

to rescue contaminated batches. In present work, bacteria were screened from natural environments to test their DON-detoxification capacity. Two enrichment cultures were obtained able to detoxify DON originating from soil from a monoculture maize field and activated sludge from a wastewater treatment plant. The metabolites have been characterized as the epimer of DON and the epimer of de-epoxy-DON, both conveying no residual toxicity for the aquatic bio-indicator plant *Lemna minor*. Illumina 16S rRNA gene sequencing revealed that *Nocardioides* sp. reached ca. 17% of the total microbial community after two weeks in both enrichment cultures, while being under the detection limit in the start culture, suggesting members of this genus might have been involved in the DON degradation. Efforts are ongoing in isolating these strains from the enrichment cultures.

107B - The stressful effects of microplastics associated with chromium (VI) on the microbiota of *Daphnia magna*

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Contamination by microplastics (particles < 5mm) is a growing and alarming environmental problem in both marine- and freshwater systems. Evidence suggests that industrial effluents are a major source of microplastics spread in fresh waters. Industrial effluents will also contain other pollutants that could make agglomeration with microplastics, which could lead to increased toxicity of the pollutant. The principal issue of microplastics is their proclivity to enter food webs and affect both the organism and its associated microbiota. To test how microplastics associated with other pollutants can increase the pollutants toxicity and also alter host survival and associated bacterial diversity; *Daphnia magna* were exposed to 1µm microplastic beads with a concentration of approximately $4.55 \cdot 10^7$ particles/mL and chromium (VI) simultaneously with treatments of 2 and 5 ppm for 72 h. A DNA extraction from the *Daphnia* was done to amplify and sequence the ribosomal Bacterial 16S. The results show a low mortality of 11.25% by the microplastics alone and a mortality of 36% by the chromium alone. However, when the microplastics are in presence of chromium (VI) the mortality increase to 57%. The microbial analyses showed changes in the microbial diversity due to the effects of microplastics and chromium (VI). In conclusion, microplastics and associated pollutants in freshwater can affect both the host associated microbiota and host fitness. Furthermore, the joint synergistic effects of microplastics and metals on organisms might have pathological and physiological consequences, due to the activity of microplastics working as immobilization matrices.

Poster Pitch

108B - Interactomics of the degradation of a recalcitrant pesticide by a soil-enriched bacterial consortium

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Recalcitrant to degradation compounds used in agriculture pose a challenge for environmental management. Thiabendazole (TBZ), a benzimidazole commonly used protectively against postharvest fungal diseases and as anthelmintic in livestock farming, is highly stable ($DT_{50} > 1\text{-}2$ years) in the environment without previously known potent biodegraders. Our group has recently enriched from soil a bacterial consortium able to rapidly degrade TBZ through cleavage of the benzimidazole ring and degradation of the resulting benzyl and thiazole ring moieties. However, no pure TBZ-degrading isolate was obtained suggesting complex interactions between consortium members. We employed an “omics” approach to elucidate the microbial interactions that maintain the degradation consortium capability. Metagenome sequencing at various conditions resulted in binning 16 genomes with 84-93% completeness. These together with stable isotope probing (SIP)-amplicon sequencing of the 16S rRNA gene verified previous group findings of the key degrading role of a *Sphingomonas* strain comprising the most dominant metagenome bin. In a time-series experiment, RNA sequencing of the consortium supplied with TBZ or succinate as sole carbon showed the enhanced expression by the suspect degrader of: a highly versatile genetic armory for aromatic compound degradation; signaling and transport associated genes; secretory and conjugative system activities. Networking analysis suggested the interaction of *Sphingomonas* with a *Hydrogenophaga* strain and possible contribution of the latter to the overall cobalamin balance. Correlations among consortium member 16S rRNA gene relative abundances further support potential auxotrophy. On-going metabolomics and proteomics analysis will further elucidate underlying interactions and mechanisms and will be presented at the meeting.

109B - Bacterial community changes in response to production and fallowing at hard-bottom aquaculture sites, a potential for novel monitoring biomarkers

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Substrates surrounding salmon aquaculture sites experience physicochemical and biotic changes as uneaten feed and fish waste (flocculent matter) accumulates at the seafloor. Where hard substrates predominate, aquaculture-derived organic enrichment is assessed using time-consuming drop-camera surveys, which cannot discriminate among disturbance levels.

We explored whether phases of aquaculture enrichment (production) and recovery (fallowing) could be identified at hard-bottom sites based on bacterial community composition (microbiome). Samples of flocculent matter (N=116) and water (N=4) were collected at production and fallow sites in 2015-2017 at a range of distances from salmon cages, along with reference sediment (N=3), and their microbiomes were characterized using high-throughput 16S rDNA sequencing.

Compared to control site sediment, flocculent matter had altered microbiomes, with significant decreases in bacterial diversity detected up to 80 m (and especially within 40 m) from cages. Bacterial taxa characteristic of unimpacted and differentially