

Session: The role of microzooplankton in marine foodwebs

Conveners:

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Merging scales in food web model links microzooplankton to bacterial diversity and gives mechanistic framework for virus-to-bacteria ratios.

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Studies of pelagic bacteria often use either a “black box” approach with focus on how the bacterial community interacts as a plankton functional type (PFT) with their trophic neighbors; or they try to resolve the internal structure of the bacterial community. Addressing a major challenge in the field, we attempted to link these different levels of resolution in a model where strain-specific virus-host interactions define the internal structure of the bacterial community, which itself is embedded in a food web model resolving different microbial PFTs. In agreement with mesocosm studies, microzooplankton represented by the 'ciliate' PFT play an important role in controlling the bacterial community and its associated viruses, both in terms of diversity through indirect bottom-up effects and in terms of total abundance through top-down effects. The theoretical framework furthermore suggests a link from molecular properties of viral-defense mechanisms in bacterial hosts and the associated trade-offs between competition and defense to the abundance of PFTs and the biogeochemical cycling in pelagic microbial food webs. By linking cost of resistance against viral defense to bacterial grazer abundance, we hence propose a mechanistic model for virus-to-bacteria ratios in the pelagic environment.

Keywords: merging scales, central role of ciliates, virus-to-bacteria ratios

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