

METABOLIC CAPACITY OF A PREDOMINANT *HYDROGENOPHAGA* IN A HIGHLY-ALKALINE ANTHROPOGENIC ENVIRONMENT. J. I. Ohlsson¹, E. D. Becraft¹, B. Ritchie¹, V. Frank¹, and W. D. Swingley¹, ¹Northern Illinois University *Corresponding author: wswingley@niu.edu First author: johlsson@niu.edu

Introduction: Life on extraterrestrial bodies may have developed under conditions drastically different from our own. However, life on Earth thrives in a multitude of extreme habitats, including the full breadth of pH ranges, pressures up to 500 atmospheres, and hyperthermophilic environments (i.e. >100°C).

While many bacteria and archaea have been characterized in acidic environments, very little is known about microbes living at extremely alkaline pH. This study aims to characterize alkaliphilic microbial populations found at an anthropogenic steel waste site with the highest recorded pH in any biotic system (consistently higher than pH 13.2).

Results: 16S ribosomal RNA gene sequencing revealed that this nonsaline, highly alkaline and heavy metal-enriched site hosts microbial communities dominated by Betaproteobacteria and Actinobacteria. Aerobic sediment communities are composed almost entirely of members of the Betaproteobacterial genus *Hydrogenophaga*, which has previously been found in anthropogenic alkaline sites as well as natural serpentinizing systems [1].

Metagenomic sequence assembly efforts were focused on reconstructing the alkaliphilic *Hydrogenophaga* genome, and predicted metabolisms were used to direct culture isolation. Using conserved non-redundant house-keeping genes as an indicator of genome completeness, it was estimated that a near-complete genome of this alkaliphilic *Hydrogenophaga* was assembled from metagenomic sequence reads.

The genome was annotated and metabolic pathways were analyzed in this *Hydrogenophaga* species in order to better understand how this and other alkaliphilic organisms survive and thrive in this uncommon environmental niche.

Outlook: Genomic studies of the *Hydrogenophaga* dominating in this alkaline system will provide valuable insights into microbial coping mechanisms for alkaline conditions. Understanding such mechanisms can in turn have significant implications for studies of the origin and potential habitats of microbial life on Earth and elsewhere.

References:

[1] Suzuki S. *et al.* (2014) *Nat. Commun.*, 5, art. no. 3900.