

A NEW APPROACH TO PLANKTONIC MICROBES: THE MICROBIAL HUB

Louis Legendre¹ * and Richard Rivkin²

¹ Laboratoire d'Océanographie de Villefranche, BP 28, 06234 Villefranche-sur-Mer CEDEX, France - legendre@obs-vlfr.fr

² Ocean Sciences Centre, Memorial University of Newfoundland, St. John's, Newfoundland A1C 5S7, Canada

Abstract

When introduced in 1983, the "microbial loop" conceptual model assigned key roles to microbes in the planktonic food web. Here, we introduce the concept of "microbial hub" as an extension of the microbial loop, and develop this concept into an operational model, which provides a new, powerful tool for exploring marine pelagic community metabolism.

Keywords : *Bacteria, Food Webs, Organic Matter, Plankton.*

The conceptual model to which biological oceanographers presently refer when discussing planktonic microbes was proposed in 1983, under the name "microbial loop" [1]. In that model: dissolved organic matter released by autotrophic and heterotrophic plankton is utilised by heterotrophic bacteria; bacteria (both heterotrophic and autotrophic) are ingested primarily by heterotrophic flagellates, and these are in turn ingested by ciliates. In the microbial loop model, bacteria, flagellates and other microzooplankton have key roles, and they coexist or not with the herbivorous food web, where large phytoplankton are grazed by mesozooplankton. There is a fundamental food-web and biogeochemical difference between heterotrophic microbes, which include heterotrophic bacteria, and metazoa: microbes remineralise most of the organic carbon they ingest, whereas metazoa channel a relatively large fraction of the carbon they ingest to long-lived organisms and to sequestration. In the same vein, [2] showed that autotrophic and heterotrophic planktonic microbes, and large zooplankton are the three food-web control nodes of the main organic carbon fluxes in the upper ocean. Here, we implement the fundamental difference between heterotrophic microbes and metazoa in a model where we group all heterotrophic microbes in a "microbial hub". We propose that heterotrophic microbes represent a planktonic food-web microbial hub, into which organic carbon is channelled by various food-web processes, and from which carbon is redirected towards both carbon dioxide (respiration) and larger heterotrophs.

Considering downward export and horizontal advection), the 5 flows in Fig. 1b are respiration. Heterotrophic microbes are central to the cycling of biogenic carbon within planktonic food webs for the following reasons. Bacteria (BACT) and microzooplankton (μ ZOO) assimilate dissolved primary production (PP) and ingest particulate PP, respectively. In addition, using the model in Fig. 1a, we calculated that the network of linkages channelled up to 35-45% of total PP (i.e., up to 45-55% of particulate PP into the dissolved organic carbon pool, assuming that 20% of total PP is dissolved), and thus towards bacteria. We also calculated that BACT and μ ZOO remineralise most of the organic carbon they assimilate, with their combined respiration being at least 70% of total PP; the remainder of the organic carbon is transferred to mesozooplankton (MZOO) and larger animals (LARGE). The intense cycling organic carbon by the microbial hub (HUB) does not mean that MZOO do not have a significant role in carbon dynamics. Indeed, according to the food web under consideration, these organisms can consume directly most of particulate PP. In Fig. 1b, the pelagic food web is restructured around two poles: the HUB, introduced above, and a metazoan compartment (METAZ, comprising all heterotrophs larger than microbes). Structuring the pelagic food web around these two poles is consistent with the fundamental difference between heterotrophic microbes and metazoa. We applied the model in Fig. 1b to five planktonic food webs, from the extreme case where all particulate PP would be grazed directly by μ ZOO to the other extreme where all particulate PP would be grazed directly by MZOO. We calculated that the HUB channels directly 20-100% of total PP toward community respiration. Hence, the HUB channels carbon from total PP toward community respiration even when all particulate PP is grazed by herbivores. When also found that temperature influences the partitioning of community metabolism between microbes and metazoa, i.e., as temperature increases, microbes directly respire more carbon and channel less carbon toward metazoan respiration.

Our review introduces and develops the concept of microbial hub as an extension of the microbial loop, and built this new concept into an operational model. We thus consolidated information on the functioning of the microbial heterotrophic components of the pelagic food web that had been published in the last decades. Crucial to our approach is the fundamental difference between heterotrophic microbes and metazoa, i.e., heterotrophic microbes respire a large fraction of the organic carbon they ingest, whereas metazoa move a large fraction of the carbon they ingest to long-lived organisms and to sequestration.

In conclusion, (1) the fundamental difference between heterotrophic microbes and metazoa leads to structuring the pelagic food web around two poles, i.e., the microbial hub, which comprises bacteria and microzooplankton, and metazoa, which consists of the heterotrophic organisms larger than microbes, (2) in the resulting microbial-hub model, a large fraction of the organic carbon originating from PP is channelled toward the microbial hub, from which organic carbon is redirected towards both hub respiration and metazoa, and (3) the microbial-hub model provides a new, powerful tool for exploring marine pelagic community metabolism.

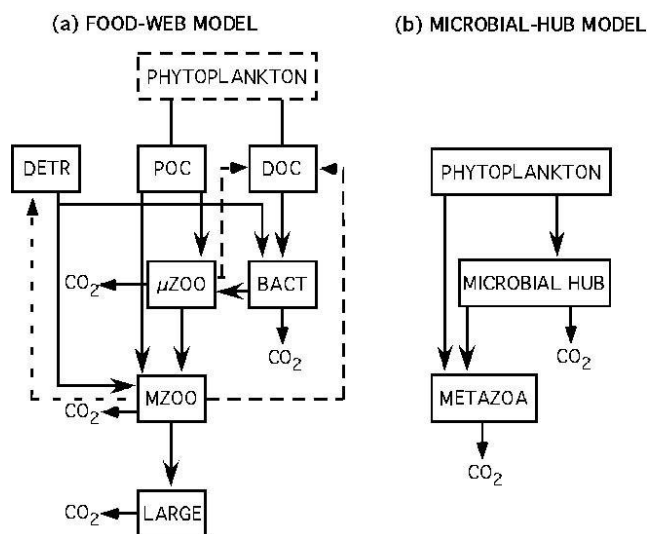


Fig. 1. (a) Food-web model with 7 compartments, and (b) corresponding microbial-hub model, with 3 compartments. Symbols are defined in the text.

Figure 1 shows two versions of a food-web model, where boxes represent food-web compartments, and arrows are flows of carbon into and out of the compartments. The model in Fig. 1a has 7 compartments, many of which are simplifications of complex in situ processes. In the corresponding 3-compartment microbial-hub model (Fig. 1b), bacteria and microzooplankton are combined in the microbial hub, and heterotrophic organisms larger than microbes make up the metazoan compartment. The flows in Fig. 1a are of various types, e.g. grazing, egestion, production, excretion, and respiration. Because the only additive property of the ecosystem is respiration (i.e. it sums up to 100% of primary production, without con-

References

- 1 - Azam F, T. Fenchel, J. G. Field, J. S. Gray, L. A. Meyer-Reil, and F. Thingstad. 1983 The ecological role of water-column microbes in the sea. *Mar. Ecol. Prog. Ser.* 10: 257-263.
- 2 - Legendre, L., and R. B. Rivkin. 2002. Fluxes of carbon in the upper ocean: regulation by food-web control nodes. *Mar. Ecol. Prog. Ser.* 242: 95-109.