Genomic Variations in *Hydrogenophilus thermoluteolus* Genomes Across a Small-Scale Hot Spring Soil Gradient and Global Geothermal Environments

Isabel Rodrigues, Zachary Garvin, Tullis Onstott, Department of Geosciences, Princeton University, Princeton, NJ

INTRODUCTION

- ***Hydrogenophilus thermoluteolus* (*H. thermo*):** thermophilic, facultative chemolithoautotroph; found globally in **hot spring environments**
- **Site:** Polloquere (PQ) hot spring, Lauca National Park, Chile; downwind side
- **Only species** with **consistent** presence and **relative abundance** (~0.1% of total community) in a set of four site soil samples

Table 1 Comparing *H. thermo* optimal growth and PQ3 conditions

Conditions	pH	Temp. (°C)	Relative *H. thermo* abundance (%)
Optimal *H. Thermo* growth	7	50–52	–
PQ, 0m conditions	2.57	(mean annual) 2.9 ± 15	0.14%
PQ, 30m conditions	8.43	(mean annual) 2.9 ± 15	0.11%

CENTRAL QUESTIONS:

- Any genomic differences between PQ samples to explain *H. thermo* persistence?
- Major genomic differences between PQ samples and cultured reference or other published genomes for *H. thermo*?

METHODS

- **Pangenome** (Anvi'o v7): *H. thermo* metagenome-assembled genomes (MAGs) (1 per sample) and all publicly available, environmentally relevant genomes
- **Completeness of metabolic pathways**
- Gene clusters that appeared:
  - Only in **closest or furthest** samples
  - Only in **cultured reference** or **PQ samples**
- Gene clusters with high geometric but low functional homogeneity (cluster **structurally consistent** but individual **amino acids may change** in a way that **impacts functionality**)

Hydrogenophilus thermoluteolus Pangenome

Items order: Presence absence (D: Euclidean; L: Ward)

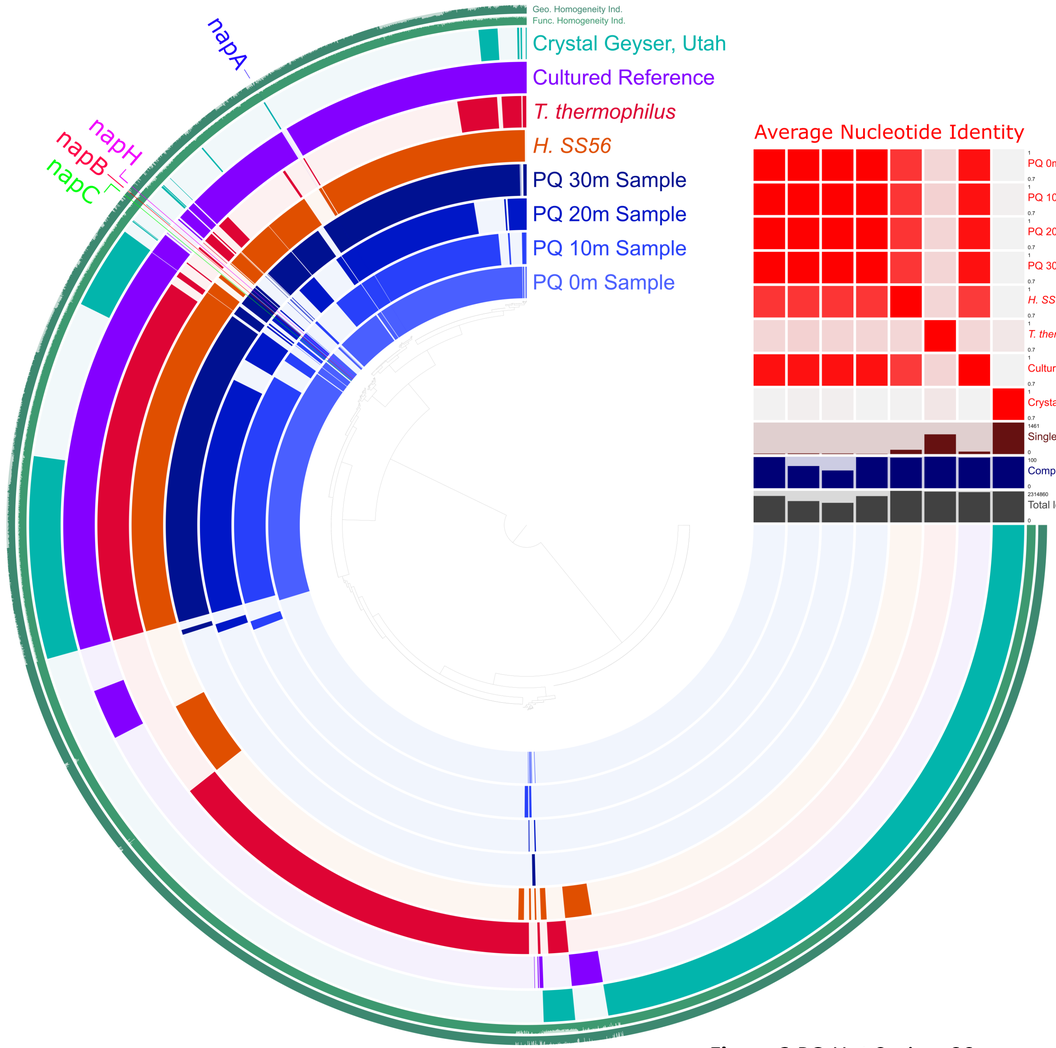
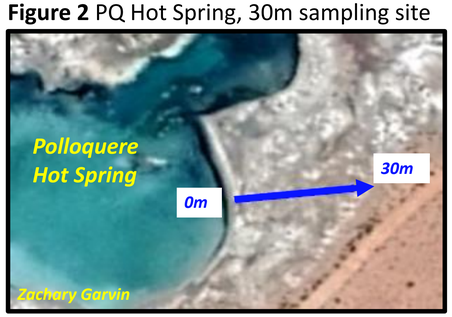


Figure 1 Pangenomic analysis from Anvi'o software, v7. Four inner-most circles represent the genomes derived from the PQ samples from 0m to 30m in 10m intervals. Three outer circles represent externally gathered genomes (outer-most: cultured reference, related organism *T. thermophilus*, related organism *H. SS56*). Genes are organized by similarity (inner tree). Average Nucleotide Identity computed using PyANI, Pritchard et al. (DOI: 10.1039/C5AY02550H)

Figure 2 PQ Hot Spring, 30m sampling site



RESULTS + DISCUSSION

- **Denitrification** (NO_3^- → N_2), **dissimilatory nitrate reduction (**NO_3^- → NH_4^+) pathways more complete in 0m and 30m samples compared to the cultured reference
  - napA, B genes (code for enzymes critical for NO_3^- → NO_2^-) present in PQ samples, not in cultured ref.
  - napH, C genes (code for membrane quinone oxidases) also present, **potential for nitrate respiration** (Sparacino-Watkins et. al, 2013)
- Total Nitrogen increases: 0.032% to 0.079% from 0m to 30m
- NO_3^- (mg/kg) increase: 12.8 mg/kg to 25.6 mg/kg from 0m to 30m
- Genomes included more similar than different — metabolic flexibility ingrained in genome?

FUTURE

- Transcriptomics; nap operon transcription
- Further investigation of nitrate respiration
- Comparison to MAGs for individuals from colder locations

SOURCES

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