UNCOVERING MARINE BACTERIAL DIVERSITY IN THE SOUTHERN ADRIATIC SEA:
FROM SURFACE TO SEABED


1. Department of Biology, Faculty of Science, University of Zagreb, Croatia
2. Division for Marine and Environmental Research, Ruder Bošković Institute, Croatia
3. Physical Oceanography Laboratory, Institute for Oceanography and Fisheries, Croatia


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WHERE?
The samples were collected from surface to seabed on total of 16 different depths at four stations in the southern Adriatic Sea during the late winter BIOTA cruise (concluded in March 2016, Fig. 1).

WHY?
To determine bacterial diversity and quantify the most represented bacterial groups in the southern Adriatic Sea.

WITH?
Sequencing: MiSeq platform
Data analysis: QIME 1.9.1, following Community ecological pipelines.
Real-time PCR quantification: Proteobacteria, Bacteroidetes, Proteocyes and Bacteroidetes.

MAJOR RESULTS

The investigated area showed an unusual general circulation that was characterized by mixed layer down up to 200 m, which differed from usual winter convection event, typical for middle-altitude ecosystems and important for seasonal picoplankton dynamics in the South Adriatic Sea (Fig. 2). A different oxygen utilization (AOU) had positive values indicating the respiration as a main process in the southern Adriatic Sea (Fig. 4). The AOU increased as the POC decreased and the best fit had a slope of 1.5 indicating that the respiration is mainly resulted from heterotrophic bacteria (Fig. 4).

The bacterial community was dominated by Alphaproteobacteria accounted for the largest fraction (42.31 % of the total) - mainly represented by the SAR11 clade (90.84 %) and Marinimicrobials (18.44 % of the total) represented with the clade SAR406 (Fig. 5). The bacterial community differed between euphotic and aphotic samples and the highest dissimilarity contribution had OTUs from class Deltaproteobacteria, Bacteroidetes, and Cyanobacteria (Fig. 6). Highest abundances of targeted bacterial populations were recorded for Alphaproteobacteria, followed by Gammaproteobacteria and Bacteroidetes. Abundances were found to vary between different sampling points and sampling depths, with values ranging from 8.7x10^3 to 9.13x10^3 genes/mL for Alphaproteobacteria, from 1.44x10^4 to 5.11x10^4 genes/mL for Gammaproteobacteria and from 1.8x10^4 to 2.4x10^4 genes/mL for Bacteroidetes (Fig. 6C). NMDs analysis clearly showed grouping of aphotic and euphotic samples, showing correlation of aphotic samples with temperature, POC, oxygen Chl a and nitrite, while aphotic samples were correlated to density, depth and nitrate (Fig. 7).

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