O8-3: Challenges, Approaches and Future Work in the Deep-sea Anoxic Brine Lakes of the Red Sea

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The Red Sea hosts several deep-sea anoxic brine lakes, which are considered some of the most remote and extreme environments on Earth [2]. The brines markedly differ from overlying seawater and provide unique biotopes combining multiple environmental extremes ranging from high salinity (7-fold increase), high temperature (up to 70°C), high concentration of heavy metals (1,000- to 10,000-fold increase in concentration), high hydrostatic pressure, to anoxic conditions. Despite this combination of multiple environmental extremes, they have been shown to be teeming with life and harbor a very high biodiversity, with identification of several new phylogenetic lineages (e.g. [1],[3-5]).

As observed for other environments (e.g. [6-7]), targeted cultivation and isolation of new microbes from the brines of the Red Sea is often quite challenging. The lack of isolates from such phylogenetically predicted lineages prevents us from accurately predicting their physiological and metabolic characteristics hampering their successful isolation. Also, the brine-seawater interfaces exhibit characteristic steep environmental gradients (e.g. salinity, nutrients) that further hinder attempts to replicate local environmental conditions in the lab.

In this poster we describe some of the approaches used for targeted microbial cultivation and isolation from these extreme and gradient-rich environments: optical-tweezers, gel-stabilized gradient plates, and single-cell genomics. The application of these new approaches has provided highly promising results on isolation of these new microbes and phylogenetic groups, and gives us important insights for our future work.

We have only started to scratch the surface of the enormous biodiversity in these unusual biotopes. Each deep-sea brine lake of the Red Sea has a unique combination and variation of physical and chemical conditions, likely reflected in distinct microbial communities, yet most studies focused on only 2 of the 25 different brine lakes. Also, previous studies under-sampled the complex and heterogeneous brine-seawater interface, while phylogenetic and cultivation studies have unfortunately excluded the eukaryotic component.

Our approaches have been quite fruitful. Therefore, we intend to employ a similar methodology to samples from previously unstudied locations, but complement it with additional components, namely by increasing resolution at the brine-seawater interface,
expanding our analysis to include eukaryotes, and use phenotypic insights from single-cell genomics to design better suited targeted enrichments. Isolates will be characterized and described, following a polyphasic approach, combining classic with modern techniques (e.g. MALDI-TOF MS, and genotypic characterization), and will provide a clearer picture on the microbial communities thriving in these unusual biotopes, and elucidate their local environmental role and impact.

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