ABYSSAL MICROBIALITES IN THE GULF OF AQABA

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PROJECT OBJECTIVES

- The NEOM brine pool is at 1770 m water depth and the main pool is 260 m long and 70 m wide.
- The NEOM pool has the lowest sulfate/chloride ratio yet documented in the Red Sea-Gulf of Aqaba system, emphasizing the activity of sulfate-reducing bacteria that contribute to the pool's rich microbial fauna.
- At the periphery of the pool, the interface between normal marine waters and the anoxic brine delivers a niche in which a rich microbial community develops, stratified by the preferred metabolisms of its occupants.
- Abyssal chemosynthetic stromatolites are conspicuous facies in the stratigraphy of the brine pool and its surroundings.

PROJECT RATIONALE

Microbial buildups are generally considered a shallow-water phenomenon. Here, we present the discovery of diverse microbial communities associated with a 10000 sq. m brine pool in the Aragonese Deep of the Gulf of Aqaba at 1770 m depth (Fig. 1). A diverse prokaryotic fauna stratifies into a series of niches characterized by high salinity, low oxygen, lowered pH, and modestly warmer temperature, as compared



Figure 1: Bathymetric and tectonic setting of the NEOM Brine Pool in the Gulf of Aqaba. (A) The General Bathymetric Chart of the Oceans (GEBCO) provides regional context to the multibeam data acquired during the OceanX-NEOM research cruise (B). The brine pool locates at the toe-of-slope of the Saudi coastal margin in the Aragonese Deep, a pull-apart basin and the deepest point in the Gulf of Aqaba. This basin is bounded by the strike-slip Arona and Aragonese faults (red lines) which connect via normal faults (black lines). The NEOM Brine Pool situates at the junction between the coast-parallel Arona Fault and the NNW-trending normal fault that extends to demark the northern margin of the basin. (C) The brine-seawater interface is at 1770 m depth and the main pool is 260 m long, 70 m wide, and covers an area of 10000 m². Spot soundings (black dots) indicate a maximum thickness of the brine to be 6 m in the center of the pool. Three minor pools, each <10 m² in area were discovered within 50 m of the main pool, one to its west and two to its south.

to ambient. The microbes develop thick mats which trap and bind sediment, delivering expansive chemosynthetic deep-water stromatolites, which, in some cases, are sufficiently lithified to justify application of the term 'microbialites'. The overall goal of this study is to characterize the microbial communities in terms of their genetics and sedimentology to better understand the formation of abyssal stromatolites in rift basins and beyond.

Approach

Sampled via a transect of five push cores (Fig. 2), a defining characteristic of all the pools in the NEOM complex are the four concentric zones which develop around their rims. The outermost zone in this series is the abyssal mud which constitutes the seabed of the Aragonese Deep. As the brine pool is approached, the second zone encountered is characterized by its rich microbial community which stains the seabed dark gray. This second zone (akin to a beach in a coastal setting) is temporarily inundated by brine when even minor waves are induced into the surface of the pool. The gray zone is typically 1-2 m wide, depending on local topography at the edge of the pool. Third in line, inboard of the gray zone, lies the orange 'swash' zone which situates immediately at the brine-seawater interface. The orange color is also induced



Figure 2: Location and photo-scans of the four short cores and one long core retrieved from the bed of the NEOM Brine Pool. (A) Shows the western margin of the NEOM brine pool. Cores #1 through #4 were pushed to 50 cm depth sub-seabed, whereas Core #5 was acquired with a longer barrel and pushed to 150 cm (the depth of refusal). The transect of cores was set to sample the four zones which develop as the brine onlaps the surrounding seabed (B). (C) Shows the five cores. Note the increase in fine-grained dark intervals, indicative of reduced conditions, for the cores acquired beneath the brine. (D) Maps the geometry of the NEOM Brine Pool and the location of this transect of cores on its western margin.

by a dense microbial community. The bivalve *A. muriatica* densely inhabits both the gray and orange zones. The fourth zone in the sequence is located within the brine pool proper, which we define as permanently submerged beneath brine.

The five cores were extensively sampled for their microbial communities using 16S rRNA sequencing. The fidelity of the sequencing was sufficient to identify seven classes of prokaryotes whose per-core relative abundances were tallied to reveal gradients in the prokaryotic community in and around the brine pool (Fig. 3).

The outermost core in the transect (Core #1) penetrated the hemipelagic mud constituting the broader seabed of the Aragonese Deep. Preliminary genomic analysis from the core tops reveals that more than 75% of the microbes in this zone adopt an aerobic metabolism, with the majority identified as Gammaprotobacteria, with minor contributions from Alphaprotobacteria, and clade SO85 (Fig. 3). The second core, which sampled seabed darkened in color by a rich microbial fabric (the gray zone),



Figure 3: Lateral distribution of prokaryote communities in and around the NEOM Brine Pool. 16S rRNA sequencing of the top 20 mm of the five cores reveal that the microbes inhabiting the background sediment (Core #1) and gray microbial beach zone (Core #2) are 75% aerobic and 25% anaerobic. Moving closer to the shoreline of the pool, this distribution between aerobic and anaerobic metabolisms is reversed in the orange microbial swash zone. For the samples obtained from within the brine pool (Cores #4 and #5), only 10% of the sequenced microbes are aerobic with the remaining anaerobes splitting near equally into seven classes of chemolithoautotrophs.

boasted a similar community of prokaryotes. By contrast, ~75% of the microbes identified in Core #3, which penetrated the orange swash zone situated immediately outboard of the brine-seawater interface, were anaerobic, adopting a broad spectrum of metabolisms spanning sulfate reduction, reductive dichlorination, fermentation, and perchlorate respiration (Fig. 3). The dominance of anaerobic prokaryotes surpassed 85% of the total community sequenced in the final pair of cores (#4 and #5) which penetrated the bed of the brine pool. The abundance of sulfate reducers occupying the bed sediments of the brine pool squares with the depleted SO₄²⁻/Cl⁻ ratio measured within the overlying brine.

SIGNIFICANCE

Syn-rift microbialites associated with abyssal brine pools broadly accumulate in the Gulf of Aqaba. The hypersaline anoxic environment favors extremophile prokaryotes. Among these, the metabolism of sulfate-reducing bacteria delivers brine with the lowest sulfate/chloride ratio yet documented in the Red Sea-Gulf of Aqaba system. Subsea hypersaline anoxic brine pools are among the most extreme habitable environments on Earth that offer clues to first life and life on other planets.