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P5-11 JUDITH VAN BLEIJSWIJK

releaved from contact stress by the macroalga Halimeda macrophysa Persistent change in microbial community in massive Porites

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on coral reefs. Consequently, the interactions between macroalgae and corals increase. In the dynamics of coral hancing microbial activity. This potentially disturbs the existing balance in the composition and abundance of the disturbances, corallivory and coral diseases) allow the proliferation of benthic algae and other benthic organisms microbiota associated with corals. algae interactions an important role is ascribed to microbes; benthic algae release dissolved organic carbon en-Enhanced nutrient supply, low grazing on algae, and increase of space (due to decline of coral cover by physical

macroalga stress we recorded changes in the microbiota with particular focus on the resilience of coral microbiota To further explore unbalance in the composition and abundance of the microbiota associated with corals, due to after the stress event.

would converge to the community composition in the undisturbed part of the coral. bleached coral, appearing underneath the H. macrophysa, to have a different microbial community than the unafing the in situ stress factor, the alga Halimeda macrophysa growing in contact with the coral. We hypothesized the pyrosequencing, the shift in the coral associated bacterial community in the massive coral Porites sp. after removfected part of the same colony, but that in time the bacterial community in the part relieved from algal contact We present an in situ experiment on reefs 20 km off the east coast of Kalimantan, Indonesia. We determined, with

Halimeda macrophysa and that the change was persistent for at least 40 days after macroalga removal Our results show that the bacterial community of massive Porites was significantly altered by interaction with

Keywords: Halimeda macrophysa, massive Porites, macroalgae, microbial community, Indonesia

P5-12 STEFAN LAMBERT

Seasonal rhythm of phytoplankton picoeukaryote communities in the North Western Mediterranean Sea

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approach. Mamiellophyceae and Dinophyceae dominated the dataset in sequence numbers. The main contribuotes. Environmental and biological parameters have been recorded twice a month at SOLA Station (Bay of Banyuls spring blooms have been observed for several important phytoplankton groups such as diatoms and picoeukarywinter to spring is accompanied by an increase in abundance and diversity of the phytoplankton. Phytoplanktonic cycles, as it generates roughly 50% of the global primary production. In temperate oceans, the transition from tors of Mamiellophyceae (Micromonas and Bathycoccus) exhibited strong seasonal rhythms which are often unsur Mer, North Western Mediterranean Sea) since 2007. We have analyzed this time-series, using a metabarcoding Marine phytoplankton is at the basis of the food chain in the oceans and plays an essential role in biogeochemical

> occur in February at minima of temperature every year. Mamiellophyceae OTU was reproducible from year to year throughout the time series. Bathycoccus OTU usually coupled from less rhythmic chlorophyll annual variations, arising from spring floods. The succession order of

Keywords: Phytoplankton, Seasonality, Time Series, metabarcoding

P5-13 GRETA REINTJES

On-site microbial diversity and abundance analysis in the remotest part of the world's oceans, the South Pacific Gyre

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microbial community composition within 48 h of sampling. this pipeline, we analysed the microbial community of the South Pacific Gyre (SPG) and obtained insights into the tion, we modified a laboratory based sequencing and analysis pipeline to work on-board a research vessel. With rent sequencing techniques is that they are not suitable to directly gain results in the field. To overcome this limitathe diversity and functional potential of microbial communities. However, a major limitation of most of the curindependent techniques, such as DNA sequencing technologies. These advances enabled the in-depth analysis of Microbial ecology has progressed immensely in recent years due primarily to methodological advances in culture-

the aphotic zone the dominant organisms were the SAR406 clade, SAR324 clade, and SAR202 clade. consisting of organisms associated with organic matter degradation such as Bacteroidetes. Below the DCM and in mg m⁻³, which is comparable to other oceanic gyres. It had a diverse microbial community composition partially deep chlorophyll maximum (DCM) was at a depth of 200 – 250 m and had a chlorophyll a concentration of 0.47 by oligotrophic microorganisms such as SAR86, Candidatus Actinomarina, SAR11 clade, and Prochlorococcus. The The surface waters of the SPG had extremely low nutrient and chlorophyll a concentrations and were dominated

during our research expedition into the SPG. sity even at a remote sampling site. This enabled us to do more targeted sampling and hypothesis-driven research By developing an on-board sequencing and analysis pipeline we could rapidly assess the prevalent microbial diver-

Keywords: South Pacific Gyre, DNA sequencing, oligotrophic, diversity

P5-14 JEONARDO CERASINO

Diversity and dynamics of bioactive metabolites in cyanobacteria of southern perialpine lakes

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(species, population). We have conducted a metabolic profiling of the most important cyanobacteria species in bolic profiling can therefore provide valuable informations on the ecology of cyanobacteria at different levels species to species, and even in the same species the production of these compounds is not constant. The metaof secondary metabolites, many of which are bioactive. The nature and quantity of these metabolites vary from mopsins). Cyanobacteria have indeed an impressive chemical machinery that leads to the production of hundreds isms have the capability of producing potent toxins (e.g. microcystins, nodularins, anatoxins, cylindrosper-Cyanobacteria proliferation in natural and artificial water bodies represents a sanitary threath since theyse organ-

southern perialpine lakes, namely Aphanizomenon flos-aquae, Dolichospermum lemmermannii, Microcystis aeruginosa, Planktothrix rubescens, and Tychonema bourrellyi. I.C.-MS/MS analyses were conducted on natural sample as well as on cultured strains. We conducted targeted analysis aimed at identifying the most common toxins (microcystins, nodularins, anatoxins, cylindrospermopsins, paralytic shellfish poisons). We also conducted untargeted analysis aimed at identifying as many secondary metabolites as possible. Targeted analysis showed that M. aeruginosa and P. rubescens produced toxic peptides (microcystins), T. bourrellyi produced toxic alkaloids (anatoxin-a and possibly some paralytic shellfish toxins), Aph. flos-aquae and D. lemmermannii did not produce any of the analyzed toxins. Untargeted analysis confirmed the ability of M. aeruginosa and P. rubescens in producing a large number of peptidic metabolites, mainly belonging to three categories: microcystins, aeruginosins and anabaenopeptins. The remaining species showed a lower propency in producing peptides, being their metabolism apparently more oriented toward the production of alkaloids.

Keywords: cyanobacteria; cyanotoxins; LC-MS; alkaloids; peptides.

P5-15 MARTA VARELA

Short term variability of bacterial communities in the shelf waters off Galicia (NW Iberian Peninsula): patterns and drivers shaping the diversity

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We combined flow cytometry, CARD-FISH and 16S rRNA gene tag pyrosequencing to investigate the short-term variability of the bacterial communities in samples collected along a transect in the shelf off NW Iberian Peninsula over one week. Bacterial abundance and community composition was stable over the temporal scale of days. Higher abundance and relative activity (expressed as a percentage of high-nucleic acid content cells) was found in surface waters at stations closer to the coast. CARD-FISH analysis displayed that SAR11, SAR86 and Roseobacter were the most abundant bacterial taxa at all samples. Using pyrosequencing, we found a higher diversity and number of operational taxonomic units (OTUs) in surface waters compared to the deep chlorophyll maximum (DCM). Surface communities were mainly dominated by Flavobacteriaceae and Alteromonadaceae, whereas samples collected at the DCM were affiliated to Acidomicrobiales, SAR406 and Oceanopirillales. Bacterial communities inhabiting in surface waters were associated with higher temperature and light conditions, whereas deep samples exhibited a significant positive relationship with salinity, inorganic nutrients and chlorophyll a. Surface and DCM layers harbor significantly different-bacterial communities, following the vertical patterns of temperature, light and nutrients.

Keywords: Bacteria, CARD-FISH, 454pyrosequencing, short-term variability, NW Iberian Peninsula

P5-16 TAMARA RODRÍGUEZ RAMOS

Changes in bacterial activity and community composition in response to water mass mixing

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Mixing zones and boundaries between different water masses are "hot spots" of marine biodiversity and activity. We aimed to investigate the effects of water mass mixing in the dark-ocean microbial communities by collecting and incubating natural bacterial communities from the Mediterranean Water (MW; at 1000 m depth), the Subpolar Modal Water (SPMW, 500m) and the Labrador Sea Water (LSW, 1800 m), and comparing them with artificially mixed communities. Mixing experiment 1 consisted of incubating at in situ conditions the original LSW and MW communities, plus a mixture of both (MIX1, dilution 1:1), whereas the Mixing experiment 2 included the original prokaryotic communities from SPMW and MW and a mixture of both (MIX2, dilution 1:1). Bacterial abundance and activity was monitored every 24h over 8 days, while bacterial community composition and DOM characterization were assessed at the beginning (day 0), middle (day 4) and at the end of the experiment (day 8). Live prokaryotic cell abundance was higher in the MIX1 and MIX2 treatments as compared to the original communities. Moreover, MIX1 bacterial showed slightly higher leucine incorporation rates than MW or LSW. These metabolic responses were accompanied by changes in the optical properties of DOM, suggesting a change in the dynamics of the organic matter. Taken together, our results indicate differences in the bio-reactivity of the organic matter after mixing as compared to the original water masses that could influence the composition and activity of the bacterial community. Keywords: dark-ocean, bacterial activity, bacterial diversity, water mass mixing, dissolved organic matter

P5-17 ADRIA AULADELL MARTÍN

Community ecology of aerobic anoxygenic phototrophic (AAP) bacteria at various temporal and spatial scales

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large genetic studies with global and culerian sampling have the most powerful potential to discern the spatiohigher richness was observed at temporal scales in a single site, dissimilarities between samples at spatial scales and phototrophic nanoflagellates abundance. Comparing spatial and temporal scales, we observed that although ties and half of the variation was explained by day length, temperature, water transparency, chlorophyll a, salinity not be associated to any defined phylogroup. At temporal scales, seasonality clearly differentiated AAP communitemporal dynamics of marine microbial communities. presented more variation, which increased with geographical distance. Our work shows that a combination of ria, Roseobacter and Rhodobacter were dominant but, interestingly, in some stations half of the sequences could location and by environmental conditions. In most stations phylogroups associated with the Gammaproteobactevatory). At the spatial scale, we observed that variation in community structure was driven both by geographical Malaspina, as well as from a decade-long time-series in the NW Mediterranean Sea (Blanes Bay Microbial Obserof AAPs by analyzing the diversity of their marker gene pufM in large metagenetic (PCR-amplification and metabolism and physiology have been intensively studied during the last two decades, but there is still a lack of large-scale analyses needed to unravel their spatio-temporal dynamics. Here, we focus in the community ecology for growth, but can derive a portion of their energy harvesting light using bacteriochlorophyll a. Their ecology, Aerobic anoxygenic phototrophs (AAPs) are photoheterotrophic microorganisms that require organic substrates Illumina sequencing) and metagenomic datasets from 2 global circumnavigation expeditions, Tara Oceans and

Keywords: aerobic anoxygenic phototrophic bacteria, carbon cycle, dissimilarity, temporal dynamics