

ENERGY SOURCES LIKE IRON CONTRIBUTE TO SHAPING THE MICROBIAL COMMUNITIES IN SCALDING HOT SPRINGS

MALEKE MATHEWS MALEKE¹, ANDISIWE MATU²,
ERROL D CASON², ALBA GÓMEZ-ARIAS² AND JULIO
CASTILLO²

¹Central University of Technology

²University of the Free State

Presenting Author: mmaleke@cut.ac.za

The composition of microbial communities found in hot springs has been reported to depend mainly on temperature and pH [1]. However, the microbial communities of these oligotrophic environments might also be influenced by energy sources' bioavailability. Iron (Fe) plays a vital role in bacterial physiology, consequently, bacteria have evolved mechanisms to actively acquire from the surrounding microenvironment under Fe-limiting conditions and also control its availability under Fe-replete conditions [2]. The abundance or scarcity of iron (Fe) may influence microbial functionality and shape microbial community structure in the microenvironment. Nonetheless, the role of Fe is poorly understood in how it shapes the metabolisms of microbial communities. To elucidate the influence of Fe on microbial functionality and community, two scalding hot springs, Brandvlei and Calitzdorp with contrasting Fe concentrations, were characterised. Hydrogeochemical data demonstrated that these scalding springs present slightly acid to neutral, oligotrophic and oxidative conditions with H₂ as a main electron donor and poor in energy sources. Energy sources influential in the system were in the order of SO₄>Fe³⁺>NO₃>CH₄. Notably, Calitzdorp contained (~167.3 mM/L) 128 times higher Fe concentrations compared to Brandvlei (~1.3 mM/L). Based on the Illumina MiSeq results, at the phylum level, *Proteobacteria*, *Bacteroidetes* and *Firmicutes* dominated the hot springs. The predominant genera in both springs were *Acinetobacter* (56.4 %), *Tepidimonas* (11.8 %), *Sideroxydans* (6.8 %), *Anoxybacillus* (4.6 %), *Curvibacter* (3.0 %) and *Hydrogenophilus* (2.5 %). The presence of iron-oxidizing bacteria such as *Curvibacter* and *Sideroxydans* could be correlated to the elevated Fe concentrations in the Calitzdorp. Functional profiling of the two ecosystems revealed that genes associated with Fe regulation were predominant in Calitzdorp due to the high Fe concentrations and an array of genes encoding redox-active metalloenzymes containing iron as cofactors (Fe-S clusters, siroheme and heme) in their catalytic subunit. Altogether, evidence of Fe shaping the microbial diversity of the hot springs suggests that Fe might also influence the functionality of the microbial communities.

References

[1] Massello FL, Chan CS, Chan KG, Goh KM, Donati E & Urbietta MS (2020), *Microorganisms* 16, 906.

[2] Frawley ER & Fang FC (2014) *Molecular Microbiology*