

EFFECTS OF PHOTOCHEMICAL TRANSFORMATIONS OF DISSOLVED ORGANIC MATTER ON BACTERIAL METABOLISM AND DIVERSITY

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Abstract

The effect of solar radiation on the bioavailability of dissolved organic matter (DOM) was investigated for two lagoons and one coastal water samples from the northwestern Mediterranean Sea differing markedly in DOM and chlorophyll concentrations and salinity. Solar irradiation of DOM had contrasting effects on bacterial production and respiration, depending of the water origin. This resulted in increase in bacterial growth efficiency for the coastal water sample and a decrease for the lagoons. Bacterioplankton growth on irradiated DOM resulted in changes in microbial community structure.

Keywords : *Bacteria, Biodiversity, Lagoons, Western Mediterranean.*

Introduction

Natural solar radiation, primarily ultraviolet radiation (UVR, <400nm), has been found to induce chemical transformations of DOM with the production of a variety of photoproducts (CO₂, CO, NH₄, PO₃, numerous low-molecular-weight organic compounds). The origin and chemical composition of DOM strongly influences its photoreactivity and its subsequent bioavailability for bacteria [1]. In coastal environments DOM is derived from diverse allochthonous and autochthonous sources. The aims of this study were to investigate the effects of the photochemical transformation of DOM on (1) bacterial production, (2) respiration, (3) growth efficiency, and (4) diversity in two coastal lagoons (Canet and Leucate, France) and one coastal water (Sola station) sample in the NW Mediterranean Sea.

Materials and methods

Surface water samples were collected in June 2005 filtered through 0.2 µm membranes, distributed into quartz tubes and exposed to the natural sunlight for 8h in a circulating water bath (18 ± 1°C). Three light treatments were applied: full sun (PAR+UVR), PAR, dark. Dissolved organic carbon and fluorescence of chromophoric DOM were measured before and after irradiation. Subsamples from both irradiated and dark treatments were inoculated (10% final volume) with a bacterial community from the same origin (0.8 µm-filtered water) and incubated in the dark at 18 ± 1°C. Bacterial respiration (BR) was measured after 38h by potentiometric titration of O₂. Bacterial production (BP) was measured by ³H-leucine incorporation for 4 to 5 days (i.e. until bacterial cell numbers stabilized). Bacterial community structure was measured by CE-SSCP fingerprinting for both 16S-rDNA and 16S-rRNA PCR products at the start and at the end of biodegradation. Bacterial growth efficiency (BGE) was calculated using BP and BR measurements (BGE=BP/(BP+BR)) integrated over 38h incubation.

Tab. 1. Integrated bacterial production (BP) and respiration (BR) over 38h incubation. Numbers in parentheses are ±1 SD of mean. Bacterial growth efficiencies (BGE) were calculated as BP/(BP+BR).

Sample	Light treatment	BP(µg C/L)	BR(µg C/L)	BGE%
Coastal water (SOLA)	Dark	4.3 (0.2)	49.5 (21.1)	9.8 (5.7)
	PAR	5.8 (0.2)	50.1 (14.5)	12.5 (5.0)
	Full sun	9.2 (0.2)	39.6 (3.4)	22.5 (4.3)
Coastal lagoon (Leucate)	Dark	26.4(2.0)	74.3 (33.7)	30.7(13.0)
	PAR	10.1(0.4)	52.9 (16.2)	19.2 (6.1)
	Full sun	14.4(2.6)	81.9 (19.7)	18.1 (5.9)
Coastal lagoon (Canet)	Dark	29.0 (0.5)	62.8 (20.8)	36.6 (9.8)
	PAR	30.3 (0.4)	91.4 (17.6)	29.3 (5.1)
	Full sun	39.3 (7.8)	126.4 (19.3)	27.9 (7.7)

Results and discussion The water samples are characterized by large variation in DOC and Chl *a* concentrations (892, 234 and 80 µM DOC, 70, 2.2, 0.3 µg Chl *a* /l for Canet, Leucate and SOLA station, respectively).

DOC-specific fluorescence at 350 nm was similar between the two lagoons (0.041-0.051 QSU/µM DOC) and lower at the SOLA station (0.014 QSU/µM DOC). The exposure to full sun resulted in a decrease of this index (bleaching of DOM) by 15, 21 and 38% for Leucate and Canet lagoons, and SOLA station, respectively.

During biodegradation, we observed that DOM exposed to full sun resulted in an increase of BP for the Canet lagoon and the SOLA station, and a decrease for the Leucate lagoon (Tab. 1). In contrast, BR was modified only for the Canet lagoon, with an increase by a factor of 2 in the full sun treatment compared to the dark control treatment (Tab. 1). The sunlight exposure (mainly from the UVR part of the spectrum) of the DOM resulted in a decrease of the BGE in the coastal lagoons and an increase in the coastal waters (Tab. 1). Bacterial diversity was modified by the light treatment (again mainly from the UVR part of the spectrum) in the Canet lagoon and the SOLA station (Fig. 1). These modifications were observed both for total community (16S-DNA fingerprints) and for the active part of the community (16S-RNA fingerprints), with an emphasis for the latter (Fig. 1).

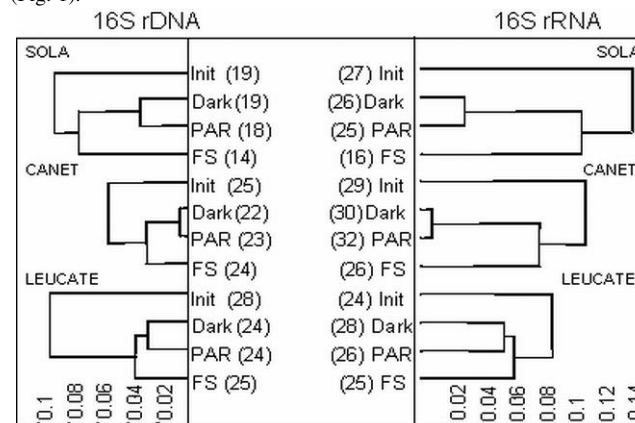


Fig. 1. Cluster analysis dendrogram based on comparison of 16S rDNA and 16 rRNA patterns from the bacterial communities before (Init) and after growth on DOM unexposed (Dark) or pre-irradiated to full sun (FS) or PAR. The numbers of ribotypes are indicated in parentheses.

Reference

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