Bacterial communities hitching a hike - a guide to the river system of the Red river, Disko Island, West Greenland

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with eukaryotes, where bacterial secondary metabolites (e.g. antibiotics) may serve as host protection. Members of the *Phaeobacter* genus can be associated with mollusks, and may also engage in dynamic symbiosis with the microalga *Emiliana huxleyi*. The antibiotic tropodithietic acid (TDA) has been proposed to be involved in the latter interaction and the aim of this study is to investigate how TDA-producing *P. inhibens* affect the microbiota associated with European flat oysters and *E. huxleyi. P. inhibens* was introduced to oysters and *E. huxleyi* and the effect on microbial community composition was assessed using V4 amplicon sequencing. Members of the *Phaeobacter* genus were indigenous to the existing oyster microbiota. Addition of the TDA-producing *P. inhibens* caused significant changes in the microbial community of the oysters allowing certain OTUs (e.g. putative roseobacters and Alteromonadales) to increase in relative abundance, while others (e.g. *Mycoplasma* and *Sulforospirillum*) decreased compared to oysters with no exogenous *P. inhibens*. Data on *E. huxleyi* are currently under way, yet based on changes in the oyster microbiome, it seems that *P. inhibens* is capable of modulating eukaryote associated microbial communities and potentially the overall functionality of the microbiome.

[P69] BACTERIAL COMMUNITIES HITCHING A HIKE - A GUIDE TO THE RIVER SYSTEM OF THE RED RIVER, DISKO ISLAND, WEST GREENLAND

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Glacier melting and altered precipitation patterns influence Arctic freshwater and coastal ecosystems. Arctic rivers are central to Arctic water ecosystems linking glacier meltwaters and precipitation with the ocean through transport of particulate matter and microorganisms. However, the impact of different water sources on the microbial communities in Arctic rivers and estuaries remains unknown. In this study we used 16S rRNA gene amplicon sequencing to assess a small river and its estuary on Disko Island, West Greenland (69°N). We describe the bacterial community through a river into the estuary, including communities originating in a glacier and a proglacial lake. Our results show that water from the glacier and lake transports distinct communities into the river in terms of diversity and community composition. Bacteria of terrestrial origin were among the dominating OTUs in the main river, while the glacier and lake supplied the river with water containing fewer terrestrial organisms and more psychrophilic taxa were found in the dominant community supplied by the lake. At the river mouth, the dominant bacterial communities from the lake and glacier were unnoticeable but became evident again further

into the estuary. This showed, that the correct resolution of samples along a network is crucial for understanding the origin and transport of microbial communities. On average 23% of the estuary community consisted of indicator OTUs from the river. Environmental variables showed only weak correlations with community composition.

[P70] MICROBIAL GRANULATION MANAGEMENT: SIMPLE CHANGES IN REACTOR OPERATION ENABLE CONTROL OF GRANULAR PROPERTIES AND THE ENGINEERING OF MICROBIAL COMMUNITIES IN WASTEWATER APPLICATIONS

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The use of microbial granules in wastewater applications is becoming increasingly popular due to their favorable properties like high settling velocity or their resilience to mechanical and environmental stress. A simple change in operational strategies of lab scale reactors was hypothesized to enable the operators to control the size of the bio-granules. The size of granules determines the fractionation of different redox zones in the biofilm and therefore affects the niche differentiation of the microbial community. With the change of the microbial community various performance parameters like the ammonium or nitrous oxide removal rate vary and are therefore a function of the granule size. Mathematical modelling was applied to support the hypothesis. Granules of two distinct sizes were grown and compared in settling velocity, substrate turnover rates and microbial community composition. The investigation shows that a simple change in process operation is feasible for managing bio-granulation and microbial communities.

[P71] CO-CULTIVATION IN A STRUCTURED ENVIRONMENT FACILITATES INTERSPECIFIC MUTUALISM

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Bacteria interact across species boundaries, resulting in highly complex communities. The knowledge of the underlying molecular and evolutionary mechanisms of interspecies interactions is currently limited and so is their response to long-term co-existence. The data presented here demonstrates co-adaptation of two species in co-culture, resulting in mutually enhanced productivity.

We used two co-isolated soil bacteria, *Xanthomonas retroflexus* and *Paenibacillus amylolyticus*, to study co-evolution. Cultures were grown as mono- and co-cultures over