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Annual variability in light modulation of bacterial heterotrophic activity in surface northwestern Mediterranean waters

Clara Ruiz-González,* Martí Galí, Thomas Lefort, Clara Cardelús, Rafel Simó, and Josep M. Gasol

Institut de Ciències del Mar-Consejo Superior de Investigaciones Científicas (CSIC), Barcelona, Spain

Abstract

The effect of photosynthetically available radiation (PAR; 400–700 nm) and ultraviolet radiation (UVR; 280–400 nm) on marine bacterial heterotrophic activity was assessed monthly throughout a seasonal cycle in Blanes Bay (northwestern Mediterranean Sea). Seawater samples amended with ^{3}H-leucine were exposed to solar radiation under three radiation treatments: PAR + UVR (280–700 nm), PAR + UVA (320–700 nm), and PAR only. Parallel reference incubations in the dark and under a fixed artificial light source (PAR only) were also performed. Exposure to high UVR doses caused strong inhibition of ^{3}H-leucine incorporation rates (LIR), whereas natural PAR doses did not cause overall significant effects. Within UVR, UVA radiation accounted for most of the reduction in LIR, and this effect was modulated by the proportionality of the experimental light to the previous light exposure history of the samples. Constant (artificial) PAR-only exposure led to a general but seasonally variable increase in bacterial heterotrophic production compared to the dark controls, with large increases in spring and lower changes during summer. This pattern was likely caused by the stimulation of the bacterial group *Gammaproteobacteria*, which showed higher numbers of cells active in ^{3}H-leucine uptake after light exposure. Again, the previous light history of the samples seemed to partly explain the measured effects. Overall, our results show variable responses of bacterial activities to light manipulations, depending on seasonally changing light conditions and communities, and stress the importance of realistic simulation of light exposure conditions for ecosystem-relevant photobiological studies with microbial plankton.

Abundance and activity of marine heterotrophic bacteria are influenced by parameters that fluctuate at different time scales. Temperature, nutrient concentration, dissolved organic matter (DOM) availability, and the composition of the microbial community have been regarded among the main factors controlling DOM consumption by bacteria (White et al. 1991; Cotner et al. 2000; Cottrell and Kirchman 2003). However, the relative importance of solar radiation as a modulator of bacterial production across spatial or seasonal patterns has received little attention. In surface waters, bacteria are exposed to damaging solar ultraviolet radiation (UVR; 280–400 nm) that can cause inhibition of metabolic activities such as synthesis of protein and deoxyribonucleic acid (DNA; Herndl et al. 1993; Sommaruga et al. 1997), oxygen consumption (Pakulski et al. 1998), or amino acid and adenosine triphosphate (ATP) uptake (Alonso-Sáez et al. 2006). Nevertheless, there might also be a positive effect of UVA (320–400 nm) and photosynthetically available radiation (PAR; 400–700 nm) on bacterial activity due to photoenzymatic repair (Kaiser and Herndl 1997), to the ability of some bacteria to derive energy from light using bacteriochlorophyll *a* (BChl *a*) or proteorhodopsin (Béjà et al. 2000; Kolber et al. 2000), or to the reported light stimulation of cyanobacterial uptake of amino acids and related compounds (Church et al. 2004; Michelou et al. 2007; Mary et al. 2008). In addition, UVR can photolyze some recalcitrant DOM into more readily utilizable forms, making it more available to heterotrophs and thus enhancing their activity or, by contrast, initially labile DOM can be rendered more recalcitrant on UVR exposure (Benner and Biddanda 1998; Obernosterer et al. 1999). Finally, heterotrophic bacteria might react to increased or decreased release of photosynthate from light-affected phytoplankton. All in all, the aforementioned processes indicate that the interactions between heterotrophic bacteria and light are far from simple.

The Mediterranean Sea is characterized by relatively high solar radiation levels because of a weak cloud cover and a high penetration of solar radiation into the oligotrophic and transparent water column. However, although some UVB (280–320 nm) and UVA underwater measurements are available for the Mediterranean (Sommaruga et al. 2005; Llabrés et al. 2010), there is still a remarkable dearth of data on UVR attenuation varying at different scales. Moreover, most of the studies on UVR effects on Mediterranean prokaryotes drive conclusions from occasional experiments conducted mostly during spring or summer (Sommaruga et al. 2005; Alonso-Sáez et al. 2006; Llabrés et al. 2010).

A current time-series study in the Blanes Bay Microbial Observatory (northwestern Mediterranean), a shallow oligotrophic coastal area, shows a great seasonal variability in underwater PAR and UVR profiles (M. Galí unpubl.). This, joined to the fact that both seasonal bacterial taxonomic succession (Schauer et al. 2003) and differential sensitivities to UVR of different bacterial groups have been described for this coastal region (Alonso-Sáez et al. 2006), suggests that seasonal variability in the bacterial responses to UVR is likely to occur in the area.

We incubated natural bacterioplankton with radiolabeled leucine in UVR-transparent vials throughout a seasonal cycle to characterize the effects of natural radiation levels on bacterial heterotrophic activity as compared to the values

* Corresponding author: clara.ruiz.glez@gmail.com

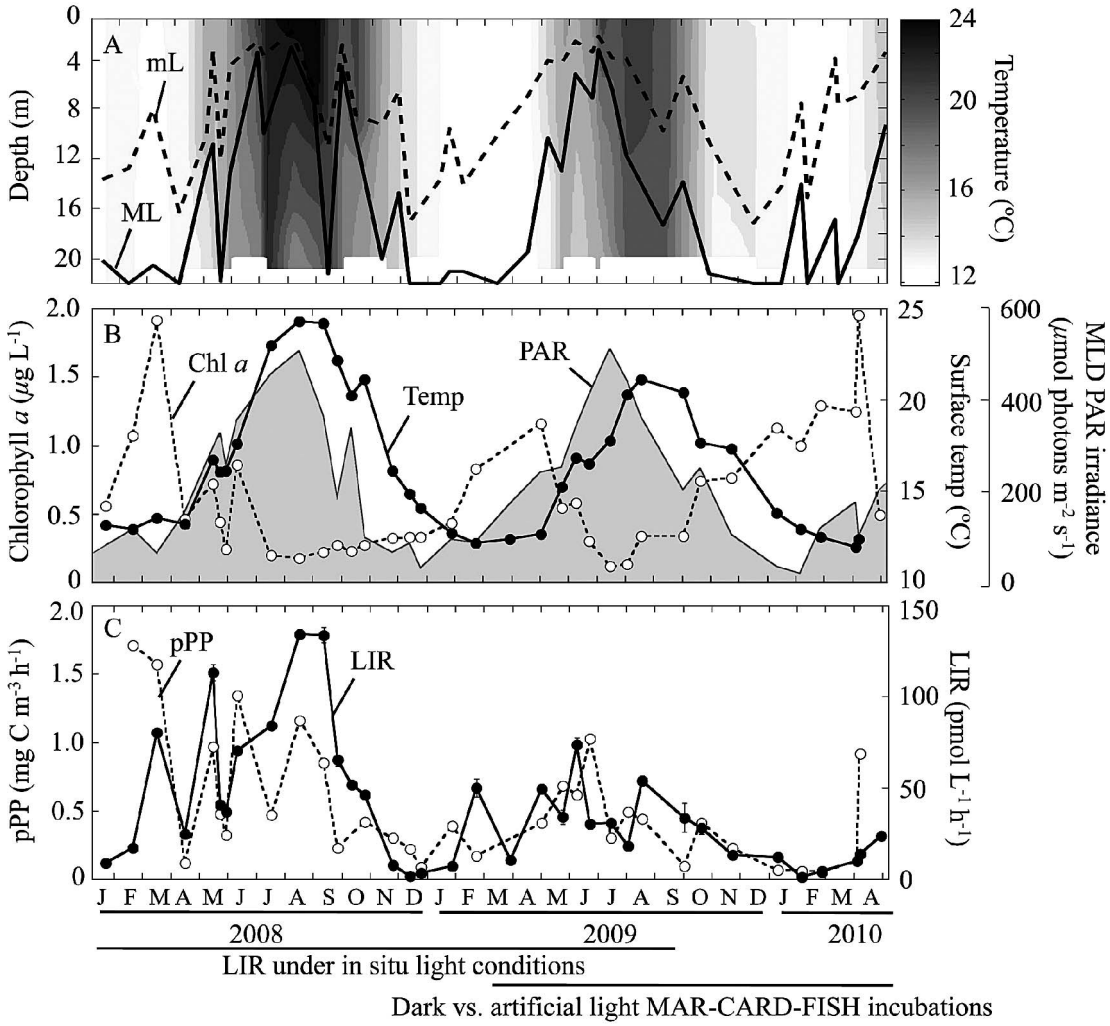

Fig. 1. (A) Temporal dynamics of water column temperature and the depths of the mixing (mL) and mixed (ML) layers (*see* Methods for calculations). (B) Surface water temperature (Temp), chlorophyll *a* (Chl *a*), and "seasonal" PAR irradiance (i.e., mean irradiance within the ML of the 3 d prior to sampling, *see* text). (C) In situ particulate primary production (pPP) and leucine (Leu) incorporation rates (LIR) over the period January 2008–April 2010 in Blanes Bay.

measured with an artificial constant light source. The observed responses were further compared with in situ changes in physical (temperature, irradiance, light history, and mixing layer depth) or biological (chlorophyll *a* [Chl *a*], primary productivity, bacterial abundance, and community composition) parameters in order to search for potential causes of the variability. Since both light levels and bacterial taxonomic composition change through the seasonal cycle, the differential responses of bacterial communities to sunlight are essential to understand the role of solar radiation as a modulator of organic matter fluxes in marine ecosystems. The results obtained have potential implications for assessing the suitability of standard dark protocols for a realistic measurement of heterotrophic bacterial activity.

Methods

Sampling and basic parameters—A series of monthly experiments were carried out with waters from a shallow (≈ 20-m depth) coastal station (the Blanes Bay Microbial Observatory [BBMO], northwestern Mediterranean Sea; www.icm.csic.es/bio/projects/icmicrobis/bbmo) between January 2008 and April 2010. Surface waters (0.5-m depth) were sampled at about 09:00 h at 800 m offshore (41°40′N, 2°48′E), filtered through a 200-μm mesh, and transported within an hour to the lab under dim light. Seawater temperature was measured in situ with a SAIV A-S 204 conductivity–temperature–depth (CTD) probe, and underwater PAR and UVR profiles were obtained with a profiling ultraviolet (PUV) 2500 radiometer (Biospherical Instruments). The Chl *a* concentration was determined by filtering 150 mL of seawater on GF/F filters (Whatman), extracting the pigment in acetone (90% v:v) in the dark at 4°C for 24 h, and measuring fluorescence with a Turner Designs fluorometer.

Experimental setup—Different experiments were performed during the study period (*see* Fig. 1). From 15 January 2008 to 14 September 2009, incubations for

bacterial heterotrophic activity measurements (hereafter leucine incorporation rates [LIR]) were conducted under natural radiation conditions inside a seawater-flushed tank placed outside the laboratory in Barcelona, ~ 100 km south of the sampling site in the same coastline. Irradiance spectrum was manipulated with light filters, and the experimental PAR and UVR doses were monitored using a PUV 2500 radiometer placed underwater next to the samples. Throughout the entire study period (January 2008–April 2010), parallel dark and artificial light (PAR only; ~ 1500 μmol photons m^{-2} s^{-1}) LIR incubations were additionally carried out inside an indoor incubator at in situ temperature. These experiments were aimed at standardizing the responses of seasonally changing communities to constant irradiance conditions. Between 17 March 2009 and 13 April 2010, additional parallel dark and artificial PAR incubations were performed for microautoradiography combined with catalyzed reporter deposition-fluorescence in situ hybridization (MAR-CARD-FISH) analyses (*see* below). The objective was the identification of the bacterial taxonomic groups responsible for the patterns found in LIR. The rest of the variables (primary production, bacterial and picophytoplankton abundances, and composition of the bacterial assemblages) were monitored throughout the whole period at the sampling site.

Abundance of prokaryotes—Aliquots for bacterial abundance were preserved with 1% paraformaldehyde and 0.05% glutaraldehyde (final concentration), frozen immediately in liquid nitrogen, and stored at −80°C until quantification with a fluorescent activated cell sorting (FACSCalibur) flow cytometer (Becton Dickinson) of cells stained with SybrGreen I (Molecular Probes; Gasol and del Giorgio 2000). *Synechococcus* and *Prochlorococcus* cells were enumerated by flow cytometry and distinguished by their different sizes and pigment properties in unstained samples (Marie et al. 1999).

Primary production—Particulate primary production (pPP) was determined using the ^{14}C technique (Steeman-Nielsen 1952). Fourteen 70-mL bottles (Iwaki) and one dark control (bottle wrapped with aluminum foil) were filled with seawater and inoculated with 10 μCi $NaH^{14}CO_3$. The incubation was carried out in a water bath at in situ temperature for 2 h in a gradient of light irradiance (~ 10–1500 μmol photons m^{-2} s^{-1}). Circulating water connected to a water bath maintained the temperature. Light was measured with a small-size spherical light meter (Illuminova AB). After the incubation, the samples were filtered at low vacuum pressure through cellulose ester filters (Millipore; 0.22 μm), and the filters were subsequently exposed overnight to concentrated HCl fumes. Scintillation cocktail (4 mL; Optiphase Hisafe 2) was then added to each filter, and the radioactivity was measured in a Beckton-Dickinson LS6000 scintillation counter. Average in situ pPP was estimated from the photosynthesis-irradiance curve and the hourly in situ PAR irradiance within the "actively mixing layer" of the 24 h prior to sampling (*see* below).

Leucine incorporation rates—Leucine incorporation rates (LIR) were monthly estimated monthly using the ^3H-leucine incorporation method described by Kirchman et al. (1985). Four 1.2-mL aliquots and two trichloroacetic acid (TCA)-killed controls (5% final concentration) of each sample were incubated with 40 nmol L^{-1} ^3H-leucine for 2 h. The incubations were carried out in a water bath at in situ temperature in the dark and under fixed light irradiance (~ 1500 μmol photons m^{-2} s^{-1}, approximately the surface PAR irradiance of a summer day in this area). The incorporation was stopped by adding cold TCA (5% final concentration) to the vials and samples were kept at −20°C until processing as described by Smith and Azam (1992). Radioactivity was then counted on a Beckman scintillation counter.

From 15 January 2008 to 14 September 2009, LIR was also measured under exposure to natural solar radiation. For that purpose, six UVR-transparent cuvettes (4 mL; Plastibrand) of which two were formaldehyde-killed controls (4% final concentration) were amended with ^3H-leucine (40 nmol L^{-1} final concentration, 160 Ci $mmol^{-1}$) and incubated for 2–3 h under different radiation conditions: full sunlight spectrum (PAR + UVR), the full spectrum minus UVB (PAR + UVA; covered with the plastic foil Mylar-D, which excludes UVB radiation), PAR only (wrapped with two layers of Ultraphan URUV Farblos, which removes all UVR), or darkness (wrapped with aluminum foil inside a black plastic bag to avoid reflection). Cuvettes were incubated at about 5 cm under the surface inside a black tank (200 liters) with running seawater to maintain in situ temperature. After incubation, 1.2 mL were transferred from each cuvette to centrifuge tubes, then killed with 120 μL cold TCA (5% final concentration) and processed as described above.

MAR-CARD-FISH—In the experiments between 17 March 2009 and 13 April 2010, 30-mL samples were amended with trace amounts of ^3H-leucine (0.5 nmol L^{-1} final concentration, 160 Ci $mmol^{-1}$) and incubated in parallel in the dark or in the light (PAR only, ~ 1500 μmol photons m^{-2} s^{-1}) for 2–3 h. After exposure, samples were fixed overnight with paraformaldehyde (1% final concentration) at 4°C in the dark and filtered on 0.2-μm polycarbonate filters (GTTP, Millipore). Sections of the filters were then hybridized following the CARD-FISH protocol (Pernthaler et al. 2002). A few horseradish peroxidase (HRP) probes were used in order to characterize the composition of in situ bacterial communities: Gam42a that targets most *Gammaproteobacteria* (Manz et al. 1992), NOR5-730 for the NOR5 clade (Eilers et al. 2000*b*), SAR11-441R for the SAR11 cluster (Morris et al. 2002), Ros537 targeting the *Roseobacter* clade (Eilers et al. 2001), CF319a for clades belonging to *Bacteroidetes* (Manz et al. 1996), CYA339 for the cyanobacteria (Nübel et al. 1997), and Eub338-II-III for inclusion of most *Eubacteria* (Daims et al. 1999). The relative abundance of each group was checked by cutting smaller pieces from each filter and staining them with 4,6-diamidino-2-phenylindole (DAPI; 1 μg mL^{-1}). Between 500 and 800 DAPI-positive cells were counted manually within a minimum of 10 fields under an Olympus BX61 epifluorescence microscope.

For microautoradiography, we followed the protocol described in Alonso-Sáez and Gasol (2007). On the basis of

previous studies (Alonso-Sáez et al. 2006; Ruiz-González et al. 2012), only potentially photostimulable groups (i.e., *Gammaproteobacteria*, NOR5, *Cyanobacteria*, and *Roseobacter*) were subjected to microautoradiographic analysis. The optimal exposure times were determined for each sampling point and ranged from 2 to 19 d. After development, the slides were dried overnight and stained with DAPI, and 500–700 hybridized cells were counted manually by epifluorescence microscopy within a minimum of 10 fields.

Measurement and calculation of PAR and UVR doses—A radiometer (Biospherical PUV 2500) was used in the field and also placed inside the incubation tanks with the sensor covered by ~ 5 cm of water, and the downwelling cosine irradiance reaching the samples was recorded at a frequency of 5 s^{-1}. The wavelengths measured included six bands in the UVR (305, 313, 320, 340, 380 and 395 nm, in units of mW cm^{-2} nm^{-1}) and one integrated band in the visible (PAR, in μmol photons cm^{-2} s^{-1}). The mean spectral irradiance in the six UVR bands was converted to mean UVB and UVA irradiance (mW cm^{-2}) by integrating over the spectrum (sum of trapezoids), between 305 and 320 nm and 320 and 395 nm, respectively. Finally, the mean UVB, UVA, and PAR irradiance was multiplied by the duration of each experiment in order to obtain the radiation dose (in kJ m^{-2} for UVB and UVA and mol photons m^{-2} for PAR).

The "light" history of microbial communities (i.e., their previous UVR and PAR exposure at the sampling site) was calculated as a function of spectral irradiance at the water subsurface, vertical mixing depth, and underwater attenuation of solar radiation (Vallina and Simó 2007). For this purpose, two distinct exposure regimes were considered: seasonal exposure and maximum daily exposure. Seasonal exposure was calculated by combining the mean irradiance of the 3 d prior to sampling with the seasonal mixed layer depth (MLD), whereas maximum daily exposure was calculated as the combination of actively mixing layer depth (mLD) with average irradiance at noon ± 2 h of the previous day. Total solar irradiance (with hourly resolution) was obtained from a meteorological station located 5 km southwest of the BBMO sampling station (Malgrat de Mar, Catalan Meteorological Service, SCM). MLD and mLD were calculated from temperature profiles obtained from CTD casts, binned at 1-m intervals. MLD was defined as the depth where a jump in temperature larger than 0.15°C was encountered relative to 1-m depth, while mLD was defined as the depth showing a 0.03°C departure from the 1-m reference. These criteria were optimized for our particular data set and yielded mLD or MLD estimates that were consistent with the vertical profiles of other variables (M. Galí unpubl.). Diffuse attenuation coefficients of downwelling radiation ($K_{d,\lambda}$) were calculated as the slope of the linear regression between the natural logarithm of spectral cosine irradiance ($E_{d,\lambda,,z}$) and depth (z). $K_{d,320}$ and $K_{d,380}$ were chosen as representative of UVB and UVA attenuation, respectively, while PAR (and its corresponding $K_{d,PAR}$) was originally measured in one integrated band.

Statistical analyses—Shapiro–Wilk's *W*-test for normality of data and Levene's test for homogeneity of variance were applied prior to analysis, and either ANOVA or the nonparametric Kruskal–Wallis test was used to analyze statistically significant ($p < 0.05$) differences in the measured variables and post hoc analyses (Tukey's honestly significant difference test) for comparison among different light treatments or seasonal averages. Correlations between variables were calculated using the Pearson's correlation coefficient. These statistical analyses were performed using the JMP software (SAS Institute).

Results

Background information—The seasonal variation of the basic parameters in the study area is shown in Fig. 1 for 2008–2010. The summer period was characterized by high surface temperatures (20–25°C), a strongly stratified water column, and low Chl *a* concentrations (< 0.4 μg L^{-1}), while the opposite trend was observed in the well-mixed winter waters showing the lowest temperatures (~ 12°C) and largest Chl *a* peaks (up to 2 μg L^{-1}; Fig. 1A,B). In situ particulate primary production (pPP) also varied seasonally, reaching higher values in late winter (> 1.5 mg C m^{-3} h^{-1} in 2008) and variable peaks during spring and summer (Fig. 1C). No winter pPP peak showed up in 2009, although it is possible that we missed it by missing the March sampling.

LIR values showed large variability among sampling dates (range 2–135 pmol leucine L^{-1} h^{-1}; Fig. 1C). Maximum values tended to be observed after Chl *a* or pPP peaks, and higher values were generally found in summer and spring compared to autumn and winter, as reflected by a positive correlation between LIR and temperature (Pearson $r = 0.65$, $n = 36$, $p < 0.0001$). Bacterial abundances ranged threefold from 0.4 to 1.2 × 10^6 cells mL^{-1} and tended to be higher during the summer. *Synechococcus* and *Prochlorococcus* abundances also varied seasonally (Fig. 2A), with greater numbers in summer and autumn, respectively.

The bacterial community (composition assessed by CARD-FISH) was always dominated by the SAR11 group (average of 35% of cell counts) followed by similar proportions of *Bacteroidetes* (15%) and *Gammaproteobacteria* (13%). The latter two groups showed a strong seasonality, increasing their numbers during winter and peaking in spring in both years, closely following the Chl *a* peaks (up to 25% or 30% of cell counts for *Bacteroidetes* and *Gammaproteobacteria*, respectively). Conversely, the SAR11 group did not show any obvious seasonal pattern, with numbers ranging from 20% to 60% of total DAPI counts. *Roseobacter* and the gammaproteobacterial group NOR5 presented much lower numbers (average 5% and 2% of total DAPI counts, respectively) with abundance peaks generally coinciding with maximal Chl *a* concentrations.

Seasonal responses of bacteria to natural solar radiation—Exposure of samples to natural sunlight radiation caused a general but variable inhibition of LIR compared to the dark control (Fig. 3). The lowest LIR were observed under

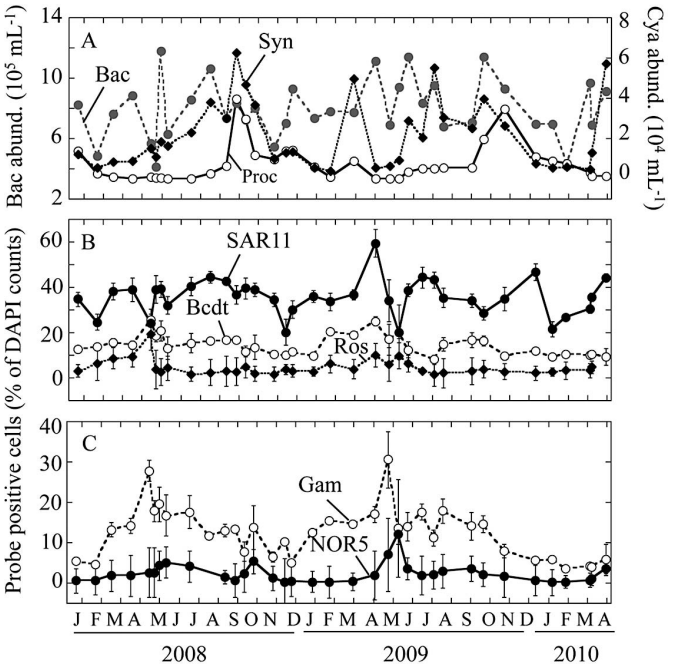

Fig. 2. (A) Seasonal variability in the abundance (abund.) of heterotrophic bacteria (Bac) and the two cyanobacterial genus (Cya) *Synechococcus* (Syn) and *Prochlorococcus* (Proc). Percentages of bacterial groups detected by CARD-FISH with HRP probes specific for (B) *Bacteroidetes* (Bcdt), SAR11, and *Roseobacter* (Ros) and (C) *Gammaproteobacteria* (Gam) and NOR5.

full sunlight (UVR inclusive) exposure (up to 60% inhibition, average 20%). PAR alone caused a significant decrease of LIR compared to the dark control in only 5 of the 25 experiments (range 20–32% decrease), and, exceptionally, significant increases (range 20–60%) were observed (Tukey's test, $p < 0.05$). The degree of inhibition due to UVR, as compared to PAR, was significantly correlated with the UVR doses measured during the incubations (Table 2; Pearson $r = 0.51$, $p < 0.02$, $n = 24$). However, this effect seemed to be driven mainly by UVA-induced inhibition ($r = 0.53$, $p < 0.01$, $n = 24$), as no significant correlation was observed between LIR measured under PAR or UVB radiation and their respective doses (Table 2).

The sensitivity of LIR to UVR was not correlated with any other measured parameter, including water transparency, salinity, Chl *a*, dissolved organic carbon (DOC) or nutrient concentration, primary productivity, depth of the mixed layer, and bacterial community composition or the abundance of the different bacterial groups as described by CARD-FISH (*n*-values from 8 to 26, *p*-values from 0.062 to 0.989; details not shown). Only sea surface temperature was positively correlated with UVR-driven inhibition ($r = 0.40$, $p < 0.05$, $n = 25$), yet probably this simply reflects the obvious relationship between warmer temperatures and greater UVR levels.

Seasonally averaged changes in LIR measured under natural light conditions are summarized in Table 1 as percentages of the dark control. No differences were found among seasons for LIR measured under PAR radiation. Conversely, a tendency for lower activities was found in spring and summer samples exposed to both UVA and UVR yet was not significantly different at the level of $p < 0.05$. When annually averaged, LIR measured under PAR + UVA and full sunlight were 15% and 20% lower, respectively, than LIR measured in the dark (Tukey's test, $p < 0.05$). LIR measured under natural PAR did not significantly differ from that in the dark (Table 1).

In order to find out which regions of the spectrum were responsible for these effects, the relative contribution of UVA and UVB to the total LIR inhibition (Fig. 4A) was calculated as follows:

$$\text{Inhibition due to UVX} = (\text{LIR}_{\text{PAR}} - \text{LIR}_{\text{UVX}}) \cdot 100 / \text{LIR}_{\text{PAR}} \quad (1)$$

where LIR_{PAR} represents the ^{3}H-leucine incorporation rates under PAR-only incubation treatment and LIR_{UVX} means the LIR measured under each UVR treatment. Inhibition due to UVB was calculated as the difference between the relative inhibition due to UVA and UVR. We found that the contribution of each type of UVR varied throughout the year, although, in most cases, UVA was responsible for most of the observed inhibition (Fig. 4A), and no seasonality was apparent in the contributions of each UVR fraction. The inhibition due to each fraction correlated not to the measured UVA : UVB ratio of irradiances during incubations (Fig. 4B) but to the ratio estimated at the sampling site (calculated from the in situ UV

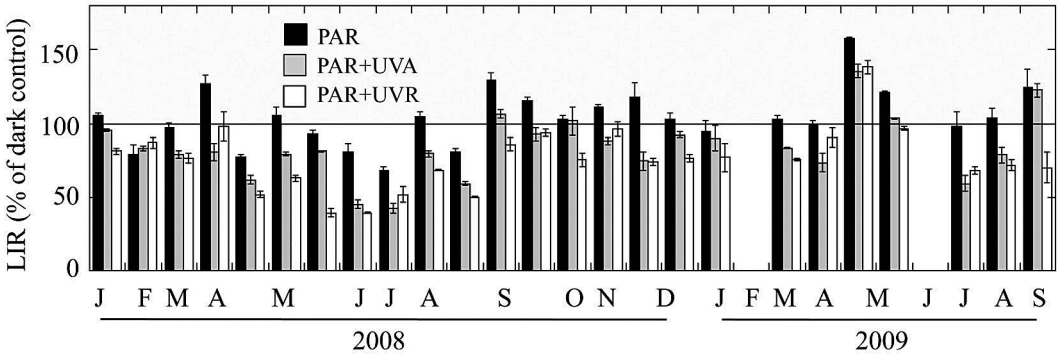

Fig. 3. Bacterial heterotrophic production measured under PAR (black bars), PAR + UVA (gray bars), and PAR + UVR (white bars) expressed as percentage of the dark control.

Table 1. Seasonally and annually averaged LIR measured under different light conditions (PAR, PAR + UVA, and PAR + UVR) presented as percentages of the dark controls. Last column: Seasonally averaged LIR measured under artificial PAR light (art. light) as percentage of the dark control. Values are average ± standard errors of sampling dates (n ranges from 4 to 25). Different superscript letters indicate significant differences among seasonal averages measured under different light conditions (Tukey's test, $p < 0.05$).

	In situ light conditions			Dark vs. art. light
	Average PAR LIR (% of dark control)	Average UVA LIR (% of dark control)	Average UVR LIR (% of dark control)	Average light LIR (% of dark control)
Winter	93±3[a]	86±4[a]	90±5[a]	119±9[a]
Spring	105±10[a]	86±11[a]	75±15[a]	151±13[a]
Summer	97±6[a]	77±8[a]	76±7[a]	96±10[b]
Autumn	100±0[a]	100±0[a]	88±7[a]	114±16[ab]
Annual average	99±4	85±4	81±5	120±6

irradiance measured during the 4 h of maximum insolation of the previous day; *see* Methods); thus, inhibition by experimental UVB was found to increase with the in situ UVA : UVB ratios ($r = 0.60$, $p < 0.003$, $n = 25$; Fig. 4C). In other words, the lower the UVB doses relative to UVA received by the plankton community prior to sampling, the higher the inhibition caused by UVB during the incubations. This was partially explained by the difference between the in situ UVA : UVB ratio and the one experienced by samples during our incubations. Experimental overexposure to UVB relative to the conditions microbial plankton was acclimated to would cause a larger deleterious effect of UVB.

Seasonal responses of bacteria to constant PAR exposure—An artificial light source (PAR only) was further used for comparison of the response of bacteria to the same light conditions across seasons. In general, LIR measured in the light was stimulated with respect to the dark control (range 20–150% increase), although inhibition (range 20–65% decrease) or no effect at all were occasionally observed as well (Fig. 5). Again, such variability in the responses was not correlated with other measured parameters, such as water transparency, salinity, Chl *a*, DOC and nutrient concentrations, primary productivity, or the composition of the bacterial community (n-values from 17 to 36, p values from 0.057 to 0.983; details not shown). However, significant relationships were found between the increase in the light-measured LIR relative to dark and the water temperature (Pearson's $r = -0.41$, $p < 0.02$, $n = 35$), the MLD ($r = 0.41$, $p < 0.02$, $n = 36$), and the maximum daily PAR irradiance (mean irradiance at noon ± 2 h of the previous day within the mLD, $r = -0.33$, $p < 0.05$, $n = 37$; *see* Methods). These observations indicate that the light LIR was generally higher than the dark LIR when lower irradiances occurred in situ, and, conversely, inhibition or no effect was found when the natural irradiances approached the artificial level (i.e., in summer). This explains the positive relationship with MLD: higher light-driven increases in LIR occurred when deeper mixed layers were found, that is, in response to experimental overexposure relative to in situ underwater irradiance conditions. In terms of seasons, the average photostimulation was maximal in spring (50% increase compared to dark LIR), whereas photoinhibition generally occurred in summer, when experimental light levels approached those in the sea (Table 1).

Table 2. Linear correlation analysis between inhibition of bacterial heterotrophic activity due to exposure to the different fractions of the spectrum and the PAR and UVR doses received by samples during the experiments. Statistically significant results ($p < 0.05$) are marked in bold.

Inhibition vs. dose	r	p-value	n
% of dark value			
PAR inhibition vs. PAR dose	−0.188	0.379	24
% of PAR value			
UVA inhibition vs. UVA dose	−0.532	**0.007**	24
UVR inhibition vs. UVR dose	−0.514	**0.010**	24
% of UVA value			
UVB inhibition vs. UVB dose	−0.035	0.872	24

Role of community structure in bulk bacterial responses to sunlight—To further investigate the reasons underlying such variability in the bacterial responses exposed to a fixed light source, several MAR-CARD-FISH incubations were performed to describe the response of potentially photostimulable bacterial groups. Probes for *Gammaproteobacteria*, *Roseobacter*, NOR5, and *Cyanobacteria* were selected for that purpose (Fig. 6), and hybridizations were carried out in the samples where the differences between dark and light LIR had been significant (either positive or negative; Fig. 5). Given the low abundances of the NOR5 group, it was not possible to quantify their number of active cells with accuracy, and they were not considered as potential drivers of the observed light-stimulation patterns.

Variable numbers of *Gammaproteobacteria* active in the uptake of ^{3}H-leucine were found all through the year (range 40–90% of active cells), showing higher percentages in summer and spring compared to autumn samples (Fig. 6A). This group showed a repeated pattern of significant stimulation due to light, except in August 2009, when they were slightly inhibited with respect to the dark control. Notably, this observation was coincident with the observed decrease in bulk light LIR (*see* Fig. 5). A good positive correlation was found between the light-driven increases in the number of active *Gammaproteobacteria* and the increase in bulk LIR caused by light ($r = 0.73$, $p < 0.001$, $n = 17$; Fig. 7A). Moreover, significant correlations were found

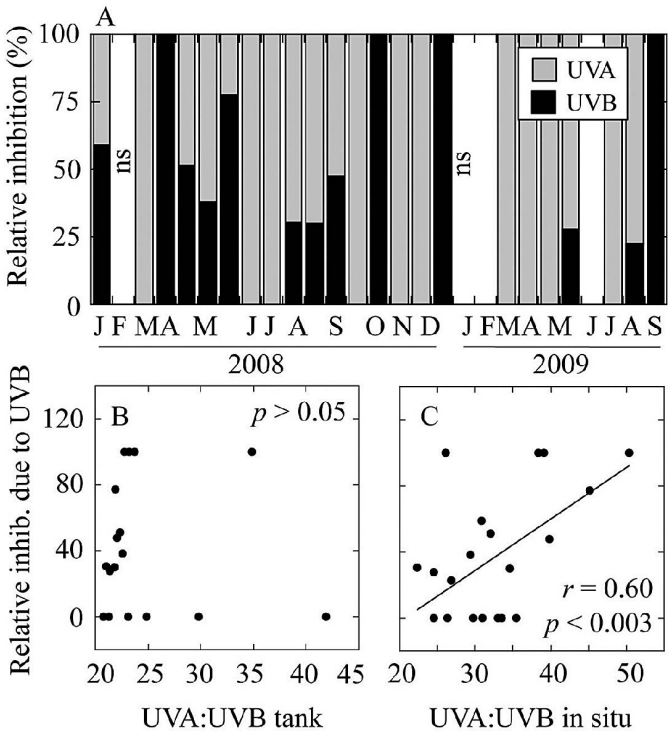

Fig. 4. (A) Relative contribution of UVA (gray bars) and UVB (black bars) to total inhibition (inhib.) of bacterial production with respect to the PAR treatment. Variation of the relative contribution of UVB to total UVR-inhibition with respect to (B) the ratio UVA : UVB experienced by samples during incubations or to (C) the in situ UVA : UVB ratio (calculated from the in situ UV irradiance measured during the 4 h of maximum radiation of the previous day; *see* Methods). "ns" indicates dates where there were no significant differences between PAR and UVA or UVR treatments (Tukey's test, $p < 0.05$).

between the number of active *Gammaproteobacteria* and bulk LIR ($r = 0.59$, $p < 0.02$, $n = 17$) and between active *Gammaproteobacteria* and active *Eubacteria* ($r = 0.66$, $p < 0.003$, $n = 17$) measured in the dark (Fig. 7B,C). These correlations were better in the light ($r = 0.67$, $p < 0.004$, $n = 17$, and $r = 0.82$, $p < 0.0001$, $n = 17$, respectively; Fig. 7B,C). Interestingly, *Gammaproteobacteria* abundances seemed to be explained in part by the underwater ambient PAR levels ($r = 0.57$, $p < 0.0005$, $n = 29$), showing greater abundances in more illuminated waters, while no correlation was apparent with temperature, Chl *a*, or primary production data. As with bulk LIR, furthermore, the magnitude of light-driven increases in the number of active *Gammaproteobacteria* was negatively correlated with the maximum daily PAR irradiance ($r = -0.49$, $p < 0.05$, $n = 17$).

No other bacterial group seemed to explain the observed bulk light-driven differences due to light in bulk LIR. Very high percentages of *Roseobacter* were active in ^{3}H-leucine uptake throughout the year (> 95% of labeled cells), but no significant differences were commonly found between dark and light treatments (only in three of nine sampling dates). The fraction of active *Cyanobacteria* rarely exceeded 10%, and although some differences were detected between treatments (up to twofold increases), their low activity and different stimulation patterns excluded them as candidates responsible for the light enhancement of bulk LIR.

Discussion

Very few seasonal studies have considered the responses of marine microbial communities to temporally variable natural radiation levels, UVR being often omitted as a significant driver of microbial activities. Given the high transparency to UVR of most oceanic waters and the reported distinct UVR sensitivity of different bacterial groups (Alonso-Sáez et al. 2006), seasonal variations in light intensity and penetration into the water column might differentially affect the year-round use of DOM by bacteria, thus modulating the effects of other environmental variables that are more easily and frequently measured.

Seasonal responses of bacteria to natural sunlight conditions—Our approach consisted of short-term incubations under natural sunlight with the radioisotope tracer already added, which allows a more realistic estimation of in situ incorporation rates since irradiation and uptake

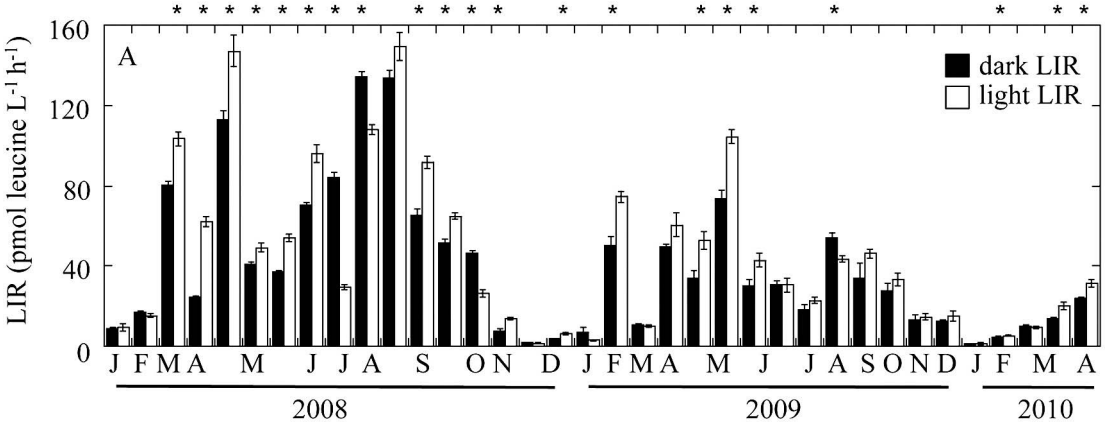

Fig. 5. Seasonal variability in bacterial heterotrophic production measured in the dark and under a fixed light source (~ 1500 μmol photons m^{-2} s^{-1}). Asterisks indicate significant differences between dark and light incubations (Tukey's test, $p < 0.05$).

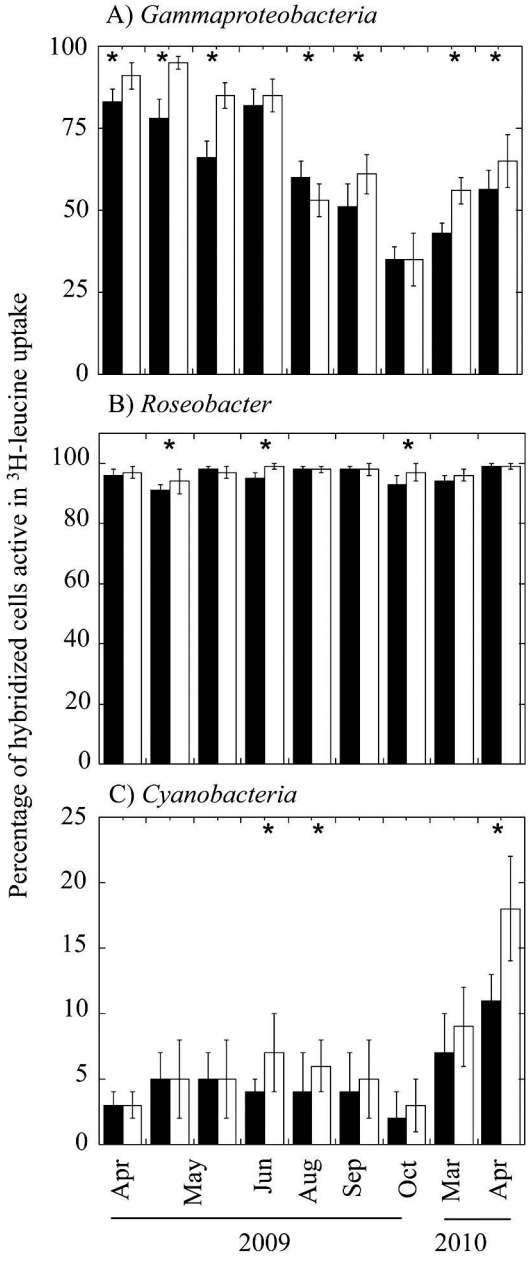

Fig. 6. Percentage of positively hybridized cells with probes for (A) *Gammaproteobacteria*, (B) *Roseobacter*, and (C) *Cyanobacteria* taking up ^{3}H-leucine (average ± standard deviation) as measured by MAR-CARD-FISH after exposure to a fixed light (~ 1500 μmol photons m^{-2} s^{-1}; open bars) or kept in the dark (black bars). Asterisks indicate significant differences between light and dark treatments (Tukey's test, $p < 0.05$). Only samples where a clear light-driven response in LIR was apparent were analyzed.

processes are not separated in time. Following Vaughan et al. (2010), any possible UVR effect on the added leucine tracer was discarded since no significant reduction in LIR was found in samples amended with previously exposed ^{3}H-leucine to both natural or artificial UVR (data not shown). Unfortunately, light-driven changes in the bioavailability of endogenous DOM could not be discriminated from direct UVR effects on bacteria. On the other hand, short-term incubations were thought to prevent or minimize other indirect interactions derived from, for example, effects on viruses or grazers. In any case, we have to bear in mind that the observed bacterial responses are the final balance among all the synergistic and antagonistic effects that are taking place at the same time inside the experimental cuvettes.

With this approach and as reported by others (Aas et al. 1996; Sommaruga et al. 1997), we found a significant UVR-driven decrease in LIR with respect to the values measured in dark incubations. In general, we found low or no inhibition when irradiance values were low (winter and autumn) and greater inhibition (up to 60%) under high irradiances (spring and summer). This suggests that, under certain circumstances, standard measurements in the dark may severely overestimate bacterial heterotrophic activity. This would be particularly dramatic in highly illuminated waters. Annually averaged, the LIR measured under full sunlight conditions was 20% lower than that measured in the dark.

In contrast, exposure to natural PAR only did not generally affect the measured LIR regardless of the irradiance, except for a few cases where a slight decrease (mainly in spring and summer) or an occasional increase were observed. Other studies have also observed different degrees of inhibition (Aas et al. 1996; Sommaruga et al. 1997; Morán et al. 2001) or stimulation (Aas et al. 1996; Church et al. 2004; Pakulski et al. 2007) when measuring LIR under in situ PAR irradiance, effects that have been attributed to photodynamic processes (Harrison 1967). Morán et al. (2001), though, suggested that PAR-mediated decrease in samples from the same area of our study was due to enhanced bacterial activity in the dark rather than inhibition by light, yet the exact mechanisms were not identified.

An interesting aspect of the UVR effects refers to the relative contribution of UVA and UVB to the total LIR inhibition. In our experiments, the contribution of UVA was generally higher than that of UVB (Fig. 4), as also seen by other authors (Sommaruga et al. 1997; Visser et al. 1999). This might be attributed to the fact that even though UVB is more energetic than UVA, the amount of UVA energy that reaches the sea surface is much larger than that in the UVB region. On some occasions, however, higher inhibition by UVB was observed. In those cases, the increase in the relative inhibition by UVB in experiments was associated with deeper in situ mixing layers ($r = 0.61$, $p < 0.002$, $n = 25$; data not shown). Vertical mixing controls the residence time of marine bacteria in surface waters, and it has been shown to be an important factor regulating the exposure to and the effects of UVR (Huot et al. 2000; Bertoni et al. 2011). Since the attenuation of UVB in the water column is much stronger than that of UVA or PAR, bacterioplankton transported within a deeper mixing layer (e.g., in winter) will be exposed to higher UVA : UVB ratios than cells confined in a strongly stratified and shallow layer (e.g., in summer), where they will be continuously exposed to deleterious UVB doses and will have fewer chances for UVA- or PAR-driven photorepair of DNA damage (Friedberg et al. 1995). A more recent study of Bertoni et al. (2011) shows for the first time that mixing reduces LIR inhibition and that large differences can be found between fixed and vertically moving

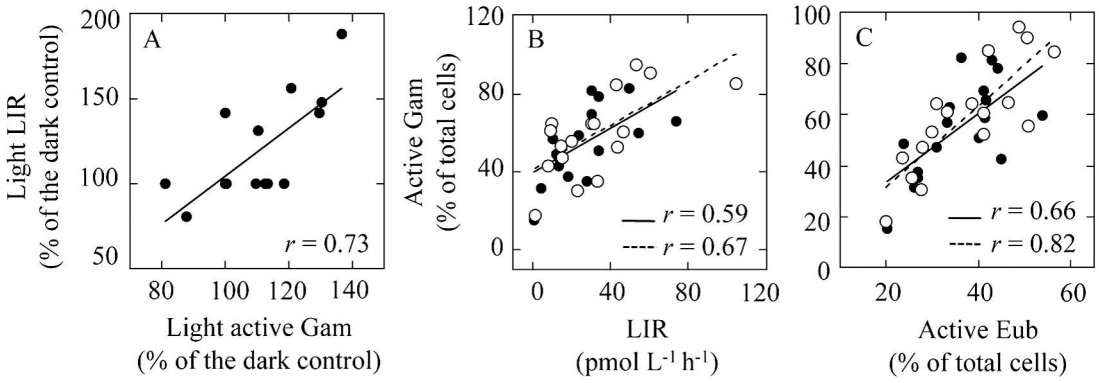

Fig. 7. (A) Comparison between the variation in LIR measured in the light (scaled to the dark control value) and the light-driven increase in active *Gammaproteobacteria* (Gam; expressed as % of the dark numbers). Relationships between the percentages of active *Gammaproteobacteria* and (B) bulk LIR or (C) percentages of active *Eubacteria* (Eub) incubated in the dark (black dots, solid line) or under an artificial light source (open dots, dotted line).

incubations. Thus, it seems that many of our static incubations led to an overexposure to UVB of organisms naturally inhabiting a well-mixed water column and thus acclimated to lower UVB doses, resulting in an enhanced UVB inhibition compared to UVA. This was supported by the fact that higher inhibition due to UVB was found with increasing in situ UVA : UVB ratios on the previous day (Fig. 4C), that is, with increasing experimental overexposure to UVB proportions relative to conditions in the sea. UVB has often been regarded as the main contributor to bacterial damage (Herndl et al. 1993), but, in view of our results and those recently reported by Bertoni et al. (2011), it is possible that, depending on the environmental characteristics of the samples, the use of artificial UVR lamps or long surface incubations that neglect natural mixing effects and cause overexposure to UVB results in unrealistic inhibitory observations. All the aforementioned point to the relevance of taking into account the often overlooked light-exposure history of samples (which is in turn dependent on the mixing regime) and further highlight the difficulty of mimicking natural underwater light conditions.

Seasonal responses of bacteria under invariable PAR conditions—In addition to the intensity and spectral characteristics of sunlight, the response of bacteria to solar radiation has been shown to depend on or interact with many other environmental or biological factors, such as temperature (Bullock and Jeffrey 2010), nutrient status (Pausz and Herndl 2002), or the specific sensitivities of different bacteria (Alonso-Sáez et al. 2006). Hence, in order to search for other potential causes of seasonality in the bacterial responses, we excluded the effect of experimental light variability by incubating a parallel set of samples under a fixed artificial PAR source (equivalent to the annual mean surface irradiance in this area). Unlike natural PAR exposure, this indoor approach led to a general stimulation of activity relative to the dark control. Unexpectedly, though, such an effect was more pronounced in spring than in summer, when no changes or even inhibition occurred. This seasonality in the light effects of different samples receiving exactly the same irradiance discarded an exclusive dependence of bacterial responses on light intensity and suggested that causes other than irradiance influenced the observed variability. During our annual cycle, neither pPP, DOC, Chl *a* or nutrient concentration, nor the composition of the bacterial communities (in terms of group abundances) seemed to influence the light-driven responses of LIR to natural sunlight. In a recent study conducted also in the BBMO, we showed that responses to natural solar radiation at the community level are influenced by taxon-specific sensitivities to sunlight and their relative contribution to total activity (Ruiz-González et al. 2012). Hence, we wanted to check whether the observed seasonality in the bacterial responses to a fixed irradiance was also influenced by the activity of some particular groups.

Role of bacterial community composition in bulk responses to sunlight—Single-cell activity analyses were performed in order to search for bacterial groups responsible for the observed light-driven changes in bulk activity. Several studies that also reported similar PAR-driven stimulation of bulk LIR attributed it to light-enhanced amino acid uptake by cyanobacteria (Church et al. 2004; Michelou et al. 2007; Mary et al. 2008). Our MAR-CARD-FISH data (Fig. 6C), conversely, discarded this group as the main driver of the observed responses because of the low numbers of active cells and the lack of significant light enhancement in these numbers concomitant with LIR increases. However, bacterial groups other than cyanobacteria have also been shown to augment their activity under the light (Alonso-Sáez et al. 2006; Mary et al. 2008; Straza and Kirchman 2011) in what has been attributed to the photoheterotrophic capabilities of some phylotypes containing light-harvesting proteorhodopsins (PR) or BChl*a* (Béjà et al. 2000; Kolber et al. 2000). With the aim to check whether photoheterotrophic bacteria were responsible for the observed increases in LIR, *Gammaproteobacteria*, *Roseobacter*, and the NOR5 group were probed on the basis of previously published data indicating that these taxa occasionally presented light-enhanced activity in this area (Alonso-Sáez et al. 2006; Ruiz-González et al. 2012). SAR11 and *Bacteroidetes* were not considered because of

the reported negative sensitivity to light of the former and the lack of responses to sunlight and low contribution to total active cells of the latter (Alonso-Sáez et al. 2006; Ruiz-González et al. 2012).

While the great majority of *Roseobacter* cells were active in both light and dark treatments throughout the year, increases in the number of active cells due to light were often negligible, so it is unlikely that they accounted for the observed light-stimulated LIR. Conversely, the numbers of active *Gammaproteobacteria* cells significantly increased in the light during most of the study period, showing a stimulation pattern very similar to that of bulk LIR. Even the observed LIR decrease in August was mirrored by a decrease in active *Gammaproteobacteria*, thus pointing to a major role of this group in the community response to light. This role, remarkable because *Gammaproteobacteria* were not the most abundant prokaryotes, was further supported by the good positive correlations observed between the number of active cells within this group, the number of active *Eubacteria* cells, and LIR. Some members of the *Gammaproteobacteria* maintain large numbers of ribosomes during extended periods of nongrowth, which allow them to rapidly initiate growth on changing environmental conditions (Eilers et al. 2000*a*). Thus, they might also take quick advantage of changes in light conditions and respond faster than other groups.

Interestingly, the *Gammaproteobacteria* showed preference for highly illuminated environments as seen by the good correlation between the seasonal irradiance and cell abundances, not seen with other variables. This is in accordance with their apparent ability to benefit from light, and it is further supported by the relatively high resistance to UVR reported for these bacteria in the study area (Alonso-Sáez et al. 2006; Ruiz-González et al. 2012).

Within *Gammaproteobacteria*, the NOR5 clade was analyzed in detail because one sequenced member of the group had shown capability for aerobic anoxygenic photosynthesis (Fuchs et al. 2007). Unfortunately, their very low abundances throughout most of the year prevented an accurate quantification of active cells and discarded them as major drivers of increases in LIR. However, in a parallel study in the BBMO, we found that their ^{3}H-leucine uptake was occasionally stimulated by natural PAR (Ruiz-González et al. 2012). On 26 May 2009, when they made up nearly 90% of all *Gammaproteobacteria*, they might indeed have driven the light response of the whole group.

Influence of the previous light exposure history on bacterial responses to light—In agreement with the observations with samples exposed to natural radiation conditions, also in the artificial light experiments, the previous light exposure history seemed to partially explain the observed light effects on LIR. Interestingly, the lower the maximal daily irradiance bacteria had been exposed to in the sea, the larger the increase caused by our artificial light source. In contrast, smaller or even negative effects of light were observed when the natural maximal irradiance was more similar to the experimental irradiance (i.e., in summer). This same pattern was also apparent in the numbers of active *Gammaproteobacteria*, supporting their role in driving the responses to light at the community level despite their low abundances. In other words, the bigger the difference between the natural and the experimental light conditions, the greater the effects we should expect. This finding is similar to that of Straza and Kirchman (2011), who found that the magnitude of the light-driven effects on bacterial activity was lower with greater light exposure prior to sampling, albeit the reasons behind this observation have not yet been elucidated.

Among the possible explanations, we may consider a seasonally variable photoheterotrophic response of the *Gammaproteobacteria* or other taxa containing PR or BChl *a*. It has been hypothesized that photoheterotrophy would be more advantageous in nutrient poor conditions (Kolber et al. 2000); thereby, highly illuminated oligotrophic waters such as those of Blanes Bay, where strong year-round phosphorous limitation of LIR is known to occur (Pinhassi et al. 2006), might select for phylotypes with photoheterotrophic capabilities. A similar strategy was described by Gómez-Consarnau et al. (2007) for a cultured PR-containing *Bacteroidetes* isolated from the BBMO that indeed showed higher photostimulation of growth when growing on low DOM concentrations; however, to date, no field measurement has consistently supported this hypothesis. In Blanes Bay it makes sense that lower PR photoheterotrophy occurs in summer, when DOC accumulates (C. Romera-Castillo unpubl.), presumably because of nutrient limitation of microbial activities. Instead, photoheterotrophy might be higher in spring, when DOC levels are at their minimum but there already is enough light. If this was the case in Blanes Bay and PR-containing bacteria were more active or abundant in spring than in summer, greater light-driven increases would be expected in spring on exposure to high light conditions.

On the other hand, preliminary data from the BBMO indicate that BChl *a*–containing bacteria are abundant in spring and summer and found at very low numbers in winter (I. Ferrera, unpubl.) and, interestingly, they have shown growth rates similar to those of *Gammaproteobacteria* (Ferrera et al. 2011). Should light supplement any energy for growth, the experimental overexposure experienced by spring microbes might have induced a photoheterotrophic response stronger than that of summer BChl *a*–containing bacteria, already exposed to high light conditions in situ. In any case, no direct evidence is so far available of photoenhanced leucine uptake by these kinds of mixotrophic organisms, so we cannot unequivocally determine whether the observed light increases in activity were mainly the result of bacterial photoheterotrophy.

A rapid response of bacteria to photosynthate leaks from phytoplankton on light exposure could provide a plausible alternative explanation. *Gammaproteobacteria* abundances seemed to follow the peaks in Chl *a*, as if they were rapidly responding to short-term variations in PP. It is thus likely that overexposure of algae with respect to their previous in situ light conditions would have resulted in an enhanced release of DOM, thus stimulating the activity of *Gammaproteobacteria*. However, the estimated excess of pPP due to the difference between the artificial and the in situ irradiances did not exhibit the same variability of the LIR and the active *Gammaproteobacteria* cells. Unfortunately, we did not measure the rates of photosynthetically

extracellular release (PER), which has sometimes been shown to increase because of abrupt changes in irradiance (Mague et al. 1980) and in this area may vary throughout the year independently from particulate PP (Alonso-Sáez et al. 2008). Thus, a potential role of light-induced PER in light LIR increase could not be ruled out.

Differences in DOM quality might also explain the variations in the bacterial responses. In the northwestern Mediterranean, Tedetti et al. (2009) reported a significant PAR-exposure enhancement of DOM bioavailability and bacterial activity in spring, whereas light exposure of DOM in summer caused inhibition of LIR, mainly because of UVA. We cannot test if this was the case in our study because we had no data of DOM phototransformations and bioavailability; nonetheless, the facts that the largest light-driven increases in LIR were observed in spring and that UVA was the main inhibitor of bacterial activity support this argumentation.

Finally, the heterotrophic uptake of DOM reported for many algae (Amblard 1991) further complicates the picture. Significant numbers of the diatom *Chaetoceros* spp. labeled for ^{3}H-leucine were found in March 2009 microautoradiography filters (details not shown), yet no differences were visually apparent between the numbers of active diatoms in the light and dark bottles. Similarly, radiolabeled *Pseudonitzschia* spp. cells were often found throughout the study period, but again no obvious differences were observed between the two treatments. Using a microautoradiographic approach like ours, Paerl (1991) unveiled that large phytoplankton (mainly diatoms) from different oceanic regions occasionally showed active incorporation of organic substrates, mainly during bloom events, which seemed to be the case in March 2009. Since diatoms dominate Blanes Bay phytoplankton assemblages in spring (Gutiérrez-Rodríguez et al. 2011), it is also possible that they contributed partially to the measured uptake of ^{3}H-leucine. Further research is needed to determine the ecological relevance of this generally overlooked role of phytoplankton in DOM fluxes.

In summary, compared to the dark incubation values, the observed light effects on bacterial activity ranged from a 60% UVR-driven decrease up to an increase of 150% due to exposure to high-intensity artificial PAR. This variability, though, was certainly not only a function of irradiance levels. It seemed to be strongly dependent on how much our incubation conditions differed from the natural irradiance levels previously experienced by the organisms. This underlines the importance of knowing the previous light exposure history in order to accurately mimic in situ light conditions or at least to avoid misinterpretation of the results. Similarly, the bacterial community structure seemed to play an important role in the observed responses since particular taxa appeared to drive some of the patterns.

Given the importance of bacteria for carbon and energy fluxes and nutrient cycling in the pelagic ocean, the observed effects of light on bacteria may have ecosystem implications, such as seasonal shifts in the dominant pathways of DOM use by different bacteria, accumulation of labile DOM in the surface ocean due to inhibition of microbial consumption, or even potential changes in community structure through selection of UVR-resistant bacterial groups. Our results may also have important methodological implications. Measurements of bacterial heterotrophic production are generally performed in the dark, which has the advantages of avoiding algal stimulation, circumventing the problem of reproducing ambient light levels, and allowing comparison among different studies. Dark measurements, however, do not capture the here described effects of sunlight on bacterial activity and may hence result in severe over- or underestimation. Incubations under realistic light conditions are recommended, particularly if the role of bacteria is to be integrated into quantitative models of carbon cycling for description on prediction purposes. How to reproduce realistic light conditions experimentally for routine measurements remains quite a challenge.

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