



Biogeography of major bacterial groups in the Delaware estuary

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ABSTRACT: We used fluorescence in situ hybridization to examine the spatial and temporal variation in the abundance of major bacterial groups in the Delaware Estuary. The abundance of alpha- and beta-proteobacteria and Actinobacteria varied systematically in the estuary and mirrored the pattern seen in lakes and oceans. Beta-proteobacteria and *Actinobacteria* were abundant in the Delaware River but were less so in the marine waters of the Delaware Bay. In contrast, alpha-proteobacteria, including the SAR11 clade, were most abundant in the Bay and rare in the Delaware River. *Actinobacteria* were active in assimilating thymidine and leucine and appeared to contribute substantially to bacterial production in the Delaware River. Among the several biogeochemical parameters we examined, only salinity accounted for a substantial portion of the variation in abundance of these bacterial groups. However, relative abundance of these groups often varied independently of salinity. *Cytophaga*-like bacteria were often abundant throughout the estuary, but they did not vary systematically over the estuarine gradient, unlike the other dominant bacterial groups. We hypothesize that this estuary-wide high abundance occurs because *Cytophaga*-like bacteria are very diverse, more so than other groups. Data on 16S rRNA sequences are consistent with this hypothesis. The consistent biogeographic patterns suggest that some bacterial groups, even at a broad phylogenetic level, operate as ecologically meaningful units for examining some processes, whereas the *Cytophaga*-like bacteria as now defined might be too diverse to be useful for ecological studies.

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