## Shallow Hydrothermal vent system at Panarea Island (Italy): a multidisciplinary study based on geochemical, geophysical and biochemical aspects in an extreme marine environment

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Exploration of Shallow Hydrothermal Vents (SHVs) is usually focused on analysis of major chemical species while few studies are focused on the fate of trace and Rare Earth Elements (REEs) and the consequences spread on the marine environment. Here, we show progress concerning trace elements and REE geochemistry and biochemical aspects about the natural system in the surrounding area of Panarea Island (Eolian Islands, Italy). Samples were collected from submerged vents at different depths and analyzed for major and trace elements and REEs from June 2017 to August 2022. Measured chemical-physical parameters, such as pH and Eh, span from 2.5 to 8.2 and from -292 to 254 mV, respectively, that express an inverse correlation compared to Mn and REEs, revealing pH Fe, Al, control precipitation/dissolution process of solid phases. A positive correlation is also observed for REEs and Fe-Al-Mn in fluid, showing simultaneous variations of these elements due to coprecipitation and adsorption onto the surface of oxyhydroxide of Fe, Al and Mn, involving scavenging process of REEs. Hydrothermal discharging fluids are responsible for generating Fe, Al and Mn-bearing minerals controlling the fractionation of REEs and trace elements. We propose a further multidisciplinary study involving geochemical, biochemical and geophysical observation, and analysis of the microbial community in two different seasons (May - August 2022) and the correlation with hydrothermal flow measurements data from a permanent multiparametric observatory (infrastructure of IPANEMA Project), located nearby the hydrothermal vent, known as Black Point (23m b.s.l.). The microbial community was investigated to understand microbial biodiversity and its role in the homeostasis of this extreme ecosystem. The metagenomic DNA was extracted from seawater, marine sediment and biofouling. The microbial community was determined by sequencing a bacterial marker gene (16S rRNA gene). We observed differences in

hydrothermal flow corresponding to variations in the abundance of different phyla, showing that the microbial community changes in dependence on physical-chemical conditions and that each sample carries its bacterial fingerprint. The study of hydrothermal flow variations could give insights into how the microbial communities and hydrothermal areas interact and to what extent.