



## Relationship between bacterial community structure, light, and carbon cycling in the eastern subarctic North Pacific

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**ABSTRACT:** Biogeochemical controls on the community structure of heterotrophic marine bacteria are not well understood, and these organisms play a critical role in the global carbon cycle. Through terminal restriction fragment length polymorphism (T-RFLP) analyses of bacterial 16S rRNA genes along a zonal transect in the eastern subarctic North Pacific, variations in community structure were compared to commonly obtained chemical and biological oceanographic measurements. It was found that heterotrophic bacterial community structure was strongly, but independently, related to both phytoplanktonic production and light. Based on computer-simulated T-RFLP analyses of database 16S rRNA gene sequences, it appeared that the relationship between bacterial community structure and light observed along the transect was driven by the distribution of  $\alpha$ -proteobacteria with phototrophic capabilities. In addition, experiments were conducted at sea to measure the growth of heterotrophic bacteria in response to amendments of amino acids, protein, N-acetyl glucosamine, and chitin. Variation in the response of heterotrophic bacteria in the experiments did not correlate significantly with variation in community structure along the transect, which suggests that the ability of the heterotrophic bacterial community to use specific components of the dissolved organic carbon reservoir was not related to its phylogenetic structure as detected by T-RFLP. However, a possible relationship between community structure and the cycling of chitin is discussed. Overall, the results stress the importance of both heterotrophic and phototrophic metabolisms when considering environmental controls on the structure of bacterial communities in the sea.

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