Changes in bacterial ß-glucosidase diversity during a coastal phytoplankton bloom

Arrieta, Jesús M., Gerhard J. Herndl

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ABSTRACT: Bacterial enzymatic hydrolysis of high molecular weight organic matter is the rate-limiting step in the bacterially mediated carbon cycling in the global ocean. Despite the importance of this process, only bulk measurements of these hydrolytic activities are available, and the dynamics and diversity of the ectohydrolases involved in the cleavage of high molecular weight organic matter are poorly understood. In this study we monitored the dynamics of bacterial ß-glucosidase diversity during the wax and wane of a coastal phytoplankton bloom using a newly developed capillary electrophoretic assay. Up to eight different ß-glucosidases were detected in a single sample and 11 over the whole study period, revealing a previously unnoticed ß-glucosidase diversity. A close link was found between the temporal succession ofß-glucosidase diversity and bacterioplankton species richness as determined by terminal-restriction fragment length polymorphism analysis. This indicates that the regulation of the ß-glucosidase activity and diversity was driven by shifts in the bacterial community structure rather than by simple induction of enzyme expression within a stable bacterioplankton community.

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