



Linking bacterial richness with viral abundance and prokaryotic activity

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ABSTRACT: We measured relative bacterial and archaeal richness and its covariation with physical and other biological parameters during six cruises in the North Sea over prokaryotic productivity levels ranging over two orders of magnitude. Relative bacterial and archaeal richness was estimated as the number of peaks detected by terminal- restriction fragment length polymorphism (T-RFLP) analysis of polymerase chain reaction-amplified prokaryotic 16S rRNA gene fragments in unfiltered (total community) and 0.8- μm filtered seawater (free-living community). Relative bacterial richness ranged from 20 to 57 peaks in the total community and from 16 to 56 peaks in the free-living community. Relative archaeal richness varied between 2 and 14 peaks in the total community and between 2 and 21 peaks in the free-living community. Coamplified plastid DNA might have influenced relative bacterial richness in unfiltered but not in 0.8- μm filtered seawater. Relative bacterial richness decreased with viral abundance and total and cell-specific prokaryotic production in the free-living and the total community. Stepwise multiple regression analysis revealed that temperature also influenced relative bacterial richness. Relative archaeal richness was not related to any other parameter. The data suggest that high prokaryotic productivity was sustained by a relatively small number of highly active bacterial populations that also maintained high viral abundance.

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