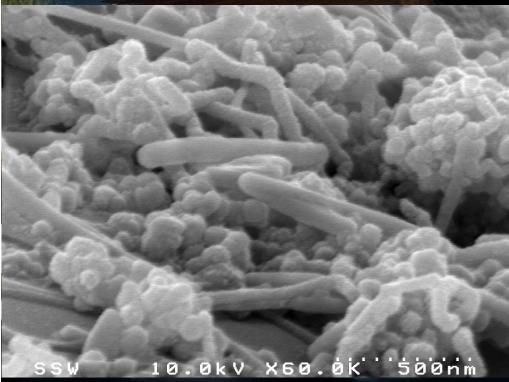
Life in the Deep Subsurface

Tom Kieft Biology Dept. New Mexico Tech



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Life in the Deep Subsurface



Subsurface life is <u>microbial</u>:

bacteria archaea fungi? protozoa viruses

NEW LINE CINEMA A Tandarde Capara



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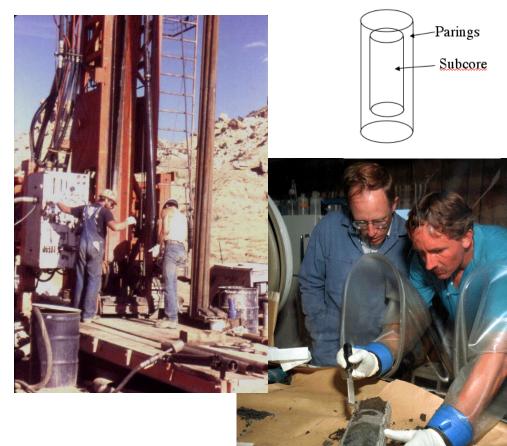
Sampling the deep biosphere



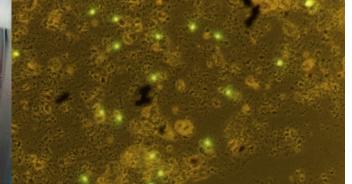
- Drilling/coring from the surface
- Access via deep mines or underground labs

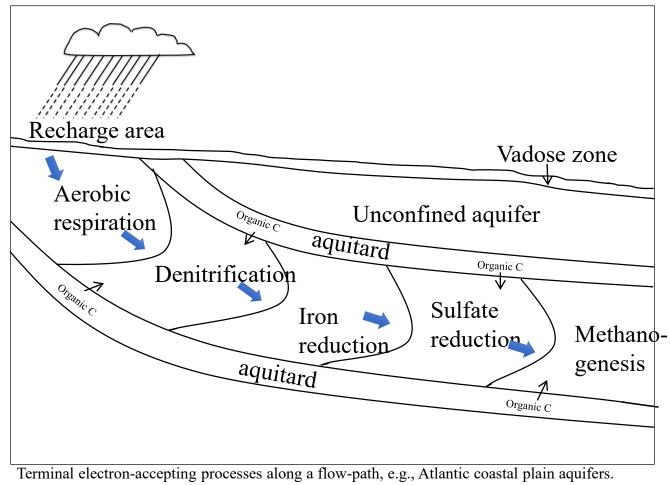


Drilling/coring needs

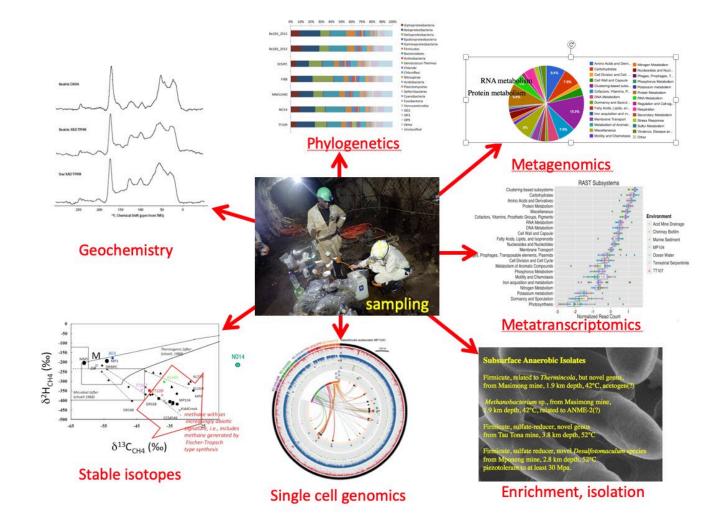


- tracers
 - Solute: Br, fluorochromes (e.g., rhodamine), perfluorinated hydrocarbons
 - Particulate: fluorescent carboxylated 1-µm microbeads
 - Microbial community comparisons
- core diameters <u>></u>2 inches preferred
- drilling methods are highly site specific.
- anaerobic glove bag
- core barrels should be steam cleaned, core barrel liners





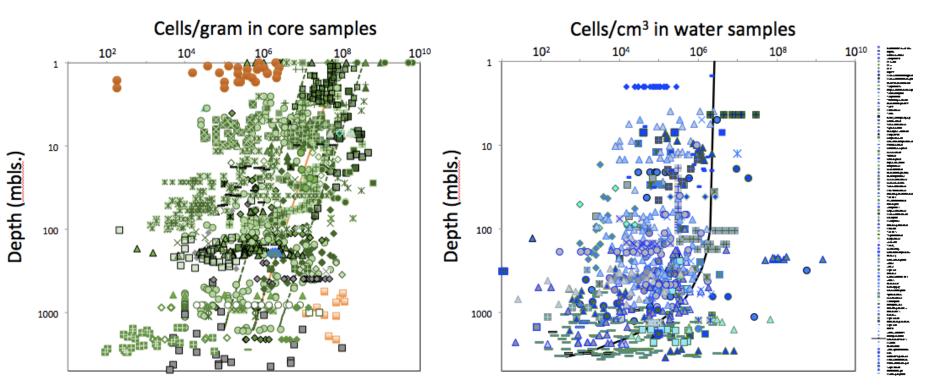
After Smith and Harris (2007)

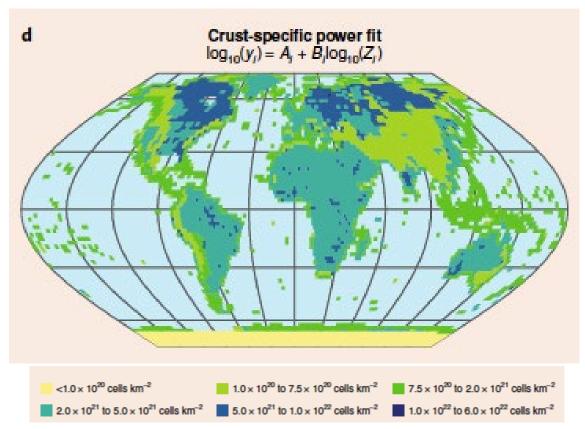


Big Objectives/Questions

- Global characterization of subsurface microbial abundance, diversity, and activities.
- What adaptations enable persistence for geologic time periods under:
 - Low nutrient flux, high temperature, extreme pH, high pressure, etc.
- How do subsurface microbes maintain/repair macromolecules?
- Do subsurface microbes represent early life on earth?
 - Deep branching phylogenies
 - Primitive metabolism, e.g. H₂ utilization

Onstott database of worldwide subsurface microbial abundance





Magnabosco et al. 2018. Nature Geoscience

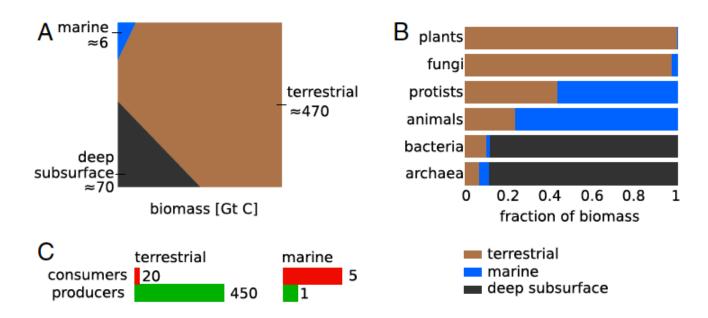
Table 2 | Biomass estimates derived from this study

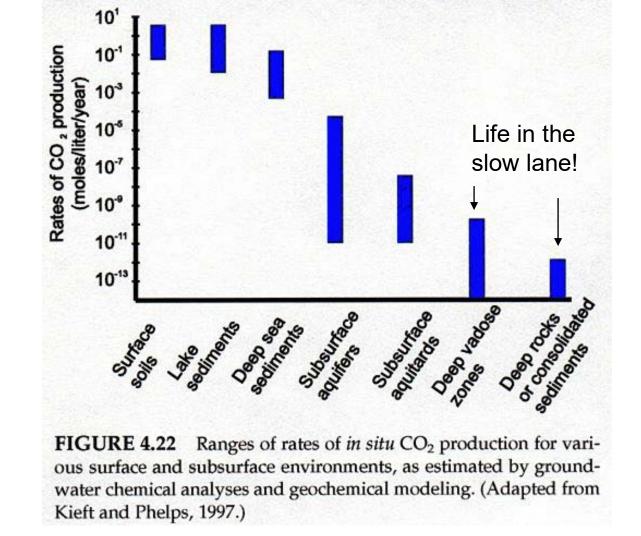
Model	10 ²⁹ cells (±95%	Mean	
	85°C isotherm	122°C isotherm	squared error ^a
Depth power fit	2.0(+0.3/-0.4)	2.3(+0.3/-0.3)	1.33
Temperature fit	10.0(+1.6/-1.2)	10.2(+1.0/-1.3)	1.13
GLM (temperature and depth)	2.6(+0.2/-0.4)	3.7(+0.6/-0.8)	1.29
Crust-specific depth power fit	5.2(+1.0/-1.1)	5.5(+1.0/-1.1)	0.27

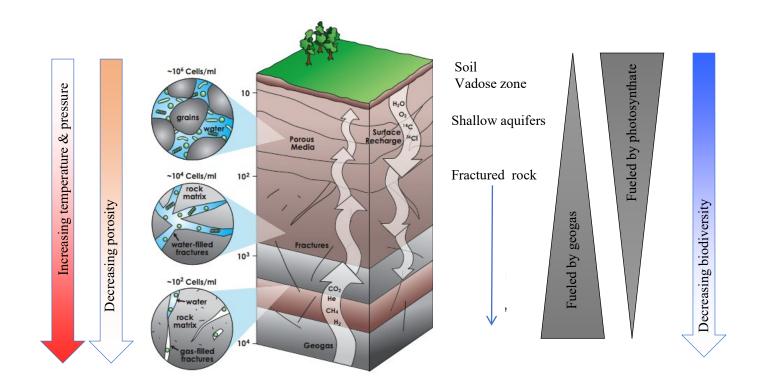
These estimates are based on the integration of each model to the designated isotherm. The parameters identified for each fit can be found in Supplementary Table 7. *Mean squared error = $\frac{1}{n} \sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2$ where *n* is the number of data points in the test set, Y_i is the log₁₀ concentration of cells per cm² of data point *i* in the test set, and \hat{Y}_i is the log₁₀ concentration of cells per cm² prediction of data point *i*.

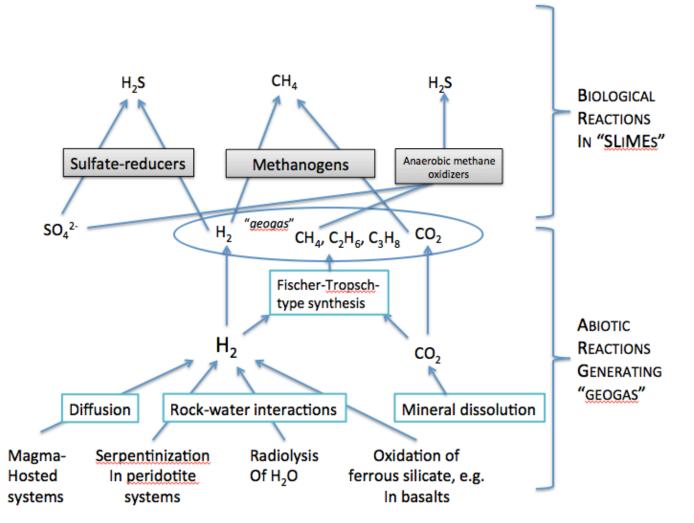
Magnabosco et al. 2018. Nature Geoscience

 ~60 Gt C in deep continental subsurface, ~10% of Earth's biomass
~2 x 10³⁰ prokaryotes

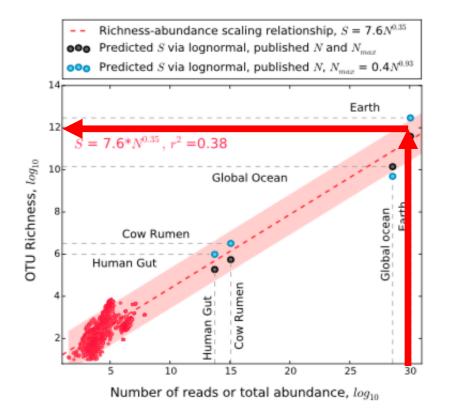








Kieft 2016. Microbiology of the deep continental biosphere

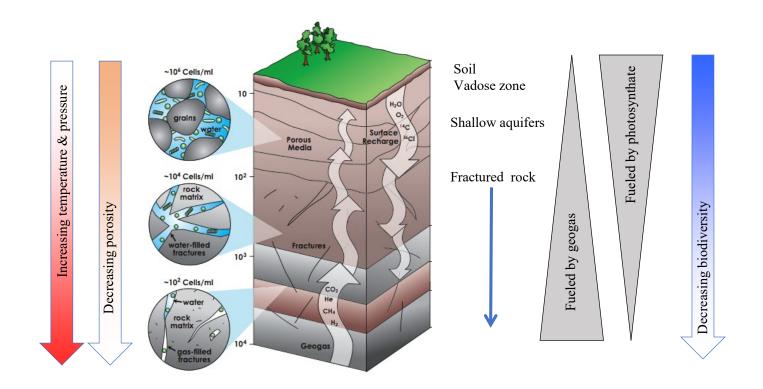


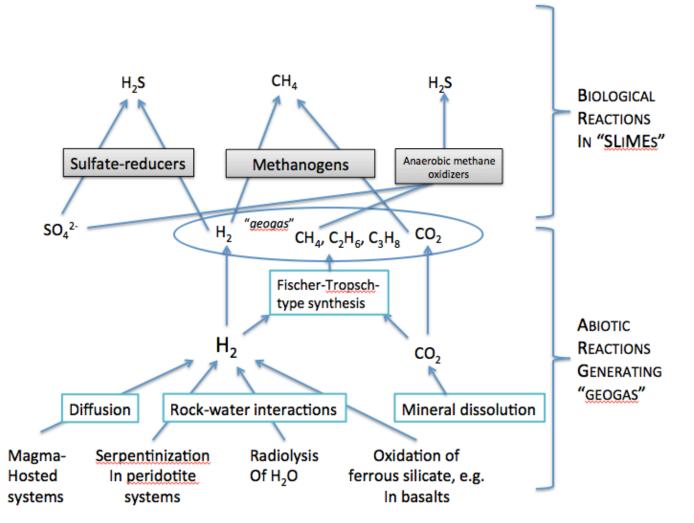
~10¹² microbial species in the continental subsurface

~1/3 of all Earth species!

Locey and Lennon, 2016. PNAS

Magnabosco et al., 2018, Nature Geoscience





Kieft 2016. Microbiology of the deep continental biosphere

More Big Objectives/Questions

- Relationship(s) between geophysics and microbes?
 - Do earthquakes stimulate microbial activities?
 - Do microbial activities increase the likelihood of seismic events.
 - Do microbial activities lead to fracture formation?
- What's the importance of viruses?
- Determine the involvements of transport, long-term survival, energy flux, and evolution in the distribution of microbes in the deep subsurface
 - As a specific example, how can nearly identical strains of *Desulforudis audaxviator* be distributed at sites thousands of km apart in deep, ancient groundwater?

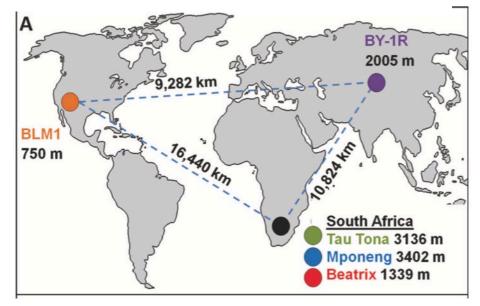
ISME

ARTICLE

Check for updates

Evolutionary stasis of a deep subsurface microbial lineage

Eric D. Becraft^{1,2} · Maggie C. Y. Lau Vetter $(0^{3,4} \cdot \text{Oliver K. I. Bezuidt}^1 \cdot \text{Julia M. Brown}^1 \cdot \text{Jessica M. Labonté} (10^5 \cdot \text{Kotryna Kauneckaite-Griguole}^6 \cdot \text{Ruta Salkauskaite}^6 \cdot \text{Gediminas Alzbutas}^6 \cdot \text{Joshua D. Sackett}^7 \cdot \text{Brittany R. Kruger}^7 \cdot \text{Vitaly Kadnikov}^8 \cdot \text{Esta van Heerden}^{9,10} \cdot \text{Duane Moser}^7 \cdot \text{Nikolai Ravin}^8 \cdot \text{Tullis Onstott}^4 \cdot \text{Ramunas Stepanauskas} (2^1)$



Hypothesis: Earthquakes stimulate microbial activity

Test with KASMS (Kinetically Activated Subsurface Microbial Sampler)

- KASMS is autonomous, triggered by seismic activity to collect formation and preserve geofluids for microbial analysis.
- Electronic control module, U-tube sampler, sample collection units, preservative pump, solenoid valve control systems.

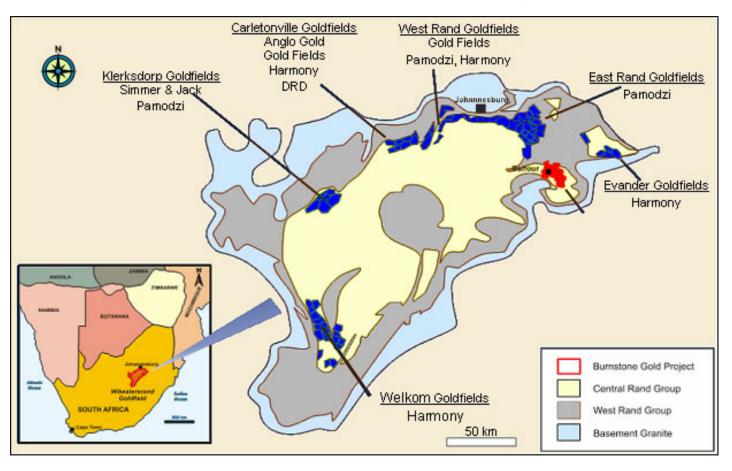








Witwatersrand Deep Microbiology Project





Moab Khotsong Mine







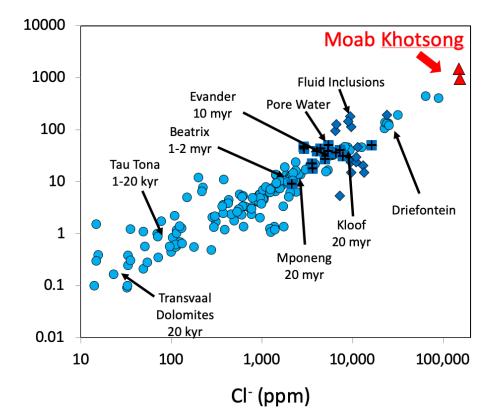
MOAB KHOTSONG COPERATIONS

he DEEPEST SINGLE LIF SHAFT in the WORLD.

3106km

Welcome to

Deep, ancient (1.2 Ga) brine: ~24% Na-Ca-Cl₂



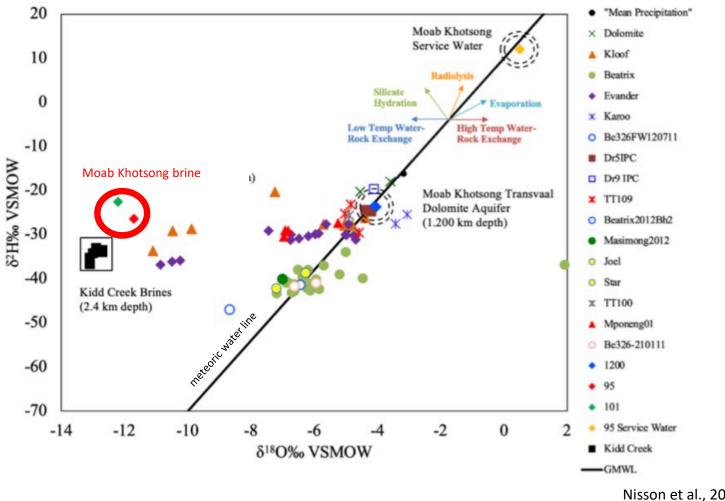
Br⁻ (ppm)

Origin of the brine:

2.9 Ga ocean water trapped and altered during metamorphosis.

Primarily radiolytic removal of water

Nisson et al., 2023 *Geochimica et Cosmochimica Acta*. 340:65-84

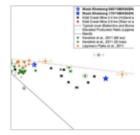


Nisson et al., 2023 *Geochimica et Cosmochimica Acta*. 340:65-84

Groundwater dating by Nobel gas isotope analyses: >1 billion year average residence time for Moab Khotsong brine

Sample	⁴ He (Ma)	²¹ Ne (Ma)	⁴⁰ Ar (Ma)	¹³⁶ Xe (Ma)	
МК95ВНА	316 ± 143	458 ±207	602 ±272	3181 ±1443	
(July 9 th , 2019)					
МК95ВНА	1028 ±466	1361 ±616	1196 ±542	4113± 1867	
(July 17 th , 2019)					
Noble Gas Residence Times in Ma for Moab Khotsong Brine					

95 level (3.2 Most radiogenic groundwaters ever described!



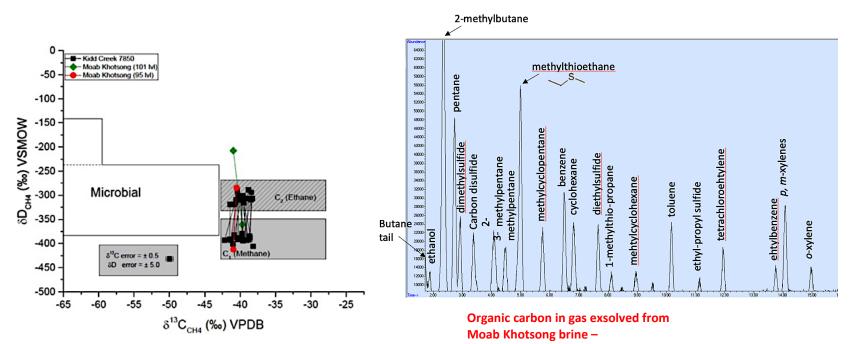
ONature

86Kr excess and other noble gases identify a billion-year...

Noble gases confirm billion-year groundwater residence times and external fluxes in deep crustal settings globally with implications for subsurface...

Warr et al., 2022. Nature Communications

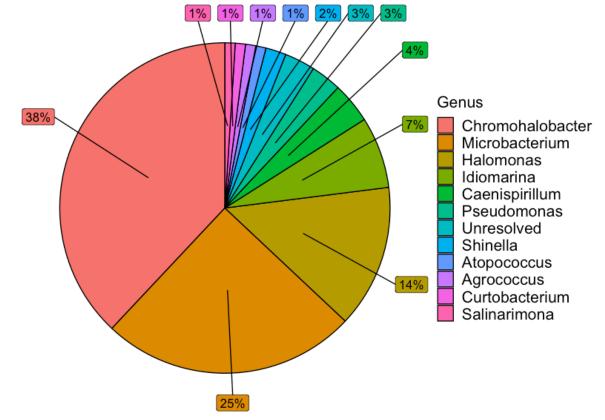
Rock-water interactions generate H₂, methane, and short-chain hydrocarbons



C₁-C₆ compounds, including <u>thiols</u>

Pre-biotic chemistry related to origin of life?

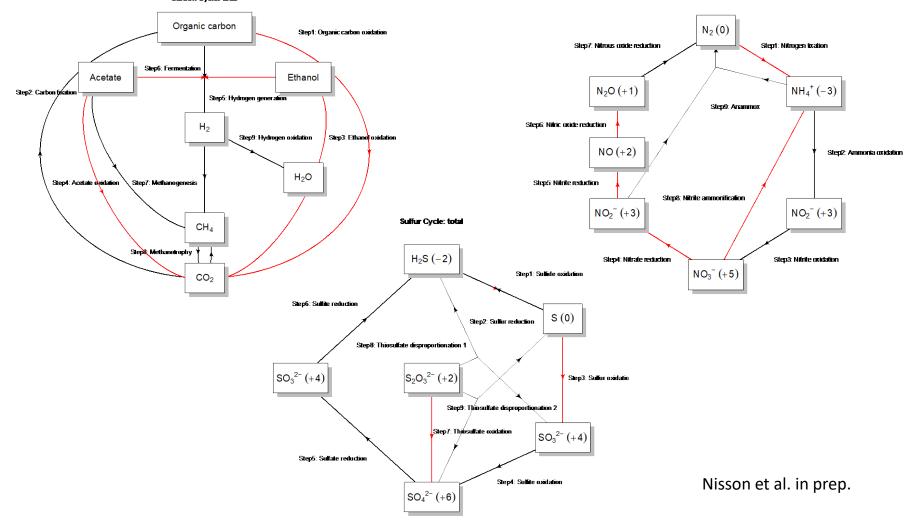
Taxonomic Distribution of MK101 SAGs



Nisson et al. in prep.

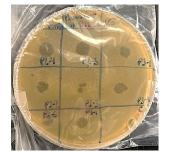
Carbon Cycle: total

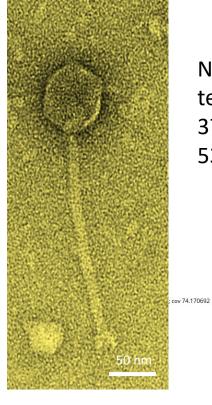
Nitrogen Cycle: total

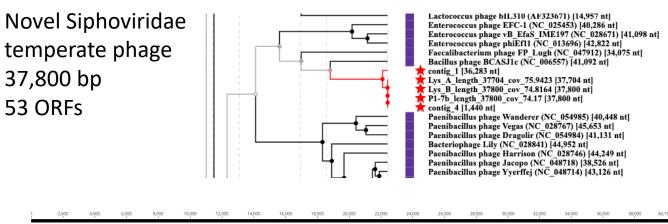


101-level bacterial isolates from ancient brine

Halalkalibacterium halodurans plus phages







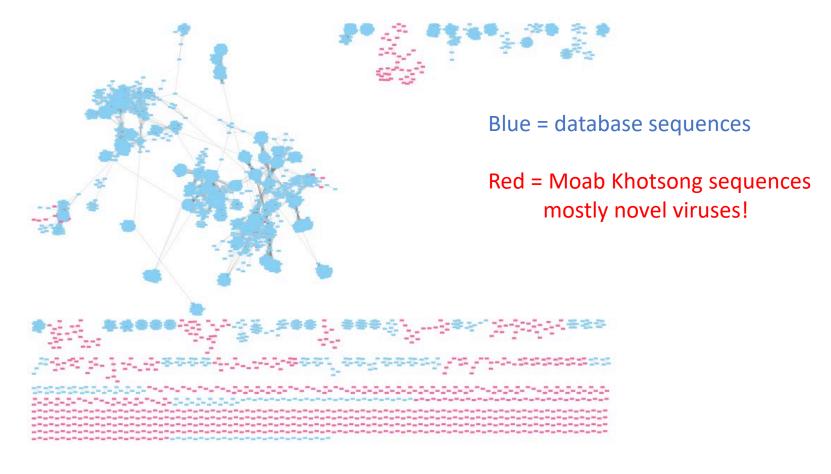
47 (concatenated sequence 3)



Also: diverse 1200L phages

134 (concatenat... 169 ...

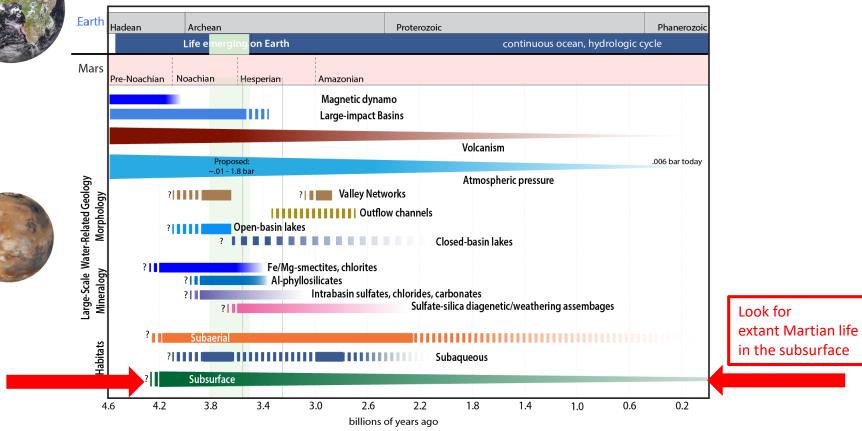
Nathaniel Jobe Cassandra Skaar 1200-level dolomite aquifer - Vcontact2 Cluster Analysis of viral sequences



Moab Khotsong DSEIS Geomicro findings

- Boreholes drilled near a fault zone intercepted a hypersaline brine.
- Noble gas isotopes indicate ~1 Ga residence times and reveal radiolysis as a contributor to brine formation.
- A large complex carbon pool is present, with contribution from both abiotic processes and chemoautotrophic activity.
- Single-cell amplified genomes reveal a low diversity bacterial community with adaptations for compatible solute synthesis and for coupling S/N oxidation to nitrate reduction.
- Moab Khotsong fracture water has yielded a diversity of phages, both through metagenomic sequencing and culture-dependent analysis.





Amador and Ehlman. In: Planetary Astrobiology, Space Science Series. University of Arizona Press, 2020

Take-home messages:

- Deep <u>continental</u> subsurface environments are important and need more love.
- Radioloysis of water generates H₂, CH₄, and a range of electron acceptors
- Radiolysis modifies buried organic C
- Deep <u>continental</u> subsurface environments are analogs for habitable subsurface environments on Mars.



Nathaniel Jobe Cassandra Skaar



Bennie Liebenberg Moab Khotsong Mine



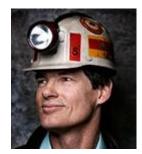


T.C. Onstott — Devan Nisson Maggie Lau Cara Magnabosco

UNIVERSITY OF THE FREE STATE UNIVERSITE IT VAN DIE VRYSTAAT YUNIVESITHI YA FREISTATA

Julio Castillo Hernandez Alba Gómez Arias Errol Cason







Barbara Sherwood Lollar Oliver Warr

Many, many others!

