Effects of increasing salinity on the biogeochemical cycle of the hypersaline biomat: Insights from the isotopic composition of pigments

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In shallow hypersaline environment, benthic microbial mat is often formed. It is densely inhabited by microorganisms such as cyanobacteria, sulfur oxidizing bacteria, sulfate reducing bacteria, and others [1]. Hypersaline microbial mat is characterized by extremely high primary production, which results from efficient recycling of nutrients inside the mat [2]. This study aims to understand the biogeochemical processes occurring in this unique ecosysytem, as well as their changes with increasing salinity.

Brine water and sediments on the bottom were collected from the solar saltern in Trapani, Italy (9 samples, salinity range 38-276). Carbon isotopic composition of dissolved inorganic carbon ($\delta^{13}C_{DIC}$) was highly variable, with lower values (-5.1~-10.6‰) recorded in the ponds where microbial mat is formed, and the highest value (~7.2‰) where salinity was high (>270) with no microbial mat developing. While high $\delta^{13}C_{DIC}$ may be attributed to degassing of CO_2 from the brine due to evaporation [3], remineralization of organic carbon or penetration of CO_2 from the atmosphere may be responsible for low $\delta^{13}C_{DIC}$ [4]. To investigate the biogeochemical cycle in the mat, we conducted compound-specific isotope analysis on pigments extracted from different layers of the mat (yellow, green, and pink, and black layers from the top to the bottom). Discussion based on $\delta^{13}C$ and $\delta^{15}N$ of chlorophyll *a* originating from cyanobacteria and bacteriochlorophyll *a* from purple sulfur bacteria will be presented, as well as their variations with different salinity.

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