Pediatric patient samples obtained from St. Jude Children's Hospital included the following: patient 9907 (Ph^1-negative T-cell ALL), 9913 (Ph^1-negative common ALL), 9453 (Ph^1-positive pre–B cell ALL), 9312 (Ph^1-positive common ALL with a deletion of the short arm of chromosome 9), 9254 (Ph^1-positive common ALL), 9378 (Ph^1-positive pre–B cell ALL) and 9556 (Ph^1-positive common ALL). Patients obtained from UCLA included the following: 045-14-02 (adult Ph^1-positive, pre–B cell ALL), 146-03-37 (Ph^1-positive blast-crisis CML), 143-57-16 (Ph^1-positive blast-crisis CML), and 133-68-56 (Ph^1-positive accelerated CML).

14. S. Clark *et al.*, unpublished data.

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Technical Comments

Bacteria: Link or Sink?

Ducklow *et al.* (*1*) conclude from an experimental study of an enclosed water column at Loch Ewe, Scotland, that bacteria were not a link (that is, a food source) to higher order consumers in the planktonic food web. We strongly disagree that "the results have great importance for our understanding of the structure and function of marine planktonic ecosystems."

First, one cannot generalize from a single "link or sink" experiment. It will be necessary to carry out many such tracer studies in different parts of the sea representing a variety of trophic states, and to have a detailed characterization of the planktonic assemblage of each, before we can begin to discover the importance of the microbial loop in marine food webs. Ducklow *et al.* do not provide information about the components of the planktonic assemblage, that is, heterotrophic microorganisms, phytoplankton, and zooplankton, at the time of their experiment. In addition, the work carried out 9 years previously (*2*) that was cited in support of the statement that "The plankton community . . . was an assemblage of bacteria, protozoans . . . typical of the . . . Scottish sea lochs in mid- to late spring" in fact contained no data on bacterioplankton or protozoan numbers. Without information on the relative abundances and production rates of organisms of the microbial loop, that is, bacteria and protozoa, compared to those of the phytoplankton and metazooplankton assemblages, one cannot properly interpret the results of the experiment.

Second, the experimental study of Parsons *et al.* (*3*), briefly mentioned by Ducklow *et al.*, provided direct evidence that bacteria can be a link in marine food webs. Addition of small quantities of glucose (1 to 5 mg per liter) to enclosed water columns enhanced bacterial production, which in turn significantly increased the total abundance of benthic larvae and gelatinous zooplankton compared to a control treatment with predominantly phytoplankton production.

Third, the speculation of Ducklow *et al.* that production of cyanobacteria as well as of bacteria may not be utilized in marine food webs is not supported by the results of their study. Cyanobacteria in the sea have an average cell volume of 0.5 μm^3 (*4*), while the average cell volume of marine bacteria is 0.07 μm^3 (*5*). The larger cyanobacterial cells are likely to be grazed more effectively than are bacteria by marine pelagic ciliates (*6*), which are abundant in the sea and are a known food source for metazooplankton (*7*). Iturriaga and Mitchell (*4*) demonstrated with autoradiography that protozoa in the size range of 10 to 50 μm actively grazed $^{14}CO_2$-labeled cyanobacteria in surface waters of the oligotrophic North Pacific Ocean. They also showed that carnivorous metazoans incorporated the label, implying at least a two-step transfer of cyanobacterial carbon in the food web.

Finally, results from a similar bag experiment previously carried out in the same system, in which the fate of phytoplankton production was assessed by monitoring the distribution of ^{14}C in the water after a spike of radiolabeled bicarbonate was added (*8*), showed that, at the end of 10 days, the herbivorous zooplankton (68-μm and 250-μm size fractions) had incorporated only 1.2% of the ^{14}C activity present in the phytoplankton (*8*). Since this apparent trophic transfer from algae to zooplankton is of the same small magnitude as that reported by Ducklow *et al.* for the transfer of bacterial production to larger organisms, it is misleading to single out bacteria as a sink.

Ducklow *et al.* are correct in stating that further ecosystem-scale experiments should be done in order to address the question of bacteria as a link or sink for organic carbon in marine food webs. Their results, based on a one-season experiment carried out in a coastal ecosystem atypical of most of the world ocean, have not settled the matter.

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Response: Sherr *et al.* (*1*) criticize the design of our study, our interpretation of the results of a previous study (*2*) and of our own, and our conclusions. They imply that because an analogous experimental study of herbivory in a Loch Ewe bag (*3*) also failed to show significant transfer of carbon to zooplankton, both experiments were not performed properly. However, it is clearly shown in (*3*) that, during the earlier study, there was appreciable net primary production only on the three sunniest days. During the major part of the experiment nighttime respiration nearly balanced daytime carbon fixation, and it is thus not too surprising that the herbivores accumulated the label slowly. In contrast, in our experiment there was a rapid and sustained (4-day) accumula-