

## Session 1: Microbial genomics and metagenomics

### P01 | Changes in the *Caulerpa* microbiome due to abiotic stresses

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Morphologically complex seaweeds such as siphonous green algae are among the most notorious invasive species in many parts of the world. Their ecological success has repeatedly been linked to their association with endo- as well as epiphytic bacteria. Indeed, recent studies based on 16S rDNA barcoding revealed rich associated bacterial communities. However, little is known about their functional diversity as well as the principles underlying their assembly. To address how bacteria contribute to the ecological success of siphonous green algae and whether the competitive potential of invasive species may be at least partly shaped by associated microbes, we will apply a metagenomic approach to analyse the diversity of epi- and endophytic bacterial communities associated with native and invasive species of *Caulerpa* in the presence of abiotic stresses. In this study, natural populations of two *Caulerpa* species (*C. cylindracea* and *C. prolifera*) found along the Turkish coastline of the Izmir region were sampled. Additionally, in situ experiments combined with lab experiments were conducted in which abiotic conditions were altered to assess the role of environmental factors in bacterial recruitment and microbiome stability. Characterization of bacterial communities involved Illumina-based 16S rDNA amplicon sequencing. To provide more comprehensive insight into the functional diversity of bacterial communities, metatranscriptomics will be done. In addition we will develop and apply DNA-stable isotope probing to label bacteria and hence provide detailed phylogenetic and functional information about the microorganisms responsible for the metabolism of a particular substrate.

### P02 | An association between a neogregarine parasite and the microbial community of bumblebees

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Bumblebees are important pollinators in temperate and cold regions of the world. They pollinate a range of wild and agricultural flowering plants, and contribute to the plant diversity and human food supply. Hereby bumblebees provide valuable ecosystem services. The characterized gut microbial communities of bumblebees and honeybees have a highly specialized but species-poor community. These gut bacterial communities revealed related functions to nutrition, pathogen defense and immune response, showing their important role in the host's health status. To better understand these host-microbe interactions, the dependency of the environmental context needs to be considered, especially the presence of parasitic species is an important factor herein. Both the gut and fat body microbial communities of foragers (*Bombus terrestris*) originating from two locations were analyzed, using the 16S ribosomal amplicon sequencing with the Illumina technology. Also the relation with the neogregarine parasite *Apicystis bombi* was explored. *A. bombi* infection disturbs the microbial association network, as positive correlations between the Operational Taxonomic Units (OTUs) residing in the gut and fat body increase from 0.18% to 0.69%. Also the OTU identified as *Arsenophonus* sp., which has a location dependent interaction with *A. bombi*, is a possible candidate to influence the bee health in collaboration with *A. bombi*.

### P03 | Temporal dynamics of bacterial colonization of plastic debris in the North Sea

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Previously we have demonstrated that bacteria can colonize marine plastic debris. We hypothesized that three major factors may influence the bacterial colonization of plastic: changes in environmental conditions (e.g. salinity, temperature), differences in biofilm formation stages and plastic-related factors (shape, colour, polymer type). Additionally, it has been proposed that bacteria could use plastic debris as a transport vector or that within the plastic colonisers, bacteria are present that are able to degrade these polymers.

Whereas bacterial colonization has been shown to occur within weeks, little is known about the temporal dynamics of marine bacterial communities on plastic debris and the influence of environment or plastic type. Therefore, we exposed two polyethylene materials (sheet and dolly rope) to the marine environment for six months on two locations: the harbour of Ostend and near the offshore wind farm, the “Thornton bank”. Once a month, plastics were sampled and the temporal dynamics of the bacterial communities was analysed using 16S V3-V4 rDNA amplicon sequencing.

For both locations and plastic types, Bacteroidetes and Proteobacteria dominate the bacterial communities. Temporal shifts in community composition were observed, especially during the first months. The bacterial community composition of plastic materials sampled at the harbour of Ostend are substantially different from those at the Thornton bank, indicating a major influence of the environmental parameters. Furthermore, differences in bacterial community composition and richness were found between the two plastic items, independent from the sampling location, suggesting that the shape and/or colour of the plastic influences the bacterial colonization. Further on, we investigated if a core microbiome could be found on plastic items across all time points. This could indicate the presence of bacterial genera that can easily colonise marine plastic debris and are therefore omnipresent.

#### **P04 | The microbiome of sympatric cryptic nematode species reflects resource differentiation which alters by ecological interactions**

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Differences in resource use or in tolerances to abiotic conditions are often invoked as potential mechanisms underlying the sympatric distribution of cryptic species. Additionally, the microbiome can provide physiological adaptations of the host to environmental conditions. We determined the intra- and interspecific variability of the microbiomes of three cryptic nematode species of the *Litoditis marina* species complex that co-occur, but show differences in abiotic tolerances. Roche 454 pyrosequencing of the microbial 16S rRNA gene revealed distinct bacterial communities characterized by a substantial diversity (85 – 513 OTUs) and many rare OTUs. The core microbiome of each species contained only very few OTUs (2 – 6), and four OTUs were identified as potentially generating tolerance to abiotic conditions. A controlled experiment in which nematodes from three cryptic species (Pm1, Pm3 and Pm4) were fed with either an *E. coli* suspension or a bacterial mix was performed and the 16S rRNA gene was sequenced using the MiSeq technology. OTU richness ranged between 1118 – 7864. This experiment confirmed the existence of species-specific microbiomes, a