



Response of marine bacterial community composition to iron additions in three iron-limited regimes

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ABSTRACT: In high-nutrient low-chlorophyll (HNLC) regimes, iron additions consistently result in primary productivity increases, and the phytoplankton community shifts from small species toward large diatoms. Heterotrophic bacterial production and abundance also increase in HNLC Fe addition experiments, but whether changes in bacterioplankton community composition also occur when Fe is added is unknown. We used trace metal clean shipboard incubation experiments, and molecular biological methods to examine this question in three Fe-limited environments: the subarctic Pacific, the subantarctic Southern Ocean, and the California coastal upwelling region. After Fe additions and subsequent phytoplankton community shifts, changes in bacterial community composition were examined using denaturing gradient gel electrophoresis and terminal restriction fragment length polymorphism of polymerase chain reaction-amplified bacterial 16S rRNA genes. Responsive bacterial phylotypes in either +Fe or control treatments were classified using phylogenetic analyses of DNA sequences. In general, iron-mediated changes in bacterial communities in all three environments were surprisingly minor compared to the changes in phytoplankton community composition. Responsive phylotypes were mostly - proteobacteria in the subarctic and California HNLC areas, but no changes were noted in the subantarctic experiments. Although bacterial growth and biomass are closely linked to phytoplankton-derived carbon supplies, our results suggest that on the time scale of our experiments (4-5 d), species composition of algal and bacterial communities can be decoupled in Fe-limited waters.

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