

# BACTERIAL PRODUCTION AND RESPIRATION IN THE SEA-SURFACE MICROLAYER OF THE WESTERN MEDITERRANEAN SEA AND THE SUBTROPICAL ATLANTIC OCEAN

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## Abstract

We measured bacterial production and respiration along with physico-chemical parameters in the sea-surface microlayer (SML) and the underlying water (ULW) of the western Mediterranean Sea and the subtropical Atlantic gyre. Dissolved organic nitrogen and amino acids were significantly enriched in the SML as compared to the ULW, however, bacterial production was consistently low. The low bacterial production and the low bacterial growth efficiency in the SML coincided with high contributions of dissolved free amino acids to the total dissolved amino acid pool in the SML. This indicates that nitrogen rich dissolved organic matter is accumulating in the SML due to retarded DFAA availability or bacterial uptake.

**Keywords :** *Western Mediterranean, Secondary Production.*

The sea-surface microlayer is the boundary layer between the atmosphere and the oceans covering 70% of the earth's surface. Despite the long-lasting interest in the physico-chemical properties of the SML, studies on microbial metabolism in the SML are scarce, particularly for open oceans. To gain more knowledge on the biological dynamics of the open ocean SML we studied a stable anti-cyclonic eddy system in the western Mediterranean Sea (WMED), and a transect from the Mauritanian upwelling into the subtropical North Atlantic gyre (SATL).

In the WMED and the SATL, the SML was significantly enriched in dissolved organic carbon (DOC), dissolved organic nitrogen (DON) and inorganic nutrients with enrichment factors (EF = SML/ULW) ranging from 1.2 up to 12. In the SML at both study sites the contribution of dissolved free amino acids (DFAA) to the total hydrolyzable amino acid pool (THAA) was remarkably high, averaging  $61 \pm 14\%$  and  $47 \pm 10\%$  in the WMED and the SATL, respectively. In contrast, the contribution of DFAA to the THAA pool was significantly lower in the ULW and 12-37%.

Bacterial production in the SML of the WMED was not significantly different from that in the ULW (Fig. 1a). Enrichment factors for bacterial production in the SML of the WMED ranged from 0.1-3 and were therefore highly variable. In the SATL, bacterial production in the SML was generally low (Fig. 1b) with enrichment factors 0.13. In the WMED, bacterial respiration was highly variable between the different stations (Fig. 1c). On average, bacterial respiration in the SML and ULW was similar although considerable differences in the respiration rates between SML and ULW were detected at individual stations. Comparing average bacterial respiration rates between the two study sites for the SML and ULW separately, no significant difference was found. In the SML of the SATL, bacterial respiration was high in the upwelling region ( $9.5 \pm 0.9 \mu\text{mol O}_2 \text{ L}^{-1} \text{ d}^{-1}$ ) and decreasing towards the oligotrophic gyre ( $3.6 \pm 2.0 \mu\text{mol O}_2 \text{ L}^{-1} \text{ d}^{-1}$ ; Fig. 1d). In contrast, bacterial respiration in the ULW was consistently low along the transect ( $0.8 \pm 0.8 \mu\text{mol O}_2 \text{ L}^{-1} \text{ d}^{-1}$ ). Thus, contrary to bacterial production, bacterial respiration was significantly higher in the SML than in the ULW over the entire transect with enrichment factors ranging from 1.6-66.

Generally, labile DOM accumulates if the production of this DOM pool is higher than its consumption. DFAA usually cover a considerable fraction of the bacterial nitrogen demand [2]. The enrichment of DFAA in the SML suggests that bacteria in the SML are apparently inhibited in their uptake of DFAA which might also explain the low bacterial growth efficiency (BGE=BP/BR+BP) ranging from 0.2-2%. Our data on the unusually high contribution of DFAA to the THAA pool indicate a decoupling of DFAA release and uptake. Inorganic nitrogen, DON and amino acids were highly enriched in the SML and the variability of nitrogen in the SML is independent of that in the ULW, suggesting either production of DON in the SML independent from those in the ULW [3] or selective scavenging of N-rich DOM on, e.g., rising air bubbles [1].

We found that the SML in the open ocean is a highly variable environment with generally low bacterial biomass production and high respiration. Bacterial production was not related to bacterial respiration and bacterial growth efficiency was mainly determined by respiration. Despite the significant enrichments in dissolved nitrogen in the SML, with concentrations generally higher than commonly reported for oligotrophic systems, the low bacterial production in combination with high bacterial respiration suggests that the DOM pool of the SML, and particularly the amino acid pool is not readily available for bacteria inhabiting this ocean atmosphere interface.

## References

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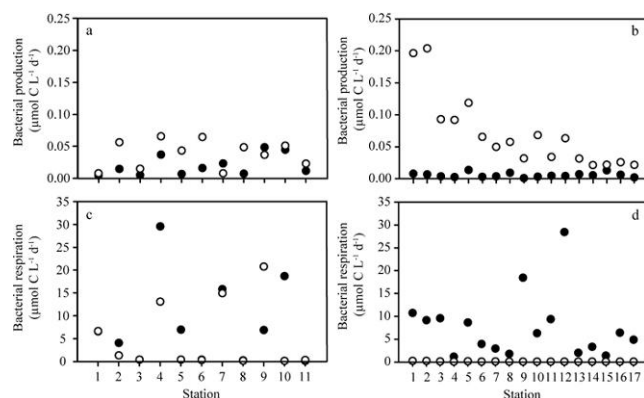


Fig. 1. Bacterial production and respiration measured in the surface microlayer (SML) and the underlying water (ULW) at the different stations in the western Mediterranean eddy (a, c) and the subtropical Atlantic (b, d).