

A photograph of a pond with water lilies and reeds. The water is dark, and the lily pads are green. The reeds are tall and thin, and some are in the foreground. The background is slightly blurred.

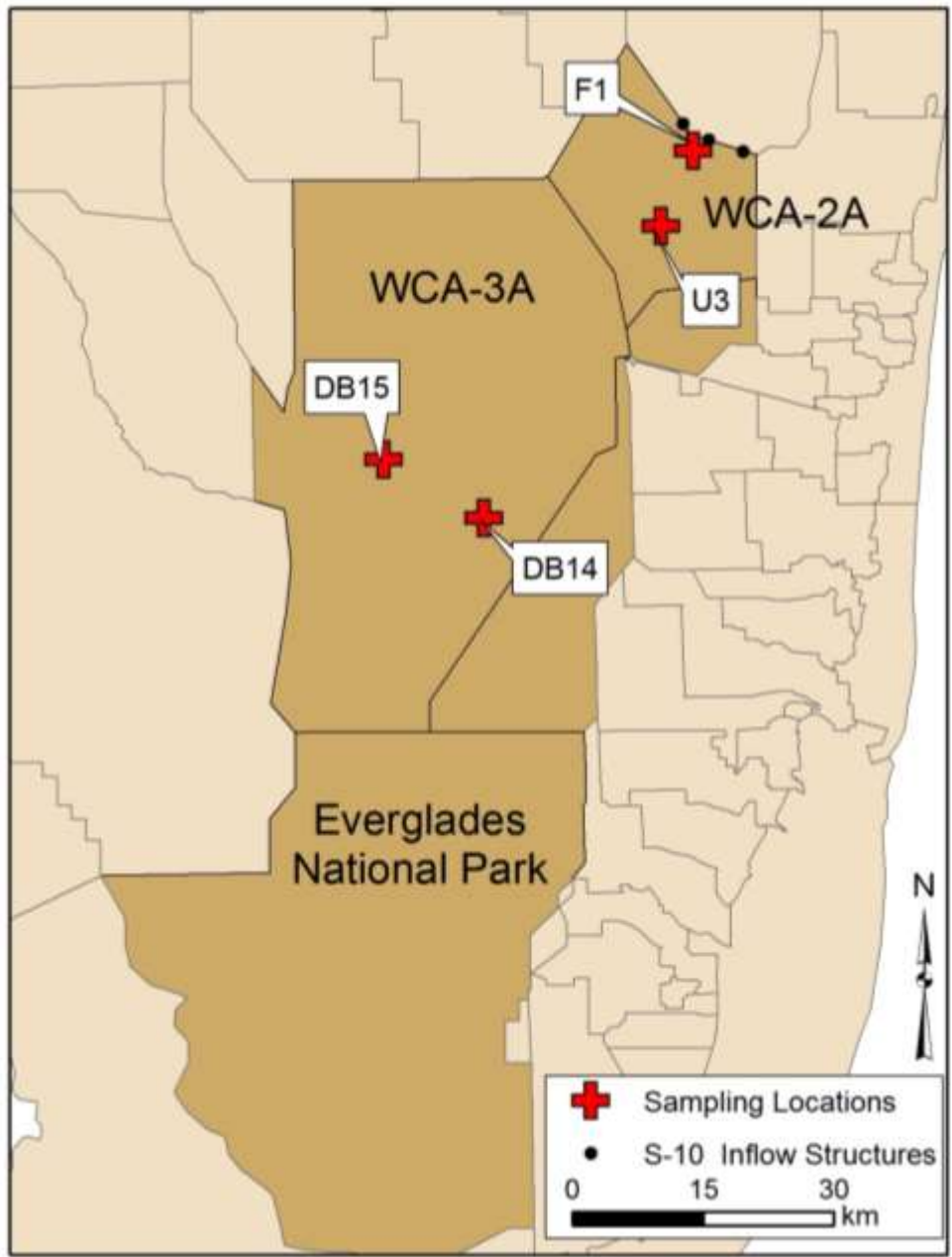
Phylogenetic Distribution of Mercury Methylators (*hgcAB*) in the Water Conservation Areas

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Outline

- The anaerobic carbon cycle in the Everglades
- Peaceful coexistence: sulfate reduction vs methanogenesis
- Distribution of *hgcAB* in different compartments down the gradient.
- *Disclaimer: genes do not indicate activities!*

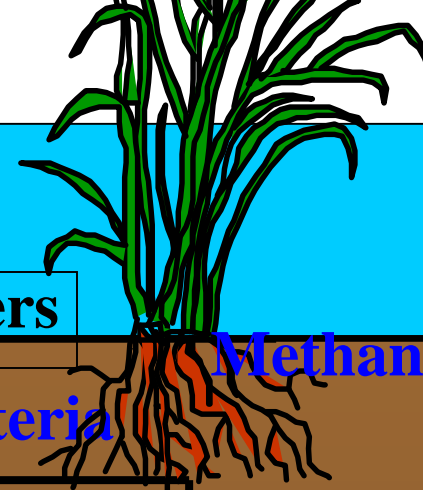


Anaerobic processing of carbon

Water (Aerobic)

Detritus (floc)

Monomers and Oligomers



Methanotrophs

ANAEROBIC

Cellulolytic & Fermentative Bacteria

H₂ and CO₂

Short chain fatty acids
(propionate, butyrate, etc);
alcohols.

Homoacetogens

Syntrophic Bacteria

Acetate

Acetate

H₂ and CO₂

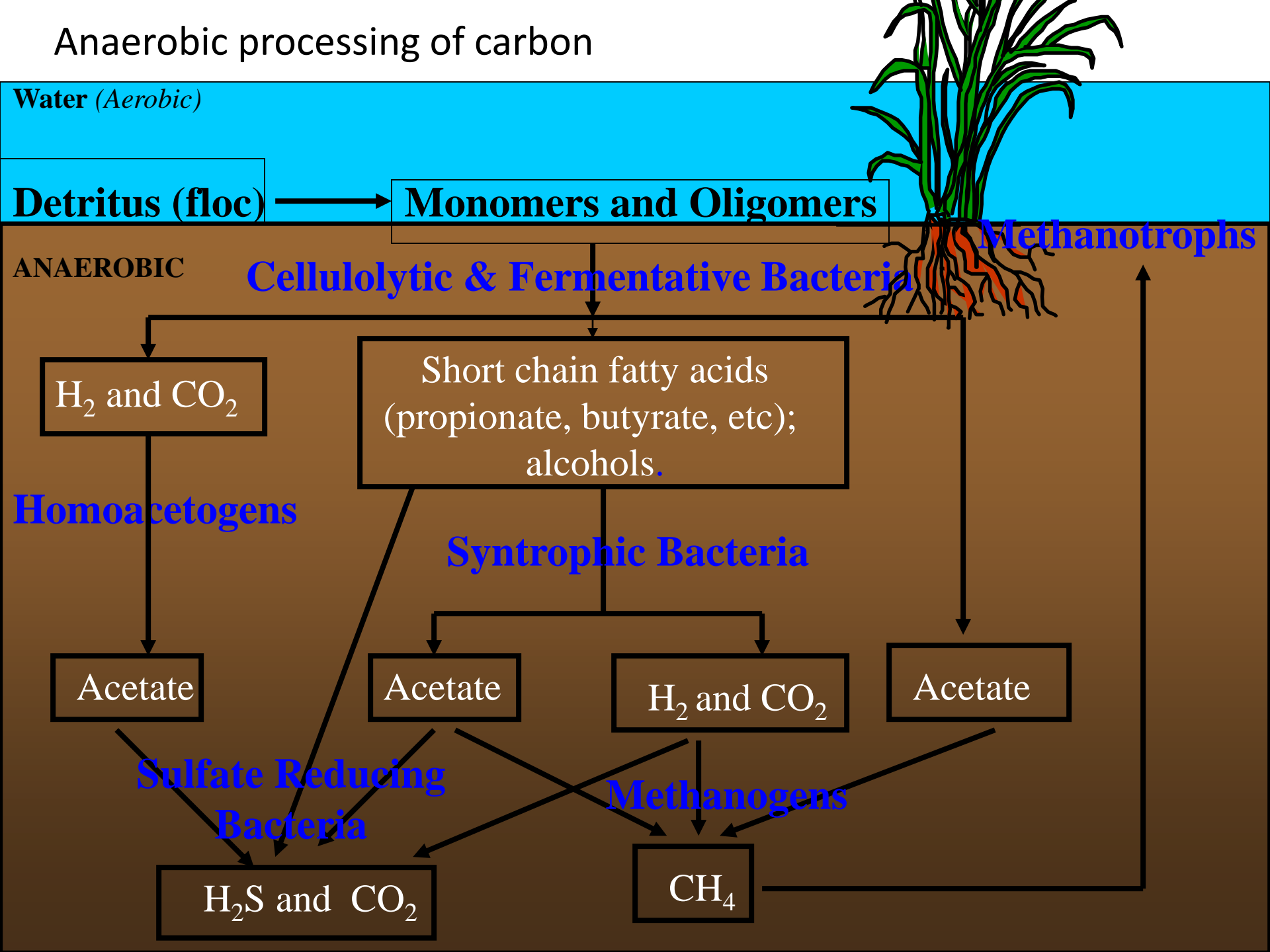
Acetate

Sulfate Reducing
Bacteria

Methanogens

H₂S and CO₂

CH₄



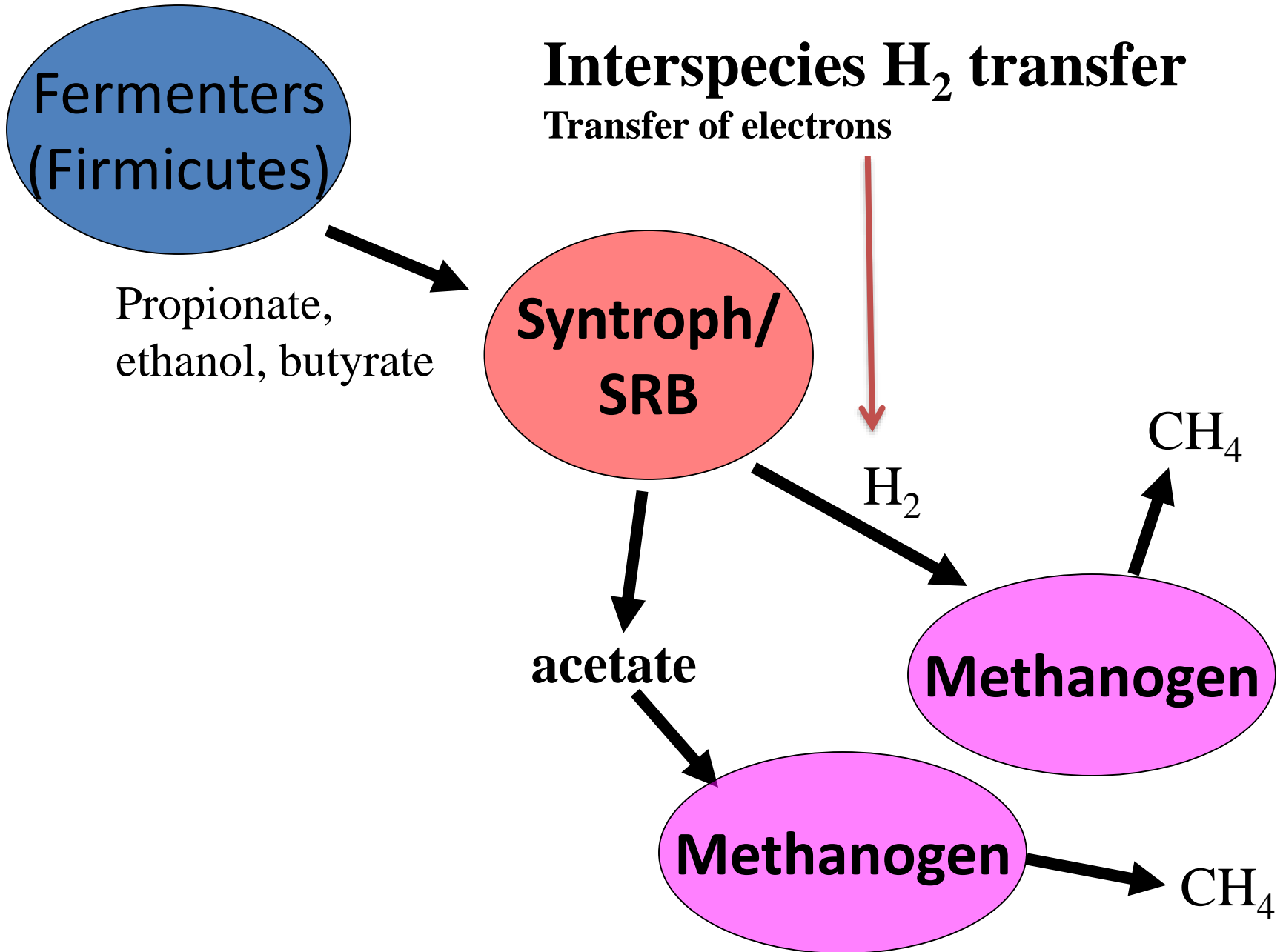
More carbon is mineralized via methane production than via sulfate reduction in soil lab incubations

| Characteristics | F1 | F4 | U3 |
|---------------------------------|----------|--------------------------------------------------------------------------------------------------------------------|-----------|
| | | CH ₄ production rate ($\mu\text{mol} \times \text{g soil}^{-1} \times \text{d}^{-1}$) | |
| Intact soils | 3.1±3.2 | 0.9±0.9 | <0.1 |
| Acetate | 5.3±1.4 | 2.7±0.5 | 0.4±1.2 |
| H ₂ /CO ₂ | 11.6±3.5 | 5.6±2.9 | 2.1±1.0 |
| | | SO ₄ ²⁻ reduction rate ($\mu\text{mol} \times \text{g soil}^{-1} \times \text{d}^{-1}$) | |
| Intact soils | 0.5±0.4 | <0.01 | 0.03±0.04 |
| Acetate | 1.4±0.3 | 0.1±0.1 | 0.07±0.07 |
| H ₂ /CO ₂ | 1.2±1.0 | <0.01 | 0.14±0.17 |

?

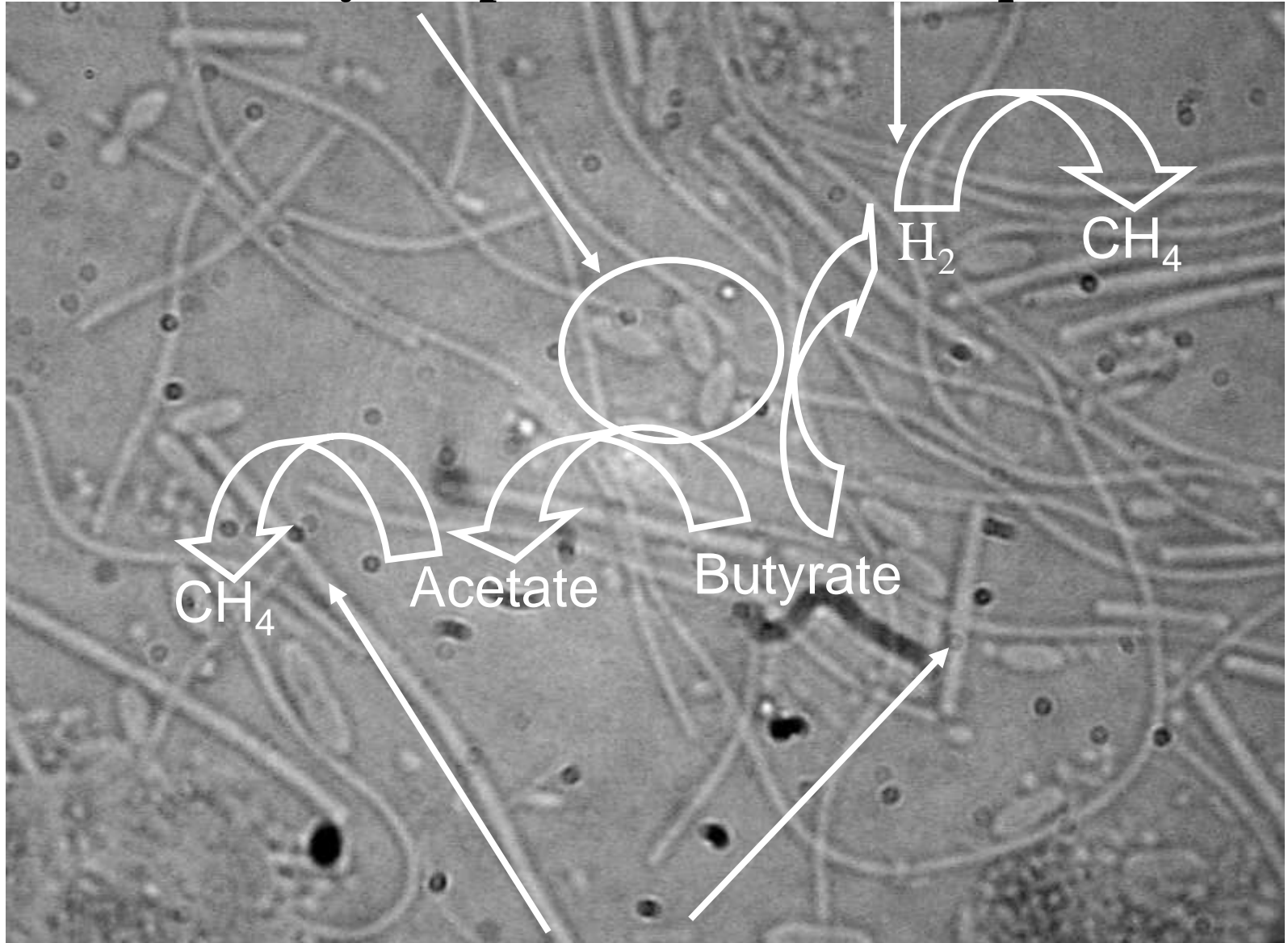
Interspecies H₂ transfer

Transfer of electrons



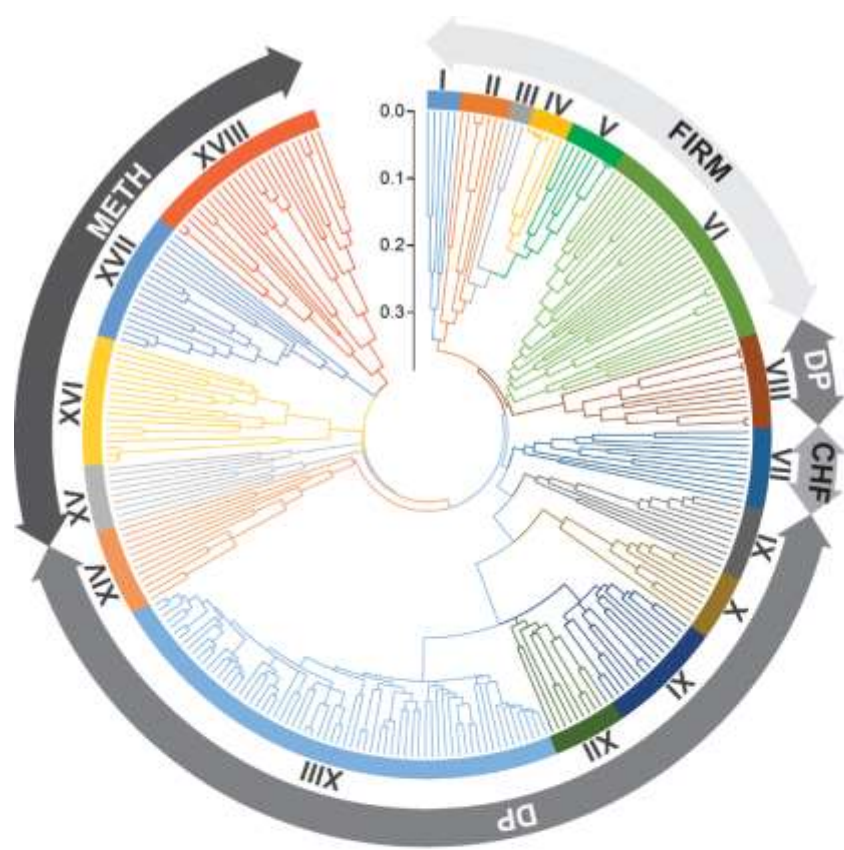
Syntrophs

Methanospirillum



Methanosaeta

Everglades *hgcAB* phylogeny



Dominant groups include:

- Deltaproteobacteria (SRB, FeRB)
 - Most affiliated with syntrophs.
 - Can also reduce sulfate
- Methanogens
- Firmicutes (Primary fermenters and *Dethiobacter*)

FIRM

- | | |
|------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|
| I: <i>Acetonema</i> | X: Unidentified DP |
| II: <i>Ethanoligenens</i> | XI: <i>Desulfomonile</i> |
| III: <i>Syntrophobotulus</i> | XII: DP NaphS2 |
| IV: <i>Dehalobacter</i> | XIII: Unidentified DP |
| V: <i>Desulfosporosinus</i> , <i>Desulfitobacterium</i> | XIV: <i>Desulfovibrio</i> , <i>Desulfobulbus</i> , <i>Desulfonatronum</i> , <i>Desulfomicrobium</i> |
| VI: <i>Dethiobacter</i> | |

CHF

- VII: *Dehalococcoides*

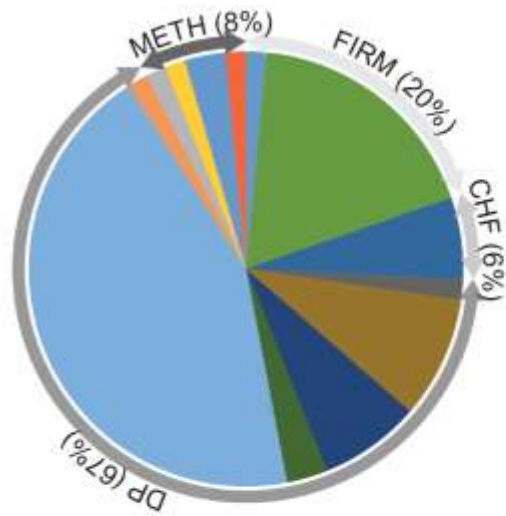
DP

- VIII: *Geobacter*
IX: *Syntrophorhabdus*,
Syntrophus

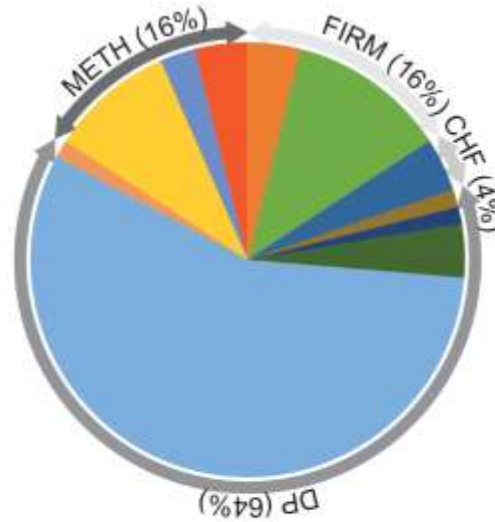
METH

- XV: *Methanosphaerula*
XVI: Unidentified METH
XVII: *Methanoregula*, *Methanospirillum*,
Methanolobus, *Methanofollis*
XVIII: *Methanocella*

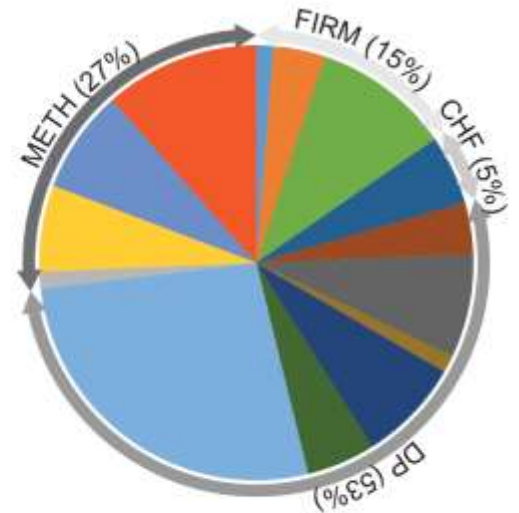
hgcAB distribution in soil down the gradient



F1



U3



DB15

DOC: SO_4^{2-}

16.8 (F2)

9.1

691

Methanogen component increases

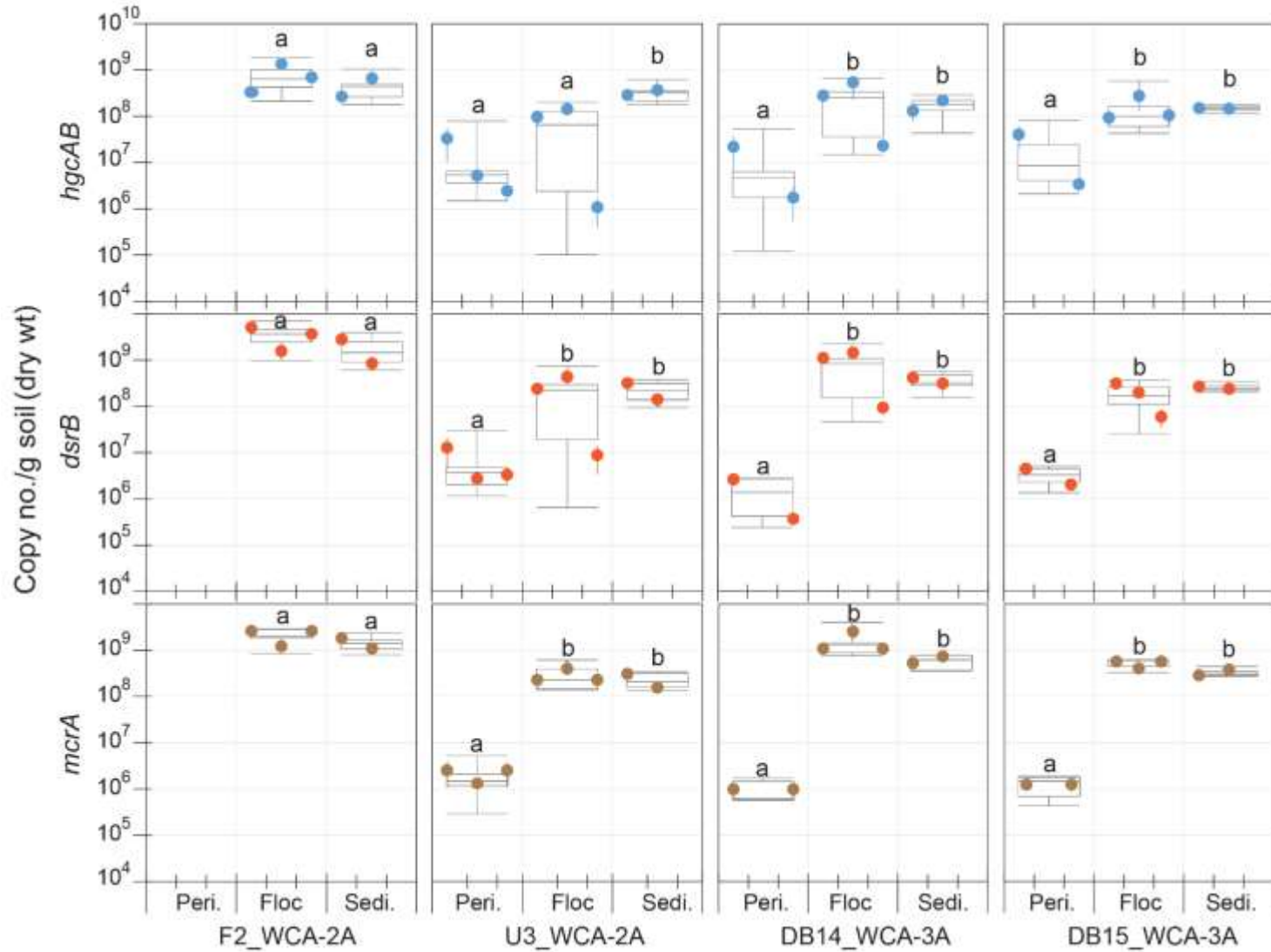


Firimicutes dominated by *Dethiobacter* (NOT SRB)

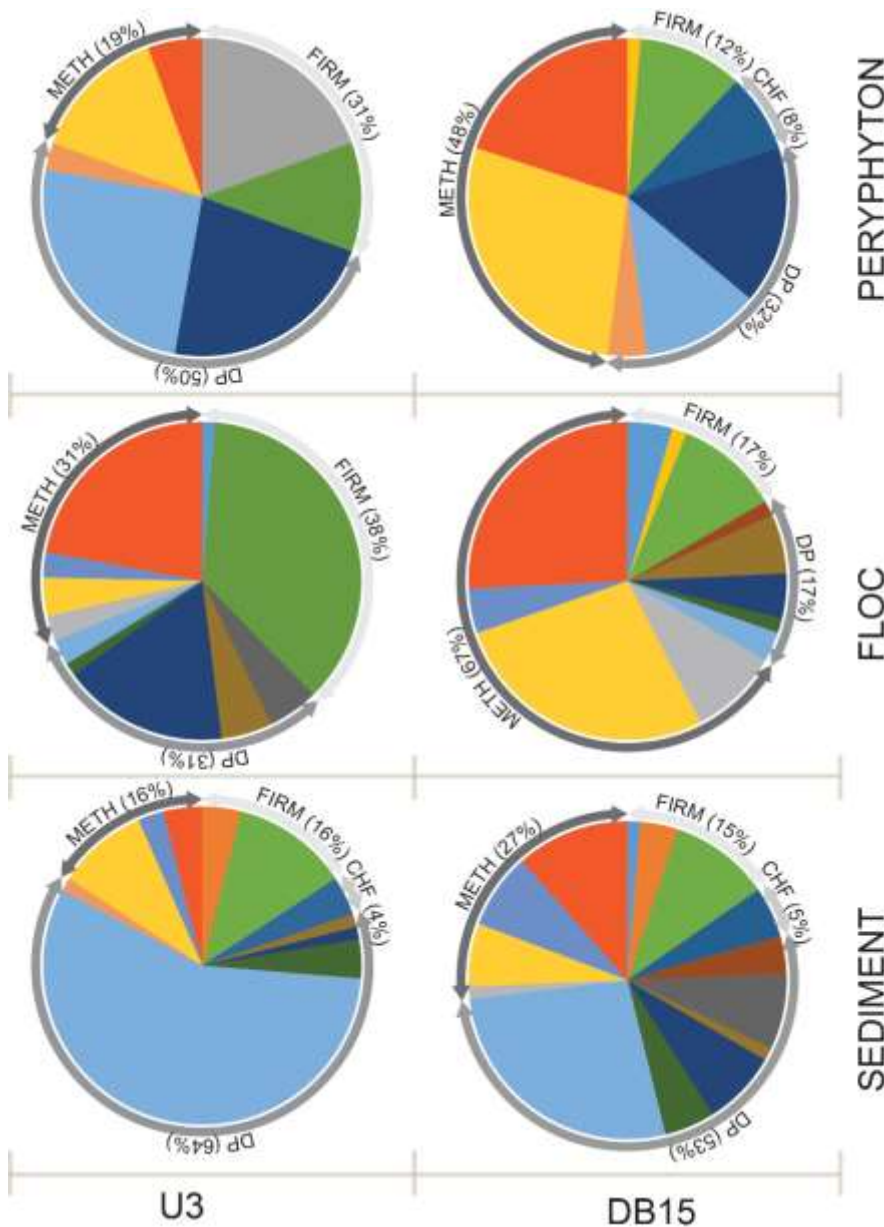
Complex ecosystem including
soil, floc, and floating periphyton



Numbers of mercury methylators (*hgcAB*), SRB (including syntrophs) (*dsrB*) and methanogens (*mcrA*). Generally higher in floc and soil than periphyton.



Methanogens and deltaproteobacteria dominate



Methanogens increase in importance at DB15

Methanogens and Firmicutes increase in importance. Firmicutes dominated by *Dethiobacter*.

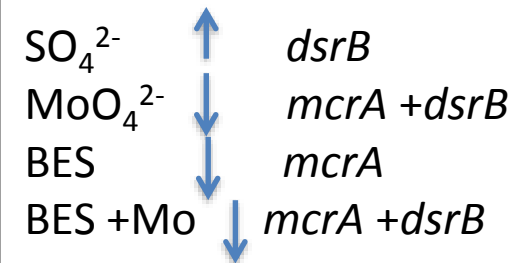
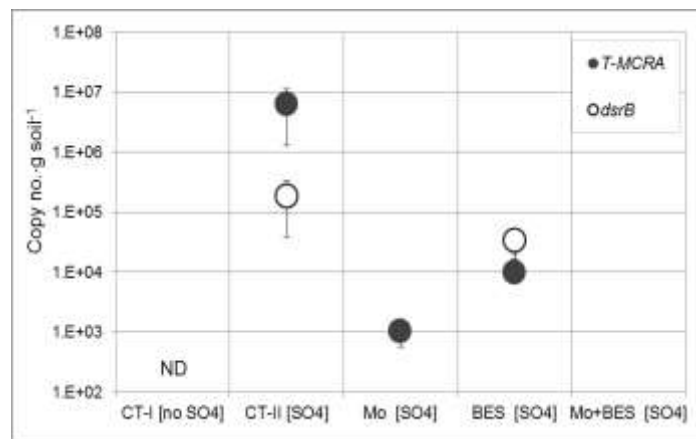
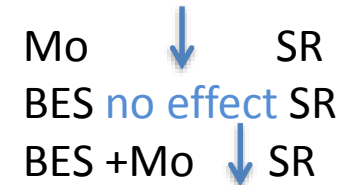
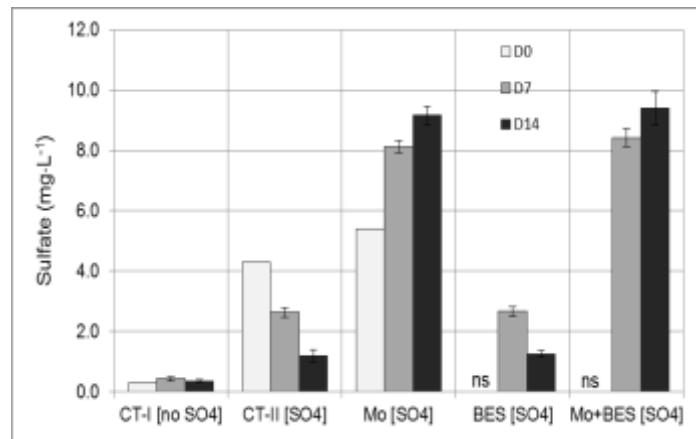
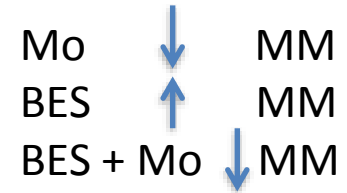
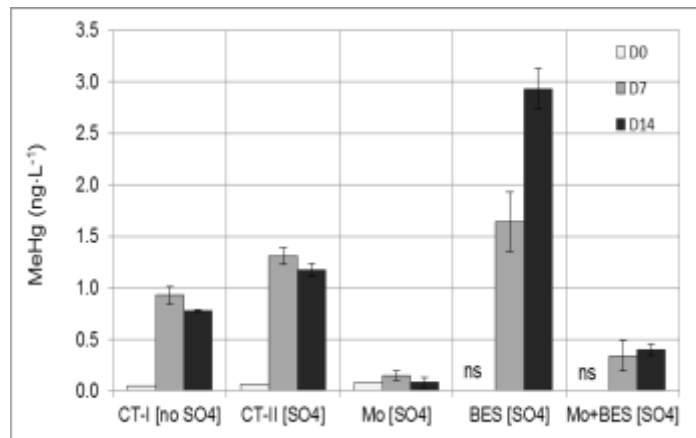
DP (SRB/Syntrophs) dominate at both sites, with increasing methanogen component at DB15

Summary

- Understanding ecological context yields insight into potential dominant processes that drive methylation.
- Mercury methylators can be viewed in the context of carbon cycle.
- Significant differences in distribution of dominant methylators in different areas and different compartments.
- Deltaproteobacteria (SRB, inc. syntrophs) dominate in WCA-2A
- Methanogens and firmicutes more important in floc, periphyton than soil. More important in DB15 (WCA-3A) than WCA-2A.
- *Presence of genes does not indicate activities.*

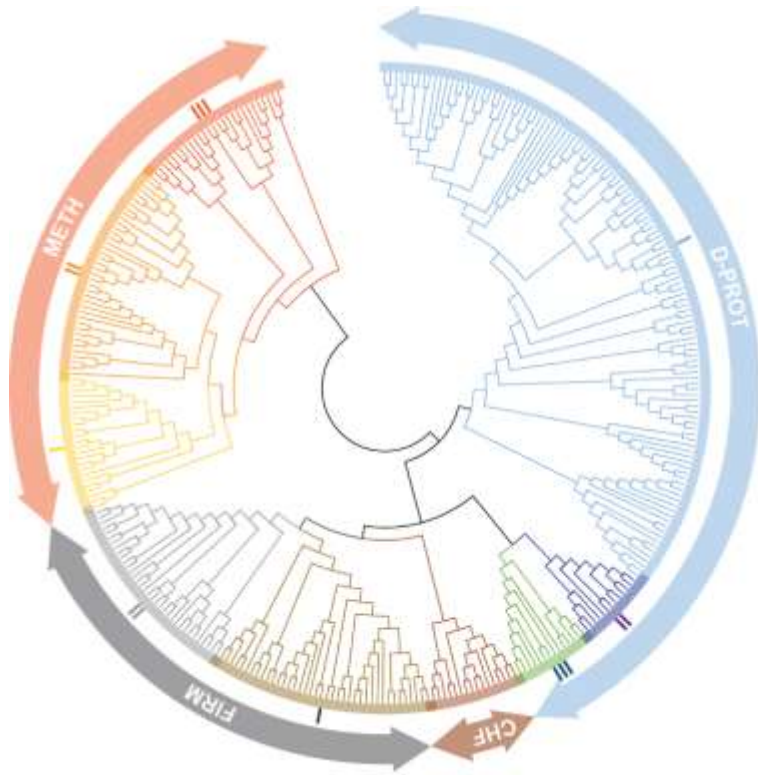
Slurry incubations with WCA-3A soil and selective inhibitors

MoO_4^{2-} inhibits SR
 BES inhibits methanogens



| Characteristics | F1 | F4 | U3 | W3 |
|------------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|---------------------------|---------------------------|
| Coordinates | 26°21'39"N, 80°22'10"W | 26°18'59"N, 80°23'01"W | 26°17'15"N, 80°24'41"W | 26°02'35"N, 80°49'39"W |
| Soil chemistry ^a | | | | |
| TP (g/kg) | 1.28±0.24 ^b | 0.60±0.26 | 0.25±0.04 | 0.38±0.02 |
| TN (g/kg) | 31±3 | 34±3 | 27±5 | 36±1 |
| TC (g/kg) | 442±31 | 424±29 | 385±69 | 424±4 |
| Porewater chemistry ^c | | | | |
| Acetate (μM) | 19.5±9.9 | 25.9±33.8 | 17.1±16.4 | ND |
| H ₂ (μM) | 0.33±0.10 | 0.28±0.20 | 0.28±0.14 | ND |
| SO ₄ ²⁻ (μM) ^d | 56±86 | 74±110 | 39±35 | ≤4 |
| CH ₄ production rate (μmol·g soil ⁻¹ ·d ⁻¹) ^e | | | | |
| Intact soils | 3.1±3.2 | 0.9±0.9 | <0.1 | ND |
| Acetate | 5.3±1.4 | 2.7±0.5 | 0.4±1.2 | ND |
| H ₂ /CO ₂ | 11.6±3.5 | 5.6±2.9 | 2.1±1.0 | ND |
| SO ₄ ²⁻ reduction rate (μmol·g soil ⁻¹ ·d ⁻¹) ^e | | | | |
| Intact soils | 0.5±0.4 | <0.01 | 0.03±0.04 | ND |
| Acetate | 1.4±0.3 | 0.1±0.1 | 0.07±0.07 | ND |
| H ₂ /CO ₂ | 1.2±1.0 | <0.01 | 0.14±0.17 | ND |

Bae *hgcAB* primers compared with ORNL primer set (DB 15)



D-PROT

- I: *Syntrophobacteriales*
- II: *Desulfovibrionales*
Desulfobacteriales
- III: *Geobacter*

METH

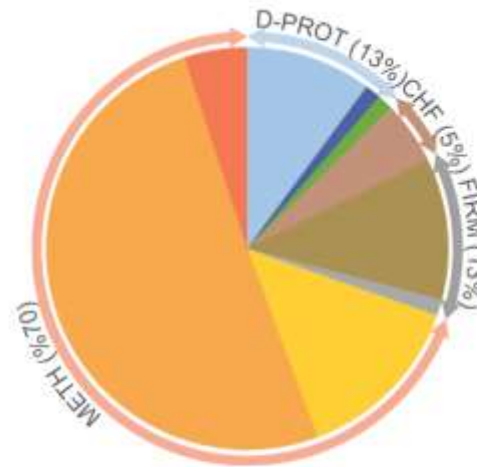
- I: *Methanomicrobiales*
Methanosarcinales
- II: *Methanocellales*
- III: Unidentified METH

CHF

- Dehalococcoidales*

FIRM

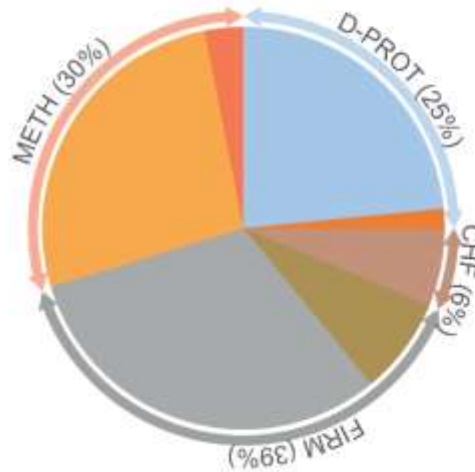
- I: *Clostridiales*,
Selenomonadales
- II: Unidentified FIRM



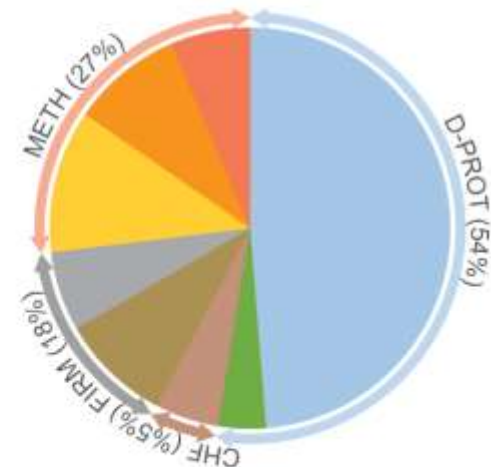
ONL_Floc



BAE_Floc



ONL_SEDI



BAE_SEDI

