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P5-11 JUDITH VAN BLEIJSWIJK

Persistent change in microbial community in massive *Porites* released from contact stress by the macroalgae *Halimeda macrophyssa*

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

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

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

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

Keywords: *Halimeda macrophyssa*, massive *Porites*, macroalgae, microbial community, Indonesia

P5-12 STEFANI LAMBERT

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

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

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

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

The surface waters of the SPG had extremely low nutrient and chlorophyll *a* concentrations and were dominated by oligotrophic microorganisms such as SAR86, *Candidatus Actinonarina*, SAR11 clade, and *Prochlorococcus*. The deep chlorophyll maximum (DCM) was at a depth of 200 - 250 m and had a chlorophyll *a* concentration of 0.47 mg m⁻³, which is comparable to other oceanic gyres. It had a diverse microbial community composition partially consisting of organisms associated with organic matter degradation such as *Bacteroidetes*. Below the DCM and in the aphotic zone the dominant organisms were the SAR406 clade, SAR324 clade, and SAR202 clade. By developing an on-board sequencing and analysis pipeline we could rapidly assess the prevalent microbial diversity even at a remote sampling site. This enabled us to do more targeted sampling and hypothesis-driven research during our research expedition into the SPG.

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

P5-14 LEONARDO CERASINO

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

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

