

BACTERIAL INFLUENCE ON THE EXTRACELLULAR CARBOHYDRATE POOL IN EXPERIMENTAL *EMILIANIA HUXLEYI* BLOOMS

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Bacteria are key players in the non-sinking biological carbon pump. But how do they affect freshly produced sugar compounds? We investigated the interactions between the extracellular carbohydrate pool of the coccolithophore *E. huxleyi*, and associated bacterial communities, and how these affect the sugar dynamics and carbon partitioning in the microbial loop. By comparing the sugar concentration and (isotopic) composition, by means of HPLC-IRMS, and TEP formation between *E. huxleyi* cultures with and without bacteria, we are investigating the influence of bacterial activity on this major extracellular carbon pool. Furthermore, we studied the evolution of both the active particle-associated and whole bacterial communities by means of DGGE fingerprinting of 16S rRNA. This approach allows the identification of the dominant active bacterial taxa which may be involved in the cycling of carbohydrates and TEP. Future stable carbon isotope pulse-chase experiments using compound-specific isotope analysis will focus on the carbon flows between the sugars in extracellular carbohydrates and bacterial communities in experimental *E. huxleyi* blooms.