Combining such models with 3-D models of physical oceanography may therefore require excessive computing power ?

We have proposed a different approach where either parts of (1), or the whole microbial complex (Fig. 1) is assumed to be in internal equilibrium. When this assumption is used, the whole state of the microbial part of the food web can be solved from the set of algebraic equations formed by the equilibrium conditions :

$$\text{Growth} = \sum \text{Losses}$$

for each functional group of micro-organisms, and the mass balance requirement that :

$$N_t = N + \sum N_i$$

where Nt is the total concentration of limiting element in the microbial community, N is concentration in the pool of free mineral nutrients, and N_i is the concentration in functional group i of micro-organisms (*e.g.* P in bacteria biomass).

In the Mediterranean, bacterial, as well as phytoplankton growth rate have been suggested to be P-limited (2, 3). In the case where there is a surplus of silicate, this means that all osmotrophs in the microbial food web in Fig. 1 are limited by the same mineral nutrient. In this case the solution to the steady state equations become particularly simple. Using this simple solution as a reference, the significance of observations such as the bacterial P-limitation and the dominance of bacterial over phytoplankton biomass in the eastern Mediterranean (4) will be discussed.

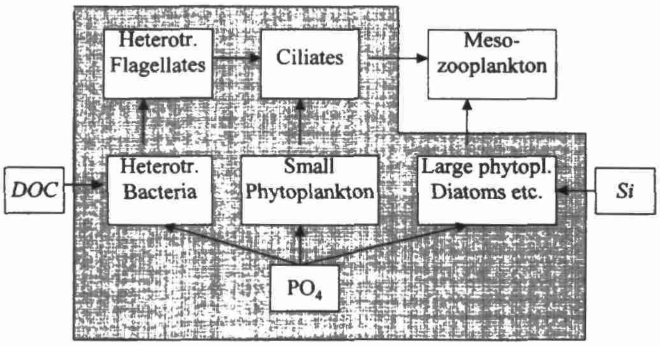

Figure 1. Schematic diagram indicating the microbial part of the food web inside the shaded area. The approach suggested is to assume steady state inside the microbial complex. This steady state can then be found as a function of the total nutrient content in the microbial part of the food web, and the mesozooplankton biomass. In more complex models where changes in the zooplankton population and in the total nutrient content is obtained from differential equations, the state of microbial food web may be derived from solving a set of algebraic equations. These equations will be particularly simple when there is an excess of both DOC and silicate.

In the simplest case, the algebraic solutions contain only the total nutrient content, the mesozooplankton biomass, and the water exchange rate as independent variables. In the ideal case, this approach therefore delivers an algebraic microbial 'module' that can be inserted into larger models. If the larger model describe loss terms, reproduction, and migration of zooplankton by differential equations, the algebraic module may in principle produce zooplankton food availability as well as the whole state of the microbial food web (bacterial biomass, bacterial consumption of organic-C, phytoplankton size-distribution, etc.).

Further research aimed at validation of this approach, and at defining the conditions under which it is applicable, is needed.

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