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Supplement of

Carbon isotopes of dissolved inorganic carbon reflect utilization of different carbon sources by microbial communities in two limestone aquifer assemblages

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Supplement material

1) NETPATH input parameters

Flowpath: **HTL H-31 to HTL H-41**

Used constraints: Carbon, Nitrogen, Potassium

Phases: "CH₂O", Calcite, Exchange (Na/K), K-Mica, NH₃-Gas

Initial C-14: 56.75 pmC

Model: Tamers

Flowpath: **HTL H-41 to HTL H-51**

Used constraints: Carbon, Nitrogen, Potassium

Phases: "CH₂O", Calcite, Exchange (Na/K), K-Mica, NH₃-Gas

Initial C-14: 56.42 pmC

¹⁴C Model: Tamers

Flowpath: **HTU H-32 to HTL H-43**

Used constraints: Carbon, Sulfur, Iron, Redox, Calcium

Phases: "CH₂O", Calcite, Exchange (Na/K), Goethite, Gypsum, Pyrite

Initial C-14: 55.86 pmC

¹⁴C Model: Tamers

Flowpath: **HTU H-32 to HTL H-52**

Used constraints: Carbon, Sulfur, Nitrogen, Calcium, Magnesium, C-14, Carbon-13, Potassium

Phases: "CH₂O", Calcite, Dolomite, Gypsum, Pyrite, N₂ Gas, NH₃ Gas, NH₄/CAEX, CO₂ Gas, CH₄ Gas

Initial C-14: 55.86 pmC

¹⁴C Model: Rev. Fontes & Garnier solid ex

2) Abundance of bacterial OTU's at genus level

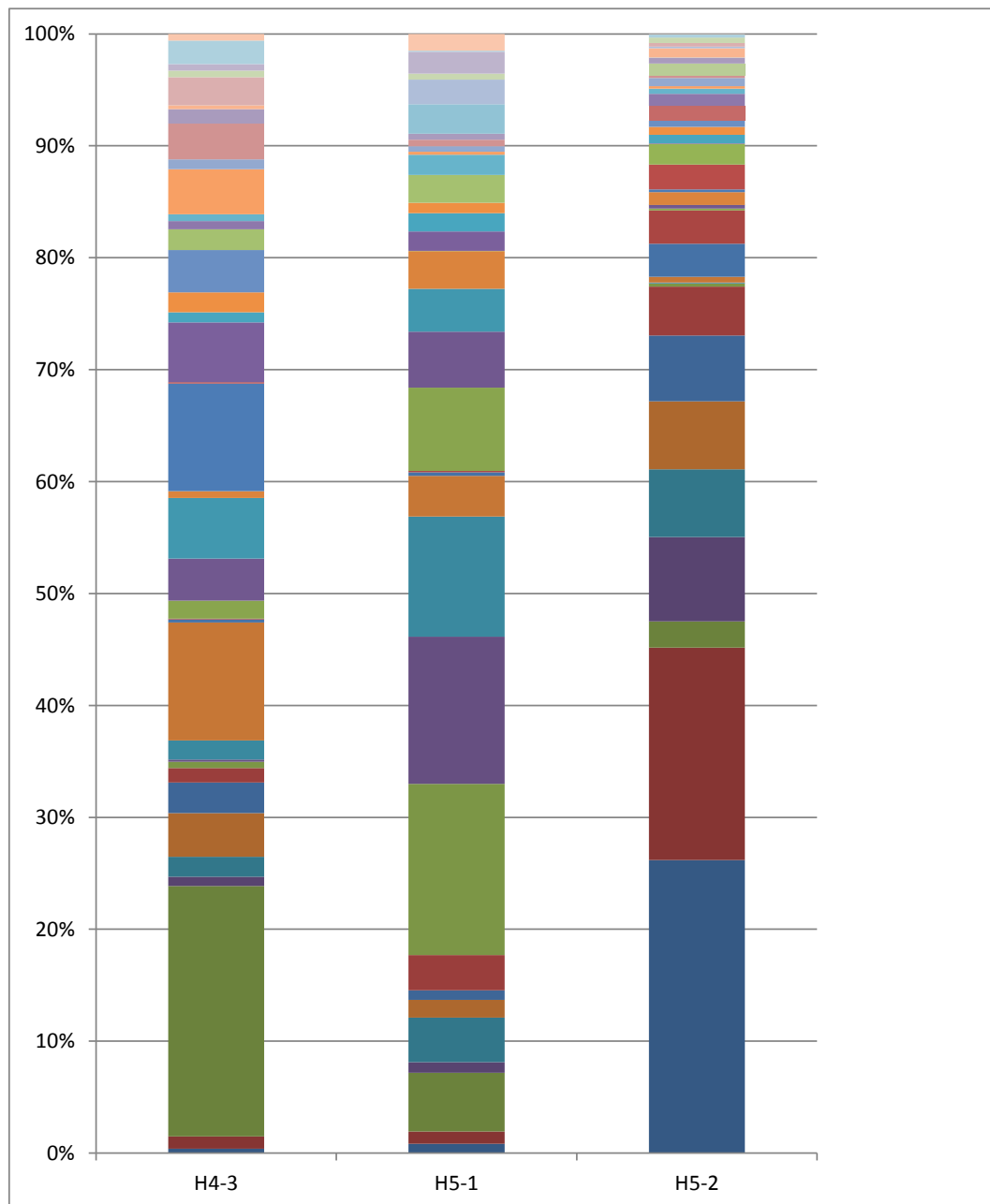


Figure S1: Abundance of bacterial OTU's at genus level:

- BSV26_unclassified; BSV26; Ignavibacteriales; Ignavibacteria; Chlorobi
- Candidate_division_TM7_unclassified; Candidate_division_TM7_unclassified; Candidate_division_TM7_unclassified; Candidate_division_TM7_unclassified; Candidate_division_TM7
- Candidate_division_OD1_unclassified; Candidate_division_OD1_unclassified; Candidate_division_OD1_unclassified; Candidate_division_OD1_unclassified; Candidate_division_OD1
- Nitrospiraceae_unclassified; Nitrospiraceae; Nitrospirales; Nitrospira; Nitrospirae
- BSV13_unclassified; BSV13_unclassified; BSV13_unclassified; BSV13; Bacteroidetes
- Betaproteobacteria_unclassified; Betaproteobacteria_unclassified; Betaproteobacteria_unclassified; Betaproteobacteria; Proteobacteria
- Syntrophus; Syntrophaceae; Syntrophobacteriales; Deltaproteobacteria; Proteobacteria
- Gammaproteobacteria_unclassified; Gammaproteobacteria_unclassified; Gammaproteobacteria_unclassified; Gammaproteobacteria; Proteobacteria
- Albidiferax; Comamonadaceae; Burkholderiales; Betaproteobacteria; Proteobacteria
- Actinobacteria_unclassified; Actinobacteria_unclassified; Actinobacteria_unclassified; Actinobacteria_unclassified; Actinobacteria
- Nitrospira; Nitrospiraceae; Nitrospirales; Nitrospira; Nitrospirae
- Candidate_division_OP3_unclassified; Candidate_division_OP3_unclassified; Candidate_division_OP3_unclassified; Candidate_division_OP3_unclassified; Candidate_division_OP3
- Sulfuritalea; Rhodocyclaceae; Rhodocyclales; Betaproteobacteria; Proteobacteria
- Ignavibacteriales_unclassified; Ignavibacteriales_unclassified; Ignavibacteriales; Ignavibacteria; Chlorobi
- Caulobacteraceae_unclassified; Caulobacteraceae; Caulobacterales; Alphaproteobacteria; Proteobacteria
- Subgroup_6_unclassified; Subgroup_6_unclassified; Subgroup_6; Acidobacteria; Acidobacteria
- O319-6A21_unclassified; O319-6A21; Nitrospirales; Nitrospira; Nitrospirae
- Deltaproteobacteria_unclassified; Deltaproteobacteria_unclassified; Deltaproteobacteria_unclassified; Deltaproteobacteria; Proteobacteria
- Desulfosporosinus; Peptococcaceae; Clostridiales; Clostridia; Firmicutes
- Desulfurivibrio; Desulfobulbaceae; Desulfobacteriales; Deltaproteobacteria; Proteobacteria
- TM146_unclassified; TM146; Solirubrobacteriales; Thermoleophila; Actinobacteria
- NPL-UPA2_unclassified; NPL-UPA2_unclassified; NPL-UPA2_unclassified; NPL-UPA2_unclassified; NPL-UPA2
- Proteobacteria_unclassified; Proteobacteria_unclassified; Proteobacteria_unclassified; Proteobacteria_unclassified; Proteobacteria
- DTB120_unclassified; DTB120_unclassified; DTB120; Deltaproteobacteria; Proteobacteria
- TRA3-20_unclassified; TRA3-20_unclassified; TRA3-20; Betaproteobacteria; Proteobacteria
- Candidatus_Magnetoovum; Nitrospiraceae; Nitrospirales; Nitrospira; Nitrospirae
- Aquicella; Coxiellaceae; Legionellales; Gammaproteobacteria; Proteobacteria
- Sulfuricum; Helicobacteraceae; Campylobacteriales; Epsilonproteobacteria; Proteobacteria
- Comamonadaceae_unclassified; Comamonadaceae; Burkholderiales; Betaproteobacteria; Proteobacteria
- Gallionellaceae_unclassified; Gallionellaceae; Nitrosomonadales; Betaproteobacteria; Proteobacteria
- Lineage_IV_unclassified; Lineage_IV_unclassified; Lineage_IV; Elusimicrobia; Elusimicrobia
- Pedobacter; Sphingobacteriaceae; Sphingobacteriales; Sphingobacteriia; Bacteroidetes
- Desulfocapsa; Desulfobulbaceae; Desulfobacteriales; Deltaproteobacteria; Proteobacteria
- BD1-5_unclassified; BD1-5_unclassified; BD1-5_unclassified; BD1-5_unclassified; BD1-5
- Caldilineaceae_unclassified; Caldilineaceae; Caldilineales; Caldilineae; Chloroflexi
- WCHB1-32_unclassified; WCHB1-32_unclassified; WCHB1-32_unclassified; WCHB1-32; Bacteroidetes
- Acidiferrobacter; Ectothiorhodospiraceae; Chromatiales; Gammaproteobacteria; Proteobacteria
- 43F-1404R_unclassified; 43F-1404R_unclassified; 43F-1404R; Deltaproteobacteria; Proteobacteria
- Bacteroidetes_unclassified; Bacteroidetes_unclassified; Bacteroidetes_unclassified; Bacteroidetes_unclassified; Bacteroidetes
- NKB5_unclassified; NKB5_unclassified; NKB5; Gammaproteobacteria; Proteobacteria
- TM6_unclassified; TM6_unclassified; TM6_unclassified; TM6_unclassified; TM6
- Anaerolineaceae_unclassified; Anaerolineaceae; Anaerolineales; Anaerolineae; Chloroflexi

Figure S2: Abundance of bacterial OTU's at genus level (legend).