ICES CM 2013/B:80

Microbial diversity and abundance in the ocean around Iceland

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Summary

A pioneering study on the diversity of small (nano- and pico- size) marine microorganisms in the waters around Iceland was initiated by some water samplings in 2011. Collection of water samples, mostly during the second half of May, has been continued annually since that, as well as some analysis of the samples. As expected, it is apparent from the preliminary result that micro organisms are most abundant in coastal regions, and the microbial numbers are high in the surface layer in comparison to deeper water. Furthermore, there is a positive trend between water temperature and abundance of micro organisms. The aim of this study is to study correlations between abundance and diversity of the small micro organisms and some commonly recorded environmental parameters (temperature, salinity, mixed layer depth, concentrations of nutrients and chlorophyll *a*, as well as index on zooplankton abundance). Special emphasis is put on registrations of the possible occurrence of known micro organisms that may be pathogenic to fish or other marine animals.

Introduction

Communities of diverse Bacteria, Archea, and Protista have been estimated to account for more than 98 present of oceanic primary production (Atlas and Bartha 1993). These are the microscopic factories and are the essential catalysts for chemical reactions within the biogeochemical cycles (Simon *et al*. 2013). However, information on bacteria and archea are very limited in the Icelandic marine ecosystems. Oceanographically, the sea around Iceland can be considered a complex system of water masses with mixed currents from the Atlantic and Arctic oceans which circulate the island, affected by freshwater from land and rising ridges on the seafloor (Fig. 1).

The aim of the present study was to obtain the first data on microbial (mainly bacteria) abundance and community structure around Iceland and to define how the microbial ecology is oriented by the environmental factors.

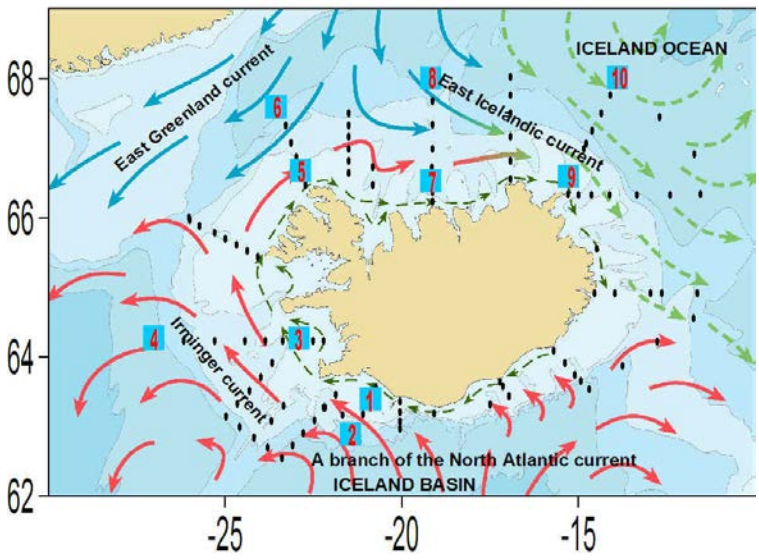

Figure 1. Surface ocean currents around Iceland (modified from Astthorsson et.al., 2007, Climate variability and the Icelandic marine ecosystem, Deep-Sea Res II, 54:2456-2477). Blue-marked numbers indicate sampling locations for genomic analysis of bacterial diversity.

Materials and Methods

Water samples were collected around Iceland at various depths in the spring of 2011 and 2012 on MRI's standard grid for environmental studies (Fig. 1), for flow cytometry analysis and cell counting. Furthermore, in selected samples bacterial communities were identified by 16S rDNA tag sequencing and the data were processed by multivariate statistics and by the use of Qiime software specially designed for 16S tag sequencing analysis. Contextual data was further recorded e.g. location, temperature, salinity, acidity, and fluorescence.

Results and Discussion

The results show that autotrophic phytoplankton is generally in higher numbers south and west of Iceland and in shallower waters near the coast line while heterotrophic microorganisms showed more even distribution. The sequencing results showed that the microbial community is reflected by environmental factors and that north samples, south samples and deep sea samples can be distinguished from one another by principal coordinate analysis of the community structure (Figure 2). Further research is essential to pinpoint shifts in these communities and to correlate them to changed environmental conditions.

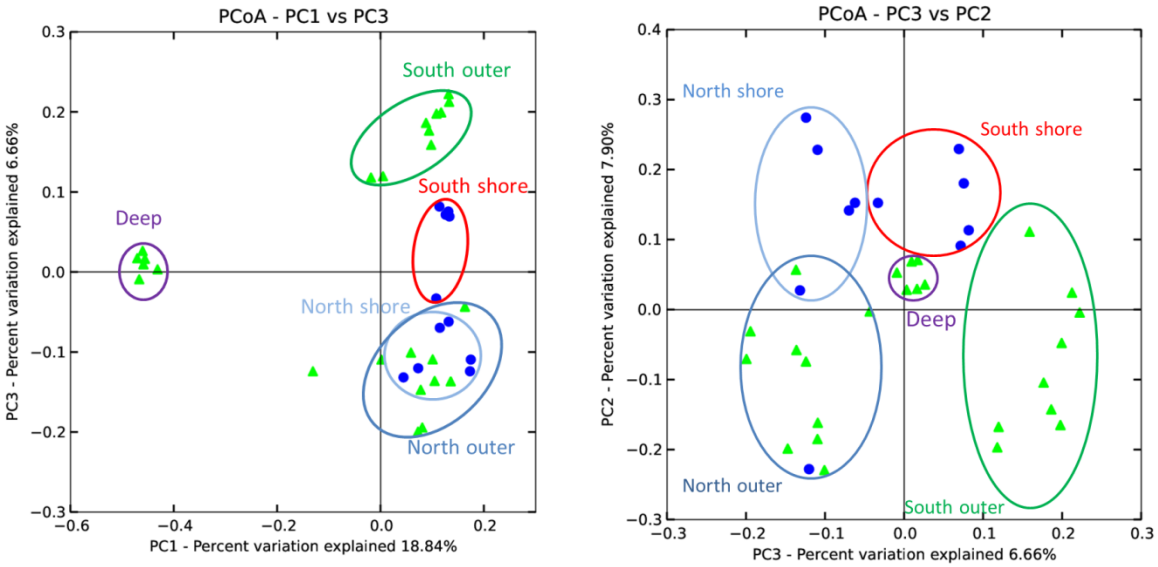

Figure 2. Principal coordinate analysis of unifrac distances between samples by Qiime analysis pipeline. PC1 is plotted against PC3 (left) and PC3 against PC2 (right).

Reference

Atlas, R.M. and R. Bartha, *Microbial Ecology. Fundamentals and Applications*. 1993, Redwood City: The Benjamin/Cummings Publishing Company, Inc.

Simon, E.J., Dickey, J.L., Reece, J.B. 2013: *Campbell Essential Biology*. ISBN 10:0-321-80729-4