

Molecular Signatures of Life in the Dead Sea A DDF Initiative



Matthew Rhodes
and
Chris House

NASA NAI Update
08/14/08

The Dead Sea as a Mars analog



Holden Crater

1. Tectonic basin ~ -418m
2. Salinity ~ 340‰
3. Acidic pH ~ 6



Matthew Rhodes



Valle Marineris

Objectives

**Comprehensively characterize life in a
unique hypersaline environment:**

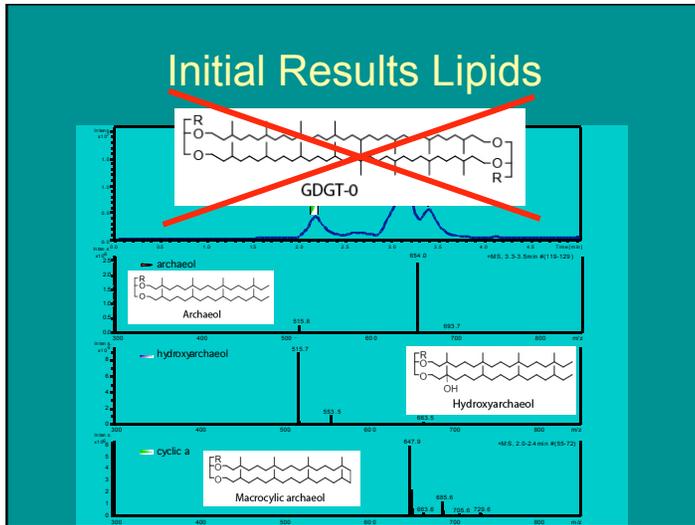
1. Cellular signatures (SIMS)
2. Lipid signatures (lipids)
3. Amino acid signatures
4. DNA signatures (metagenomics)

Cellular Signatures

SIMS to monitor uptake of isotopically
labeled carbon and nitrogen
→Reveal which organisms are primary
producers

Incubations
conducted in
the field





- ### Amino Acid Analysis Intro
- Two high salinity coping mechanisms
 1. Organic in
 - Energetically expensive
 - Does not require protein alteration
 2. Salt in
 - Energetically Cheap
 - Requires protein alteration
 - ↑ Acidic AAs ↓ Basic AAs Low hydrophobic AAs
 - Salt in more prevalent at higher salinities

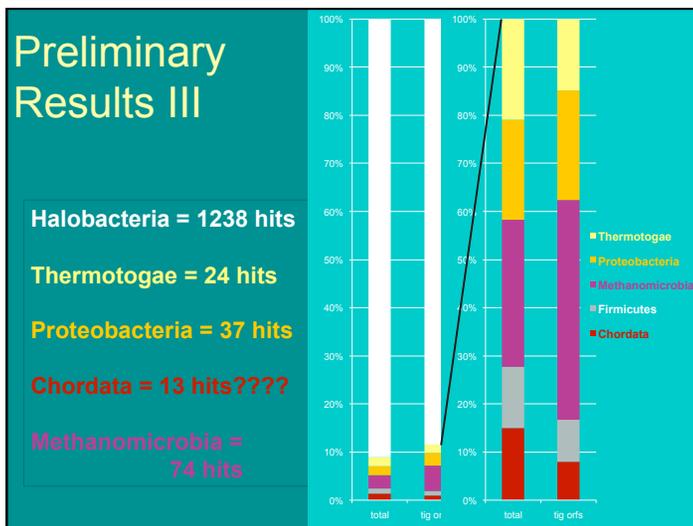
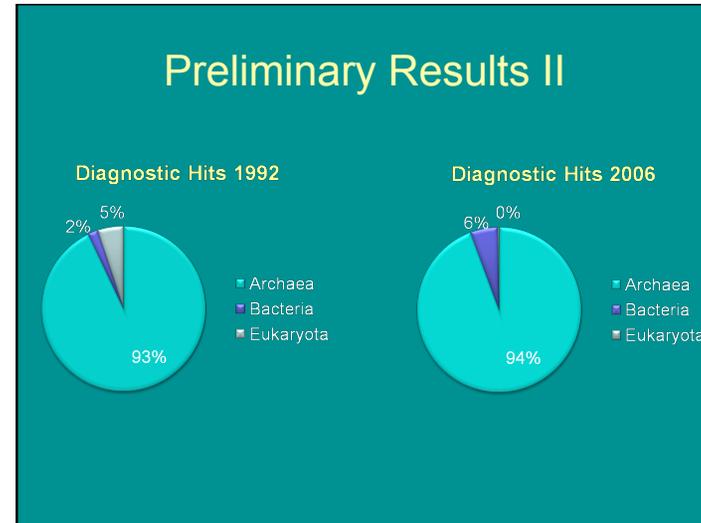
- ### Amino Acid Signatures
1. Degree of racemization
→ Reveal level of microbial activity
 2. Presence of unusual amino acids
Betaine, Ectoine, and hydroxectoine used by halophiles as osmolytes
-
- The figure shows the chemical structures of four amino acids: betaine (trimethylglycine), ectoine, hydroxectoine, and gamma-aminobutyric acid (GABA).

- ### DNA Signatures
- #### “Pyrosequencing” of the Dead Sea
- Novel sequencing method
 - Massively parallel (~400,000 sequences per plate)*
 - Yields very short reads (~200 bp)
 - PSU is a good place to do this work
- As examples,
 - our modern Dead Sea half-plate gave 273,296 sequences with an average read length of 251 bp,
 - and last week, we had a full plate yield 546,127 reads with an average length of ~194 bp (105 Mb).

454 Sequencing
(to compare today's Dead Sea with the 1992 bloom event)

1. 16S rRNA sequence tags to look at species distribution
2. Non-specific DNA sequencing (2x400,000)
3. Assembled fosmid sequences

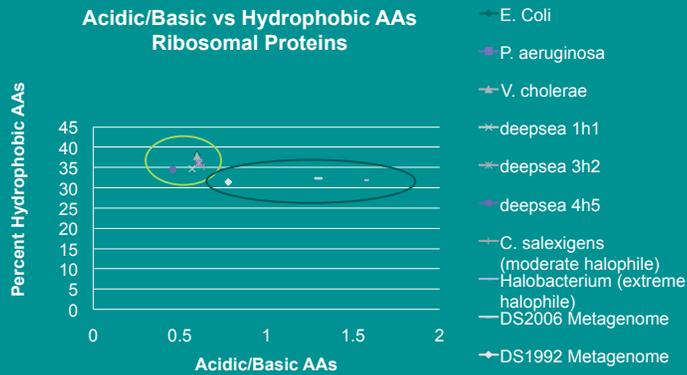
End up with close to ~200 Mb of data



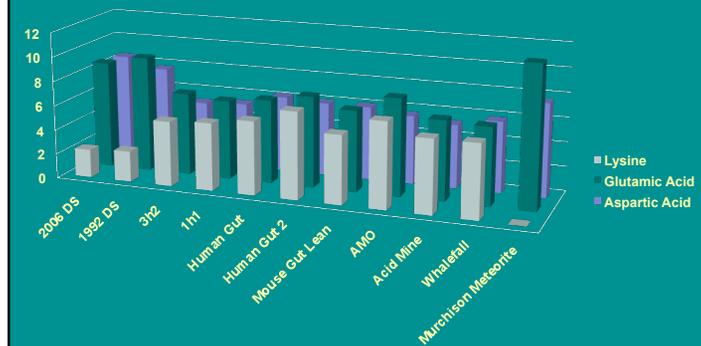
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Amino Acids I



Amino Acid Percentage Metagenomes



Summary

1. Identify a high number of DNA-based signatures of hypersaline life
2. Reveal organic biosignatures (cells, lipids, phospholipids, and amino acids) from the water and sediments
3. Integrate results with measured geochemistry
4. Involve international expert collaborators in analyzing the results

Acknowledgments

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