



Compositional changes in free-living bacterial communities along a salinity gradient in two temperate estuaries

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ABSTRACT: There is now clear evidence for major differences in heterotrophic bacterial composition between freshwater and marine ecosystems. A fundamental question that remains unresolved is whether the compositional succession occurs by a gradual replacement of the major phylotypes, or whether there are drastic compositional shifts in discrete areas along the gradient from one system to another. The aim of this study is to examine the change in the phylogenetic composition of the free-living bacterioplankton across the salinity gradient in both the Choptank and the Pocomoke Rivers, both subestuaries of the Chesapeake Bay, using fluorescence in situ hybridization (FISH). The proportion of free-living cells that could be detected using FISH varied widely (3 to 80%), and the majority of cells detected belonged to bacteria, whereas archaea represented less than 3%. The distribution of the different members of bacteria exhibited a clear pattern along the salinity gradient, with the dominance of α -proteobacteria in the lower, saltwater regions and of γ -proteobacteria in the upper freshwater regions. The *cytophaga-flavobacterium* cluster prevailed in the turbidity maximum located in the middle estuary, and the β -proteobacteria showed sporadic peaks along the transect that may have been related to local events. The replacement of α - for γ -proteobacteria along the salinity gradient was not gradual but rather occurred rapidly within the turbidity maximum region of the estuaries where the fresh and salt waters mix. The pattern of phylogenetic succession was linked to the development of the turbidity maximum, which is related to rainfall and the ensuing hydrological conditions. There is indication that the phylogenetic succession is accompanied by strong physiological changes in the bacterial assemblage, expressed as a decline in bacterial growth efficiency and community production. The transition appears not to be simply the result of conservative mixing of riverine and estuarine bacterial assemblages, but rather appears to involve cell inactivation and/or death.

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