



Temporal and spatial response of bacterioplankton lineages to annual convective overturn at the Bermuda Atlantic Time-series Study site

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ABSTRACT: We used terminal restriction fragment length polymorphism (T-RFLP), clone library, phylogenetic, and bulk nucleic acid hybridization analyses to identify and characterize spatial and temporal patterns in marine bacterioplankton communities at the Bermuda Atlantic Time-series Study (BATS) site. Nonmetric multidimensional scaling of monthly surface and 200-m bacterial 16S rDNA T-RFLP fragments from 1992 to 2002 revealed temporal trends in bacterial community structure in different depth horizons. A 200-m 16S rRNA gene clone library was used to identify fragments increasing in relative abundance following mixing events and to link observed terminal restriction fragments with those predicted from sequence data. T-RFLP fragments matching those of cloned OCS116, SAR11, and marine *Actinobacteria* rRNA genes exhibited the strongest increases at 200 m following convective overturn, and fragments attributable to SAR11, SAR86, and SAR116 rRNA genes exhibited the strongest increases at the ocean surface during summer time periods. Variability in the distribution and relative abundance of fragments assigned to different SAR11 and SAR86 subclusters was also evident. Quantitative hybridization of extracted 16S rRNA with radiolabeled, taxonspecific oligonucleotide probes provided additional data supporting spatial and temporal patterns of lineage distributions and abundances suggested by ordination. Overall increases in the relative abundance of T-RFLP fragments attributable to the OCS116, SAR11, and marine *Actinobacteria* clusters following convective overturn suggest that members of these groups may play important roles in dissolved organic carbon dynamics at BATS.

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