

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

## FROM SURFACE TO SEABED

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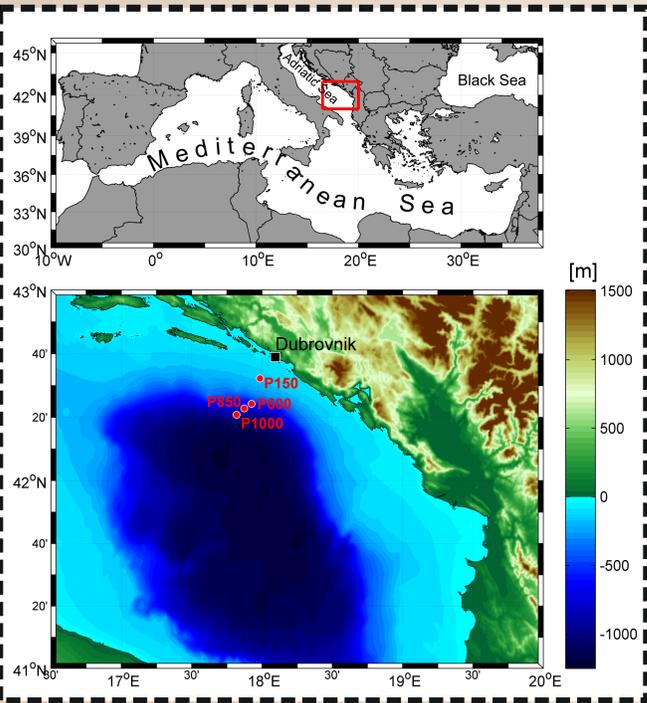


Figure 1. Map of the BIOTA 2016 cruise study area along transect from station P100 to station P1000.

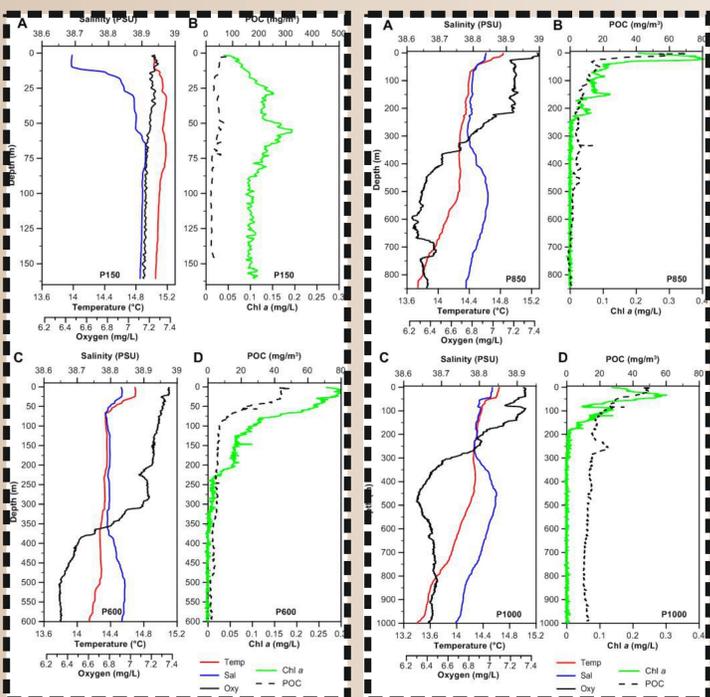
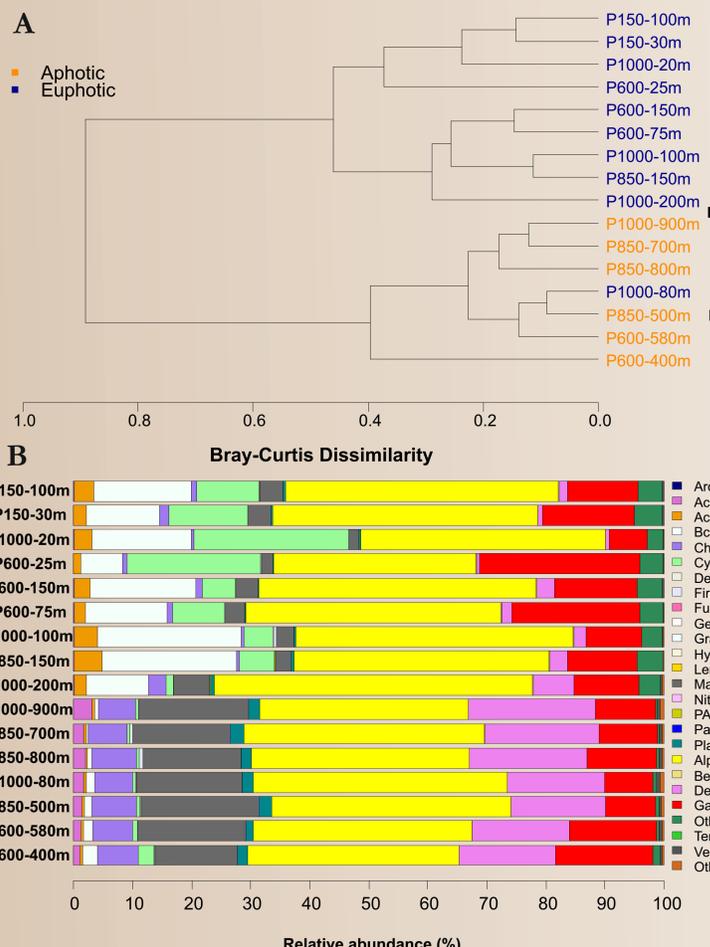
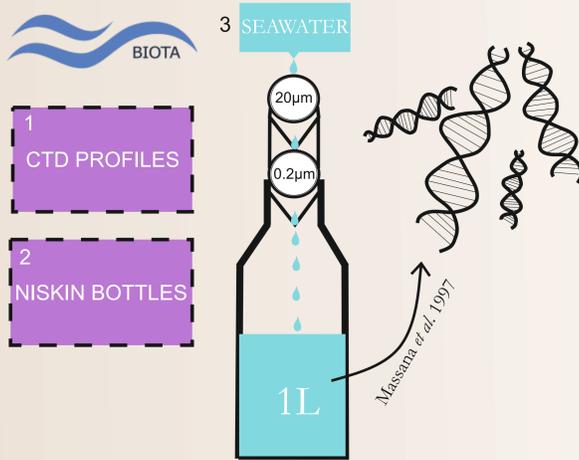


Figure 2. Stations P150 and P600. Vertical profiles of (A, C) temperature, salinity and oxygen (B, D) POC and Chl a.

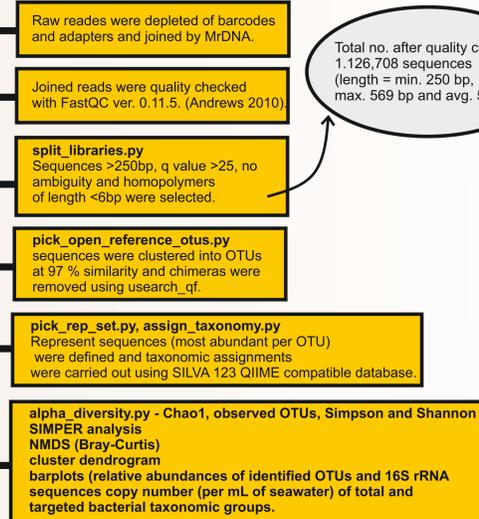
Figure 3. Stations P850 and P1000. Vertical profiles of (A, C) temperature, salinity and oxygen (B, D) POC and Chl a.



## COLLECTION, FILTRATION, DNA ISOLATION



## QIIME PIPELINE



Total no. after quality checking: 1,126,708 sequences (length = min. 250 bp, max. 569 bp and avg. 506 bp)

## MAJOR RESULTS

The investigated area showed an unusual general circulation that was characterized by mixed layer down up to 200 m, which differed from the usual winter convection event, typical for middle-altitude ecosystems and important for seasonal picoplankton dynamics in the South Adriatic Sea (Figs 2, 3). Apparent oxygen utilization (AOU) had positive values indicating the respiration as a main process in the southern Adriatic Sea (Fig. 4). The AOI increased as the POC decreased and the best fit had a slope of 1.5 indicating that the respiration is mainly result of heterotrophic bacteria (Fig. 4).

The bacterial community was dominated with Alphaproteobacteria accounted for the largest fraction (42.31 % of the total) - mainly represented by the SAR11 clade (90.84 %) and *Marinimicrobia* (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  $8.7 \times 10^3$  to  $9.13 \times 10^5$  genes/mL for *Alphaproteobacteria*, from  $1.44 \times 10^4$  to  $5.11 \times 10^5$  genes/mL for *Gammaproteobacteria* and from  $1.8 \times 10^3$  to  $2.4 \times 10^5$  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 euphotic samples were correlated to density, depth and nitrate (Fig. 7).

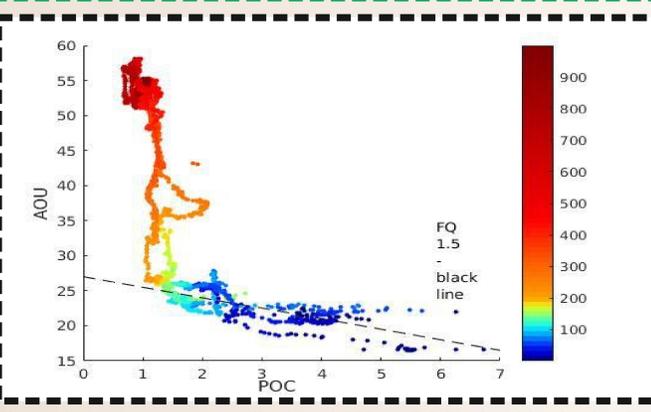


Figure 4. Apparent oxygen utilization (AOU) vs. POC colored by depth. The best fit (dashed black line) had a slope of 1.5, consistent with that expected for a respiratory quotient arising from bacterial metabolism. AOI is defined as the difference between the saturation oxygen (at measure temperature, salinity and surface pressure) and the measured oxygen.

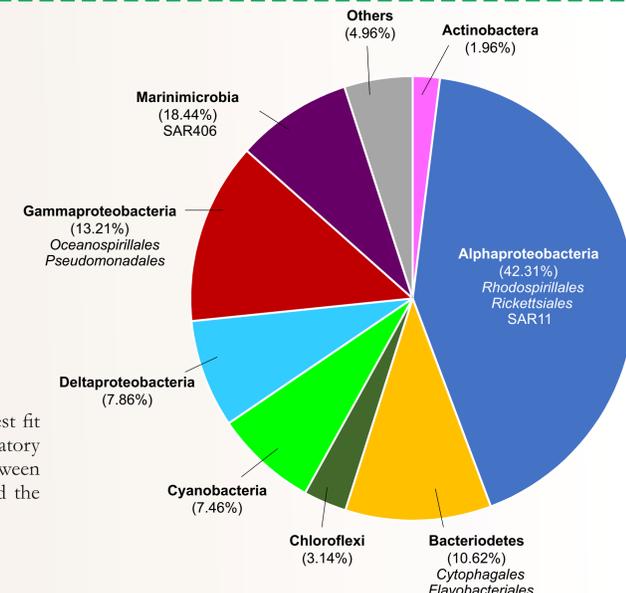


Figure 5. Taxonomic distribution of all sequences retrieved during this study (n = 1,126,708). "Others" comprises taxa accounting for less than 1 % of the total.

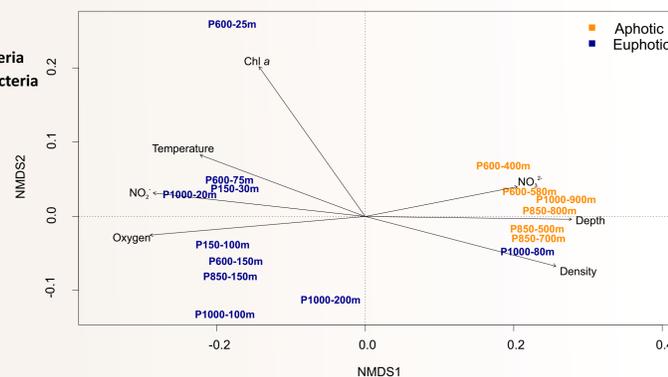


Figure 7. NMDS analysis of BIOTA 2016 stations according to Bray-Curtis distance between bacterial taxa assemblages, with fitted statistically significant (adjusted P value < 0.05) physico-chemical parameters. Samples that belong deep (Aphotic) and surface (Euphotic) assemblage have been colored according to the orange and blue color, respectively. NMDS stress value: 00013.

## ACKNOWLEDGMENTS

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