



Food web flows through a sub-arctic deep-sea benthic community

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ARTICLE INFO

Article history:

Received 1 April 2010

Received in revised form 13 December 2010

Accepted 19 December 2010

Available online 24 December 2010

ABSTRACT

The benthic food web of the deep Faroe–Shetland Channel (FSC) was modelled by using the linear inverse modelling methodology. The reconstruction of carbon pathways by inverse analysis was based on benthic oxygen uptake rates, biomass data and transfer of labile carbon through the food web as revealed by a pulse-chase experiment. Carbon deposition was estimated at $2.2 \text{ mmol C m}^{-2} \text{ d}^{-1}$. Approximately 69% of the deposited carbon was respired by the benthic community with bacteria being responsible for 70% of the total respiration. The major fraction of the labile detritus flux was recycled within the microbial loop leaving merely 2% of the deposited labile phytodetritus available for metazoan consumption. Bacteria assimilated carbon at high efficiency (0.55) but only 24% of bacterial production was grazed by metazoans; the remaining returned to the dissolved organic matter pool due to viral lysis. Refractory detritus was the basal food resource for nematodes covering ~99% of their carbon requirements. On the contrary, macrofauna seemed to obtain the major part of their metabolic needs from bacteria (49% of macrofaunal consumption). Labile detritus transfer was well-constrained, based on the data from the pulse-chase experiment, but appeared to be of limited importance to the diet of the examined benthic organisms (<1% and 5% of carbon requirements of nematodes and macrofauna respectively). Predation on nematodes was generally low with the exception of sub-surface deposit-feeding polychaetes that obtained 35% of their energy requirements from nematode ingestion. Carnivorous polychaetes also covered 35% of their carbon demand through predation although the preferred prey, in this case, was other macrofaunal animals rather than nematodes. Bacteria and detritus contributed 53% and 12% to the total carbon ingestion of carnivorous polychaetes suggesting a high degree of omnivory among higher consumers in the FSC benthic food web. Overall, this study provided a unique insight into the functioning of a deep-sea benthic community and demonstrated how conventional data can be exploited further when combined with state-of-the-art modelling approaches.

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1. Introduction

The deep-sea floor (below 200 m water depth) occupies approximately 65% of the Earth's surface, constituting the largest ecosystem on the planet (Thistle, 2003). Deep-sea sediments account for 50% of the global benthic mineralization (Middelburg et al., 1997) and host infaunal communities of high local and regional diversity (Levin et al., 2001). Despite the ecological significance of this ecosystem, the remoteness and the difficulties encountered in its exploration have resulted in the deep-sea being one of the least understood environments on earth (Tyler, 2003). As a result, the functional interactions within deep-sea benthic communities remain largely unknown. The processing of organic matter (OM) by benthic communities has significant consequences for the global carbon and nutrient cycles. Knowledge of the functional interactions between biological components in food webs is thus necessary if we are to understand and predict the response of

deep-sea ecosystems to global change phenomena (Soetaert and van Oevelen, 2009b).

The quantification of energy flows between food web components is, in most instances, hampered by the lack of sufficient empirical data (Brown and Gillooly, 2003). This is especially true for deep-sea datasets that normally consist of biomass estimates of large taxonomic groups and occasional measurements of a single flux (Soetaert and van Oevelen, 2009b). Furthermore, direct observations on the feeding mode of deep-sea fauna are lacking and most inferences on the feeding habits of deep-sea animals rely largely on observations of shallow-water analogues (Jumars et al., 1990; Thistle, 2003). In recent years, stable isotope tracer experiments have provided direct observations of the transfer of fresh phytodetritus through food webs (e.g. Witte et al., 2003b; Moodley et al., 2005). Tracer experiments involve the introduction of an artificial stable isotope-labelled food pulse to the sediment and the subsequent “chase” of the tracer in various components of the food web (pulse-chase experiments). The pulse-chase methodology enabled the quantification of the contribution of particular taxonomic groups/species to the processing of fresh OM and revealed

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