



IV ROSS SEA CONFERENCE 2023

Università degli Studi di Napoli "Parthenope"

Via Amm. F. Acton, 38 - 80133 Napoli, ITALY

3-7 July 2023, Via Acton 38, Naples-Italy

Topic: Biogeochemistry

Mauro Celussi

ABSTRACT Subject :

High dissolved inorganic carbon uptake by Bacteria and Archaea in the deep water masses of the Ross Sea

Abstract 15/02/2023 11:35:34

A deep knowledge on the ocean C cycle functioning is fundamental to predict the consequences of increased CO₂ in the atmosphere. Current researches indicate that the amount of CO₂ fixed in deep marine systems via chemosynthetic processes is comparable to the one taken up by photosynthetic organisms in the lit portion of the water column. Despite the pressing need, we still lack information on the deep sea biodiversity and metabolism of the Southern Ocean. The Ross Sea represents a key study area because (1) it is a system where dense water masses with distinct features, potentially involved in different quantity and quality of organic matter export to the deep sea, are formed and (2) these water masses, eventually forming the Antarctic Bottom Water (AABW), act as an engine for global ocean circulation, ventilating 60% of the whole ocean mass. During two oceanographic cruises in Southern Ocean (austral summers 2014 and 2016) we have performed 64 incubation experiments in order to understand the C fluxes in the dark portion (200-2000 m) of the Ross Sea. We evaluated dissolved inorganic C uptake (via chemosynthesis or anaplerosis) and production (via respiration) together with dissolved organic C utilization (via heterotrophic production) and release (via excretion or viral lysis). The study focussed on the newly formed oxygen-rich High Salinity Shelf Water (HSSW), on the oxygen-depleted Circumpolar Deep Water (CDW), and on the Antarctic Bottom Water. Results indicate that in the three water masses (in the same depth range) the metabolism of marine microbes proceeds at different rates. The fastest bulk inorganic C fixation, heterotrophic production and respiration were measured in HSSW. Significantly lower values were found in CDW, whereas AABW maintained the metabolic signature typical of both parental water masses showing intermediate values. Prokaryotic abundance mirrored the trend observed in metabolic activities. The per-cell normalization of C uptake and production did not reveal significant differences among the water masses indicating that metabolism do not spatially vary at the single organism-level. Noteworthy, the relative abundance of putatively chemosynthetic prokaryotes was significantly (yet slightly) higher in CDW suggesting that, in an environment with lower palatable organic C concentration, a higher number of microbes access its need for energy and C via autotrophic pathways. Overall, these data indicate that the signature of newly-formed water masses significantly affects the metabolism of microbes living in Antarctic Bottom Water possibly having profound implications for the global bathypelagic biogeochemistry.

