

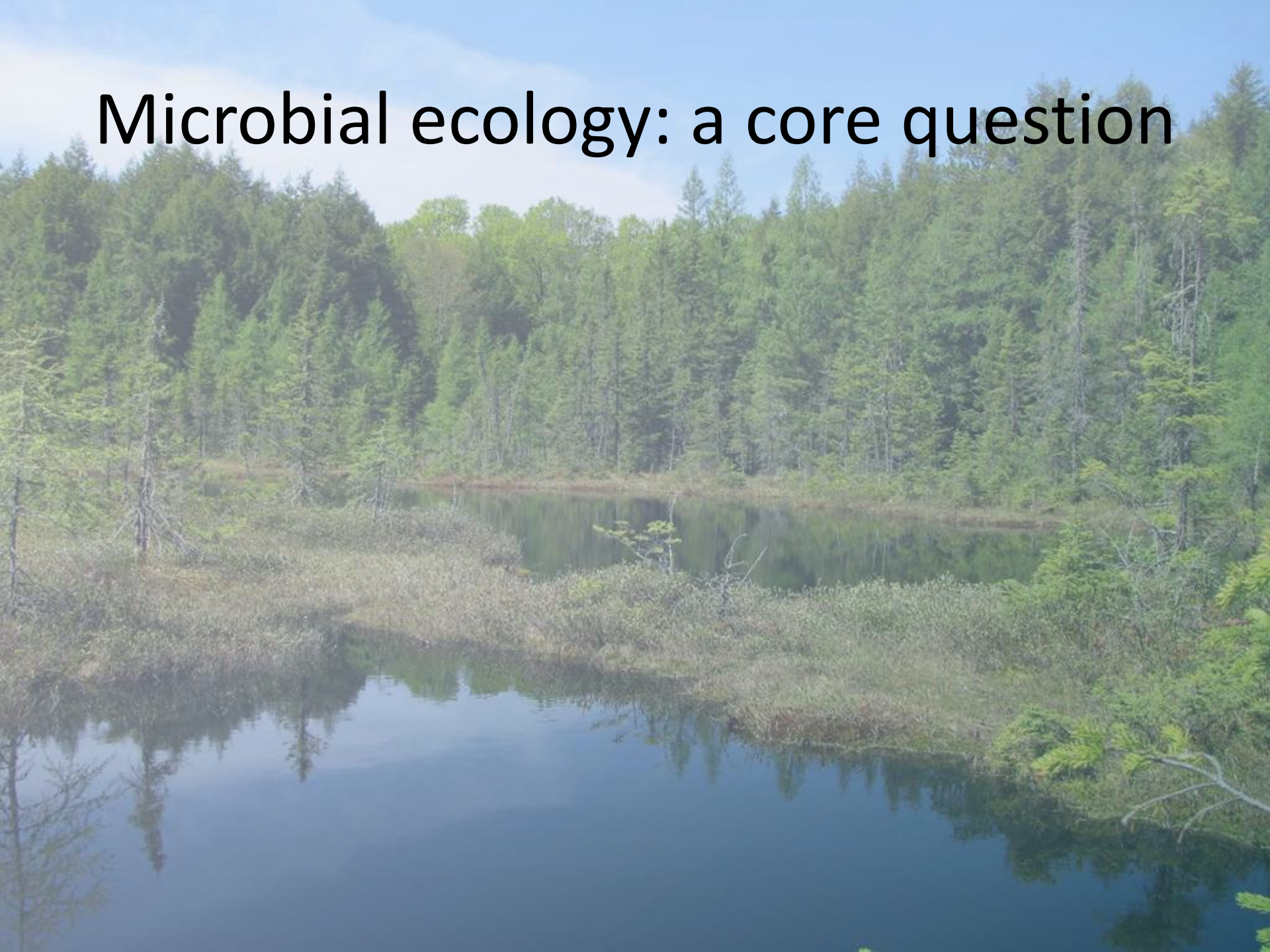


Linking Ecosystem Function to Methanogen Community Structure in Peatland Soils

**Steve McAllister, Brendan Bohannon, Rongzhong
Ye, Qusheng Jin, and Scott Bridgham**

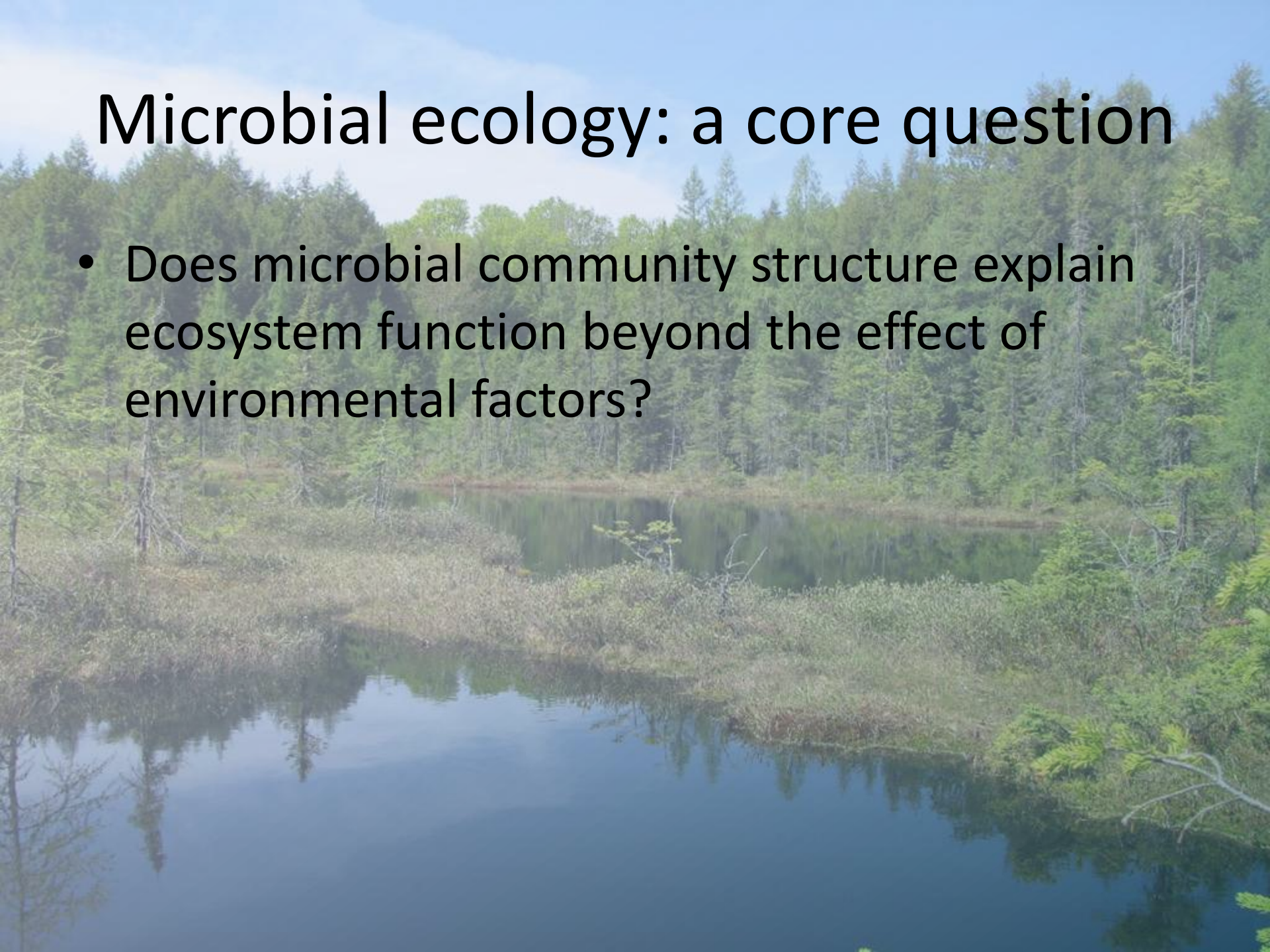
University of Oregon

Microbial ecology: a core question



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- Does microbial community structure explain ecosystem function beyond the effect of environmental factors?



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- Does microbial community structure explain ecosystem function beyond the effect of environmental factors?
- Does spatial and temporal variation in microbial diversity and activity contribute to the control of key biogeochemical processes?

Methanogens: a small community, an essential function



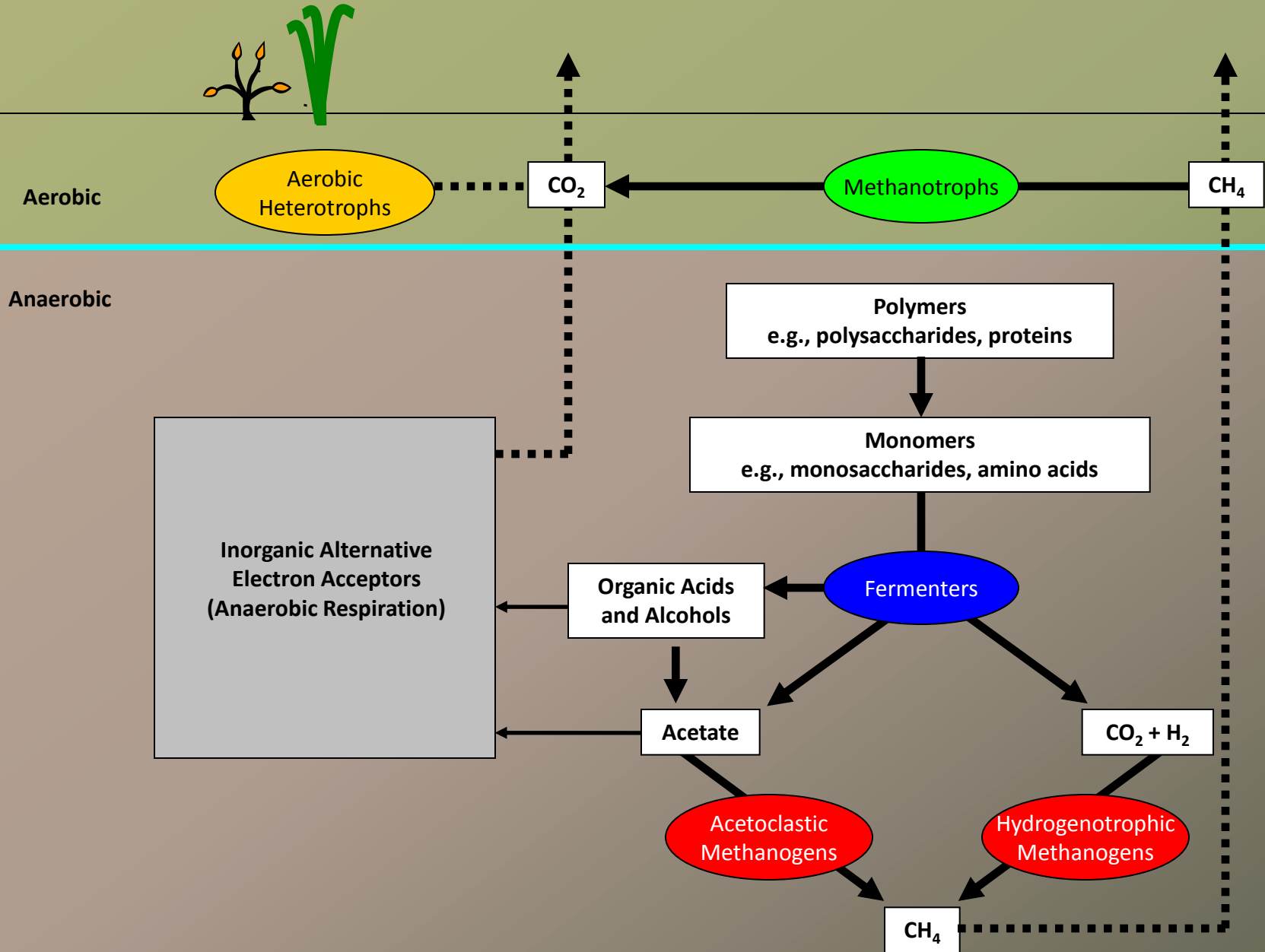
Methanogens: a small community, an essential function

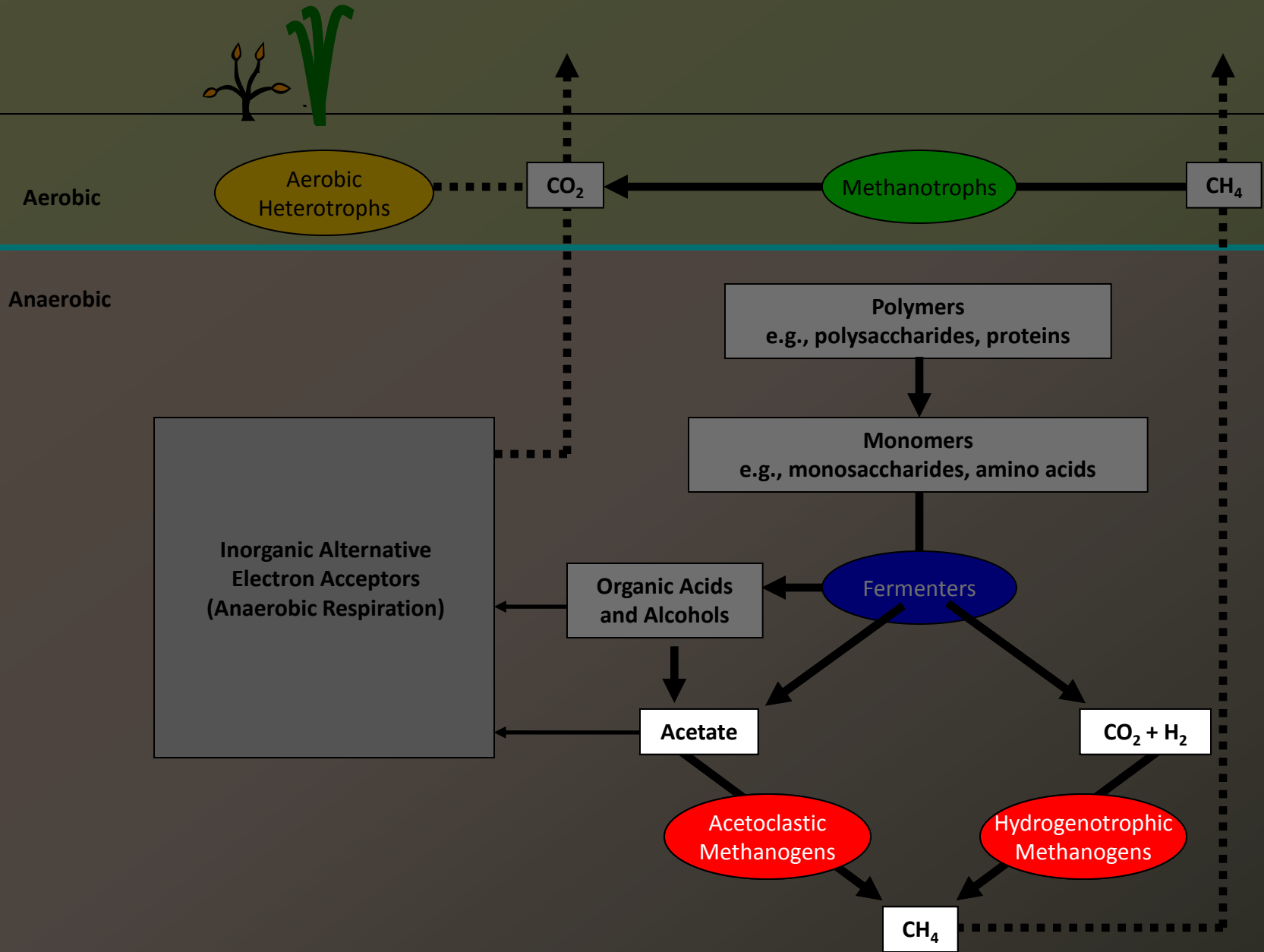
- A microbial group with a distinct, unique function and (relatively) low diversity



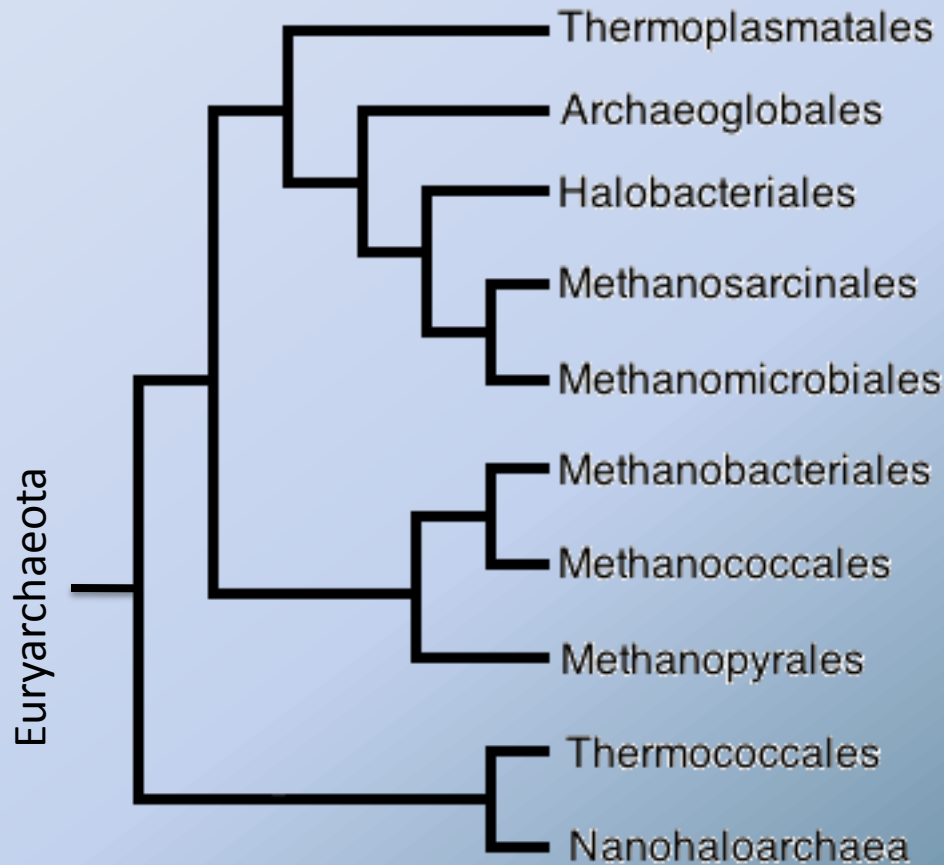
Methanogens: a small community, an essential function

- A microbial group with a distinct, unique function and (relatively) low diversity
- Two distinct biochemical pathways that are phylogenetically distributed within the methanogens, and can be quantified independently via radioisotope labeling

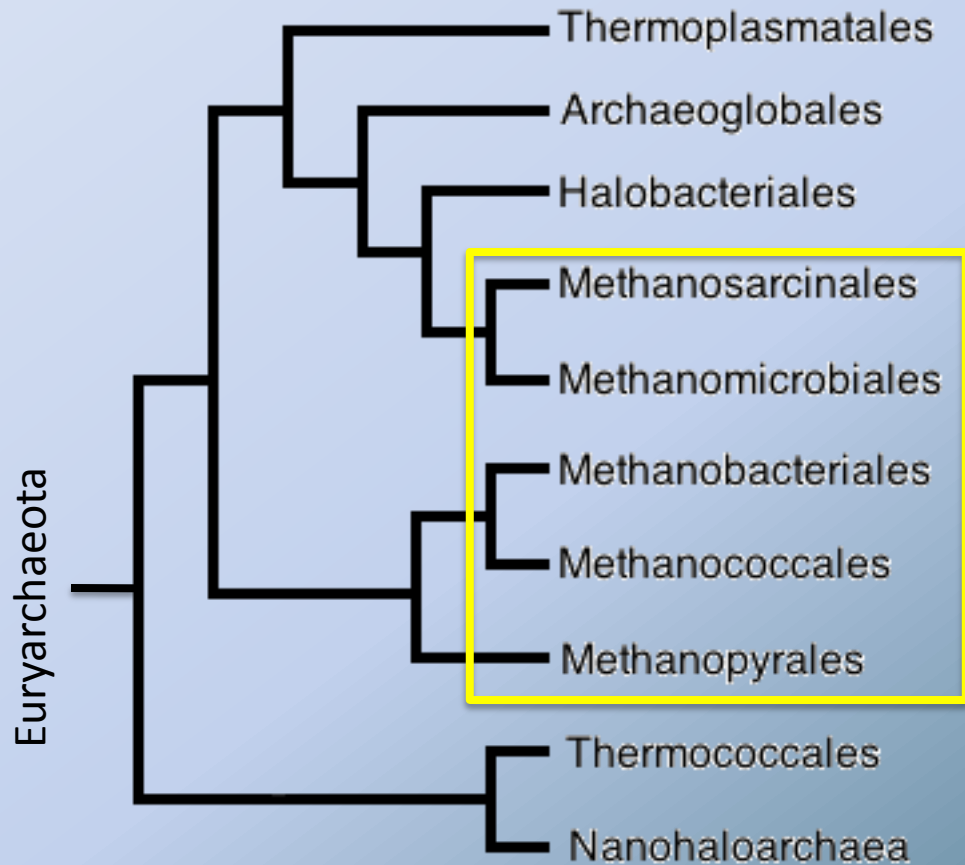




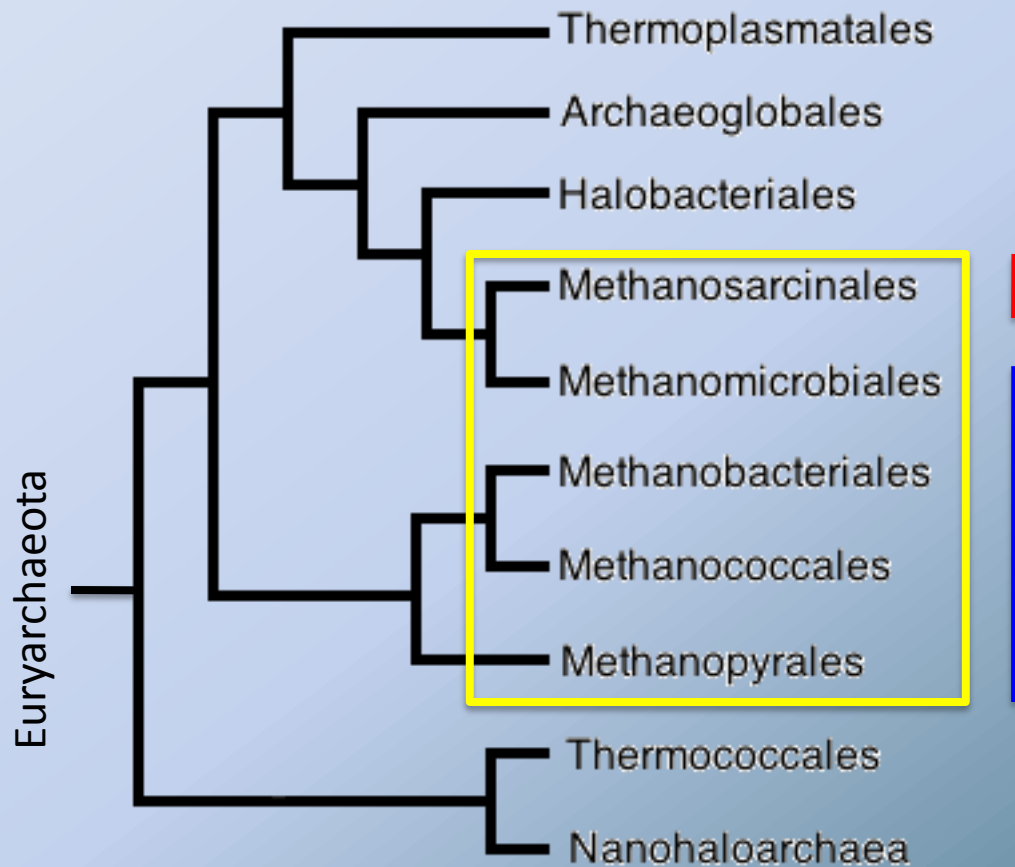
Methanogenesis pathways are taxonomically distinct



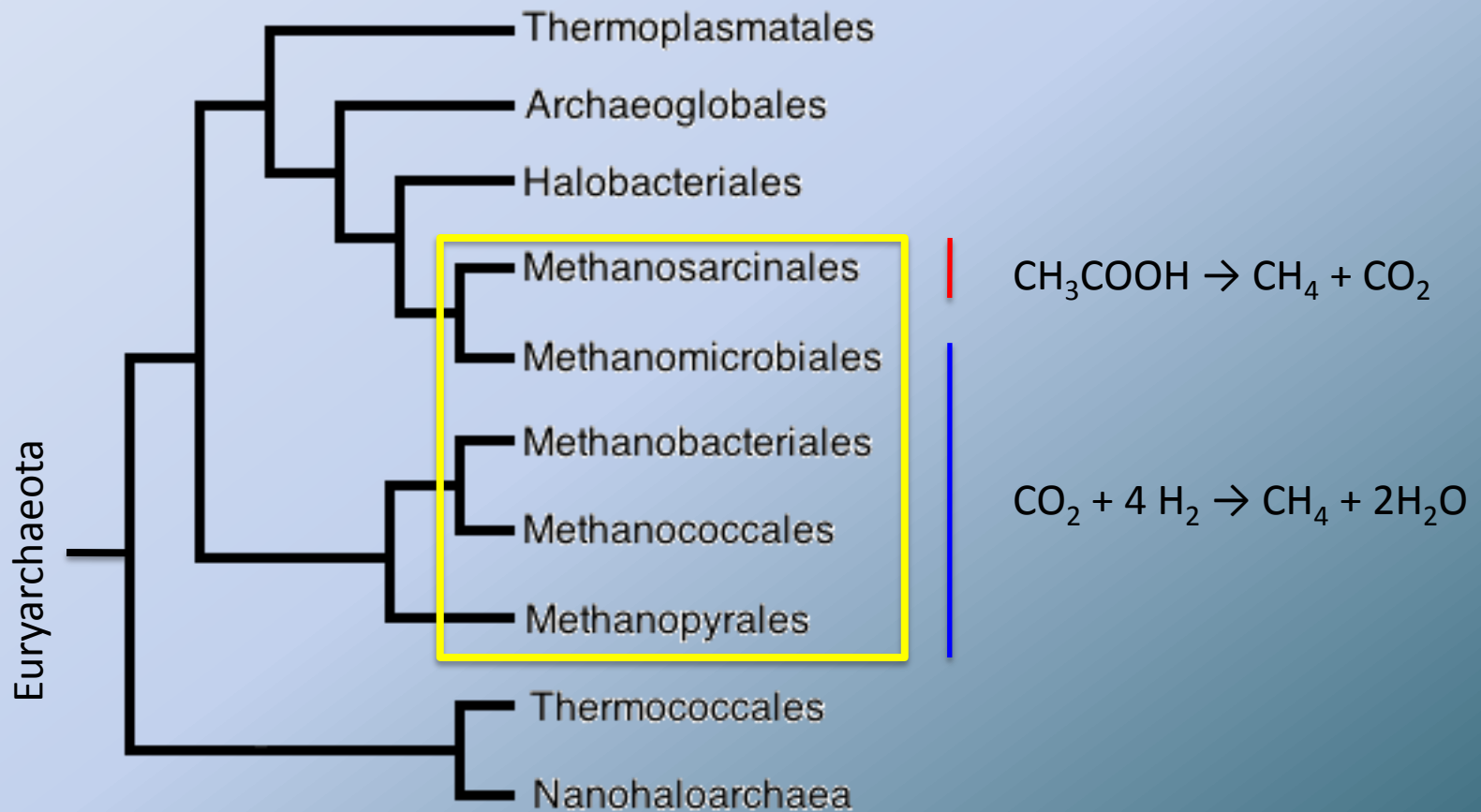
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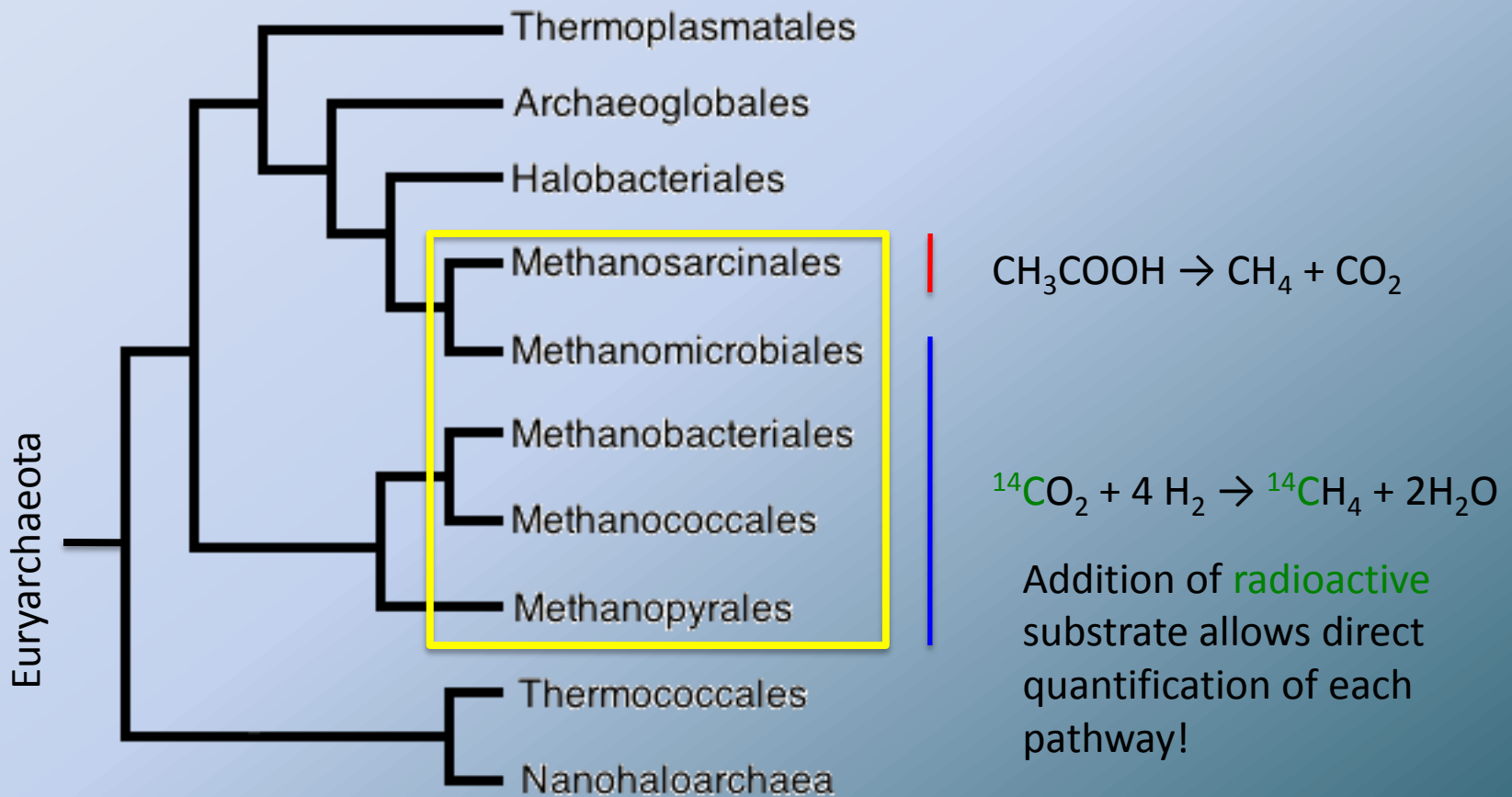
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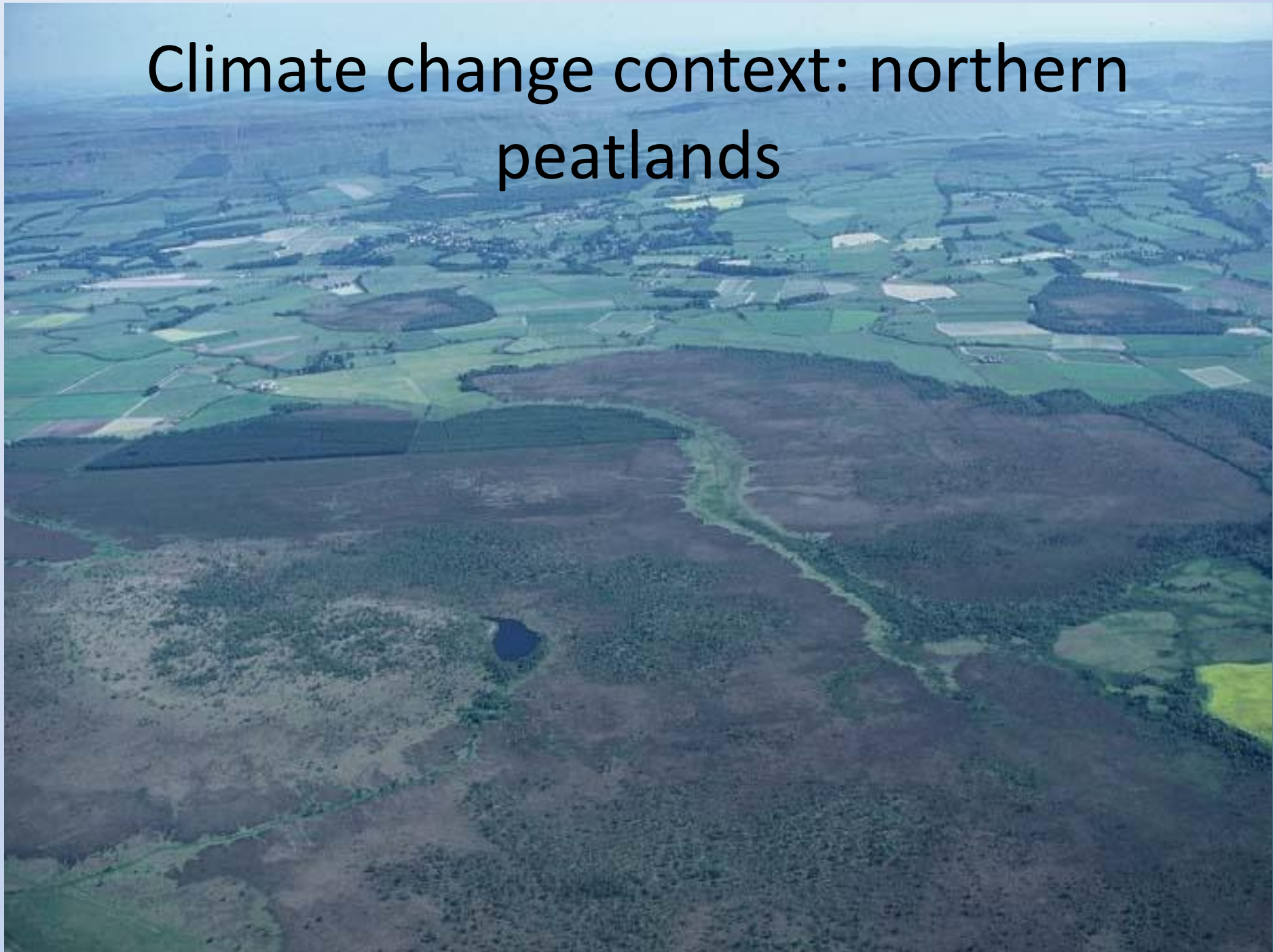
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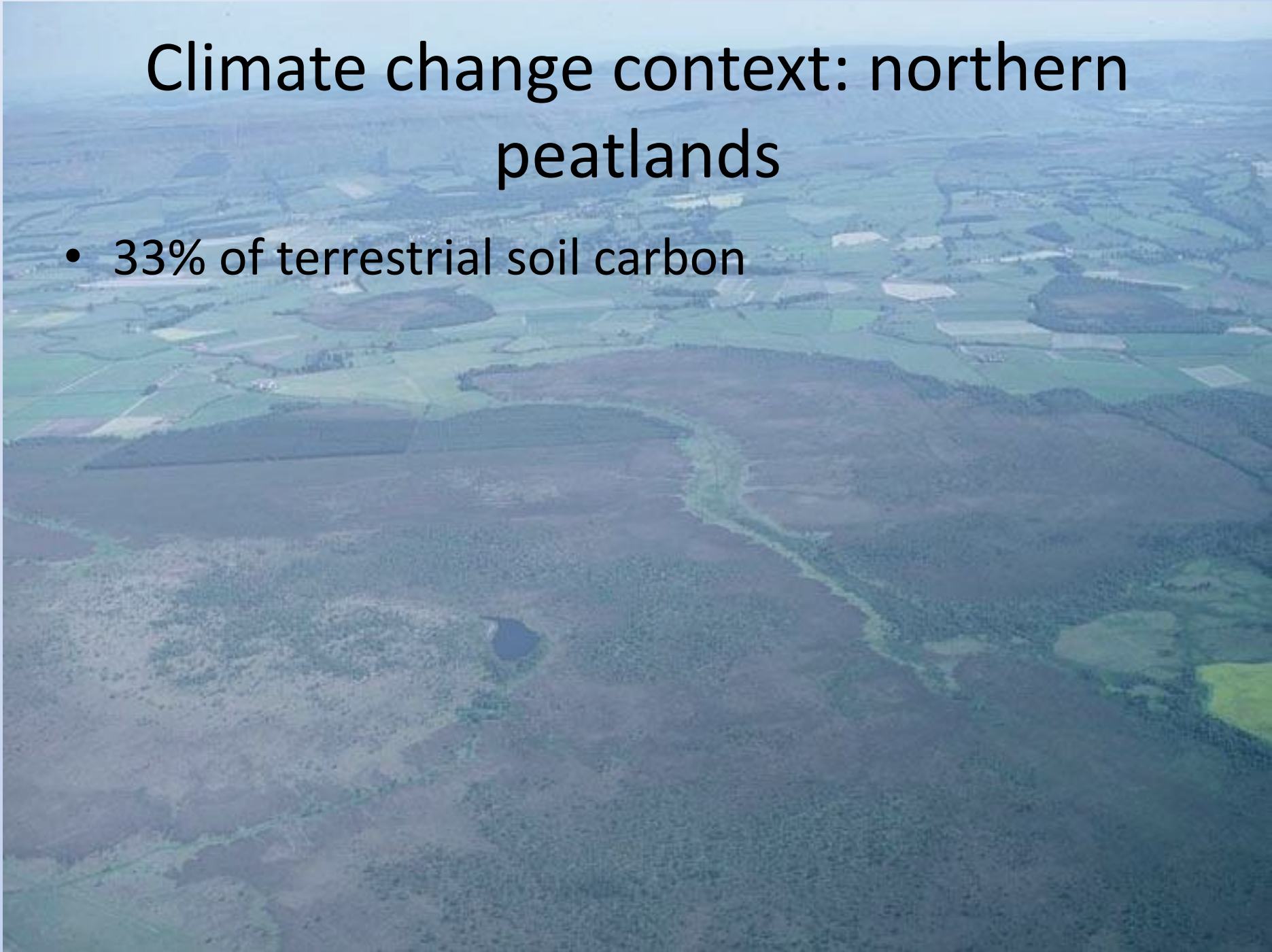


Climate change context: northern peatlands



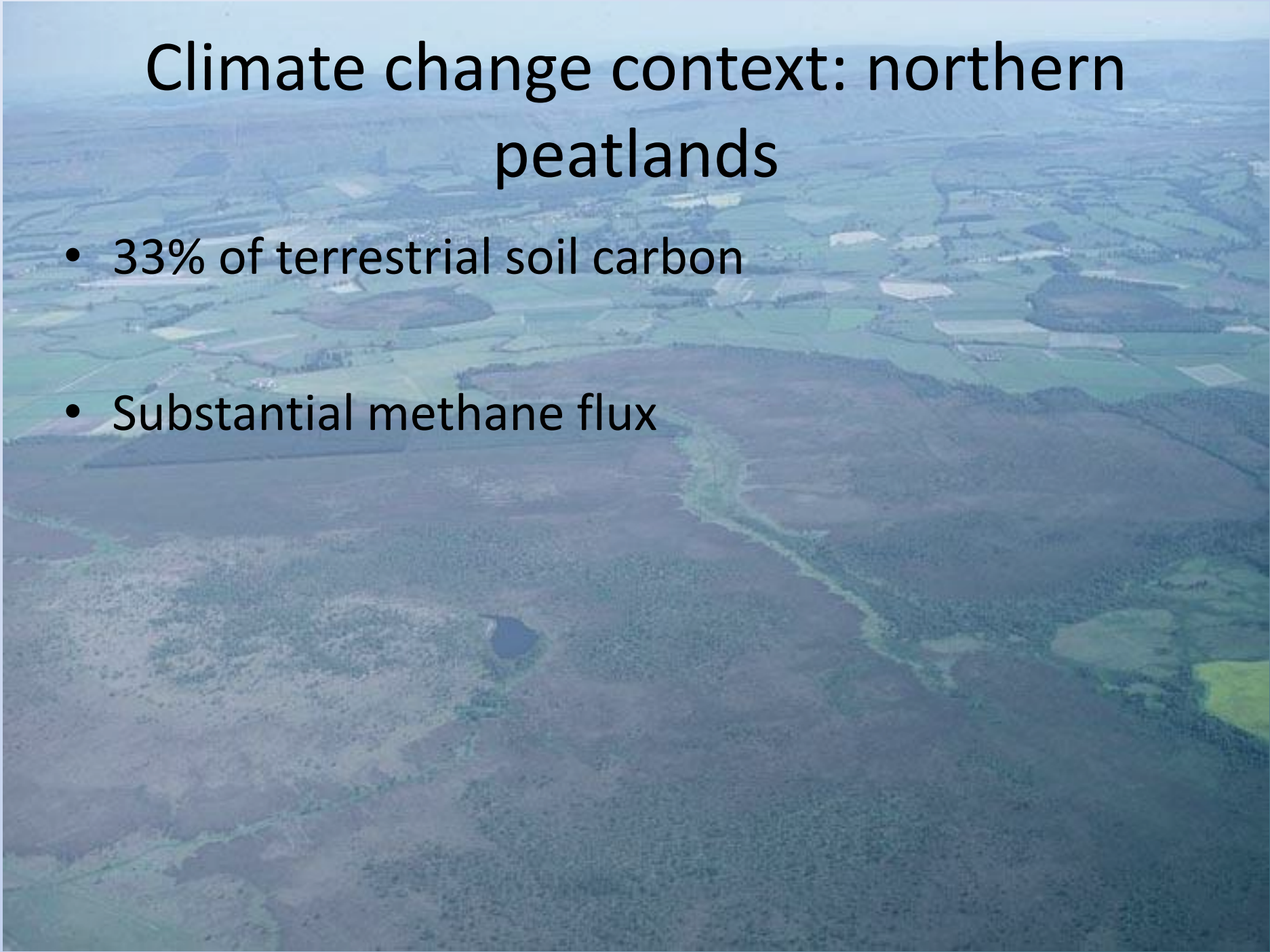
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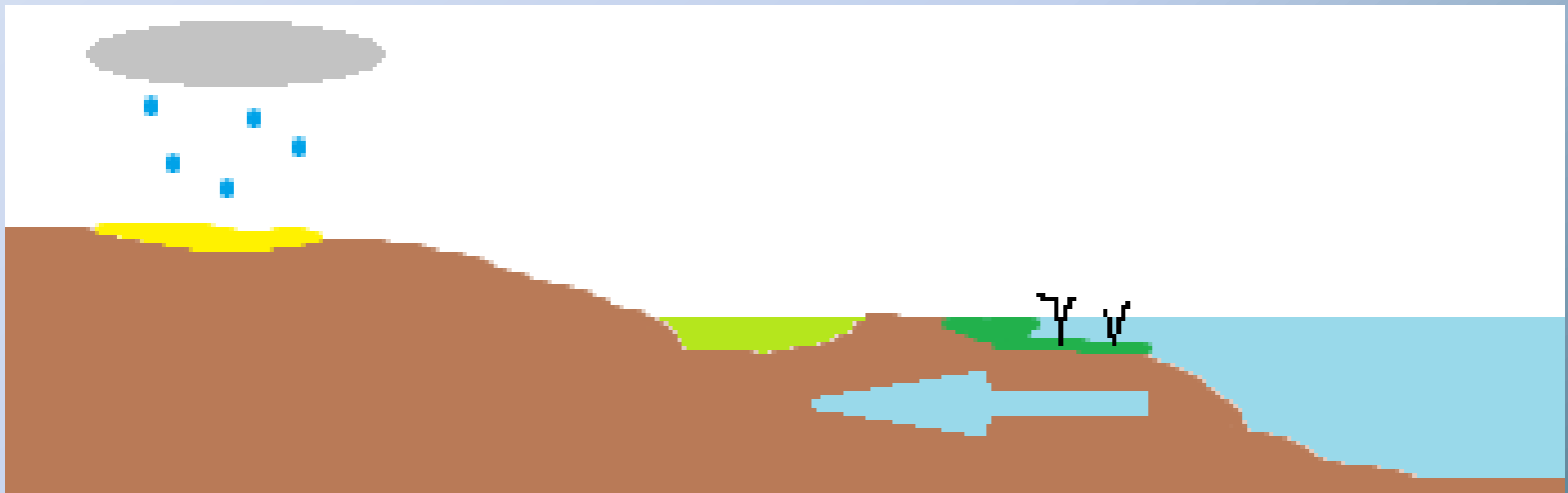
- 33% of terrestrial soil carbon
- Substantial methane flux
- A distinct hydrogeomorphic gradient that harbors a diversity of methanogen communities
- Vulnerable to large increases in mean annual temperature in the coming decades

Northern peatlands: a variety of communities and functional characteristics

pH

hydrology

methane pathway



ombrotrophic

minerotrophic

Northern peatlands: a variety of communities and functional characteristics

low

pH

neutral

hydrology

methane pathway



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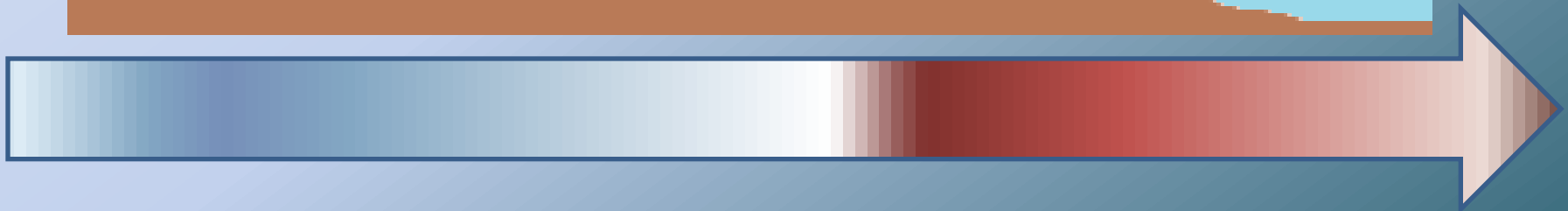
acetoclastic

hydrogenotrophic

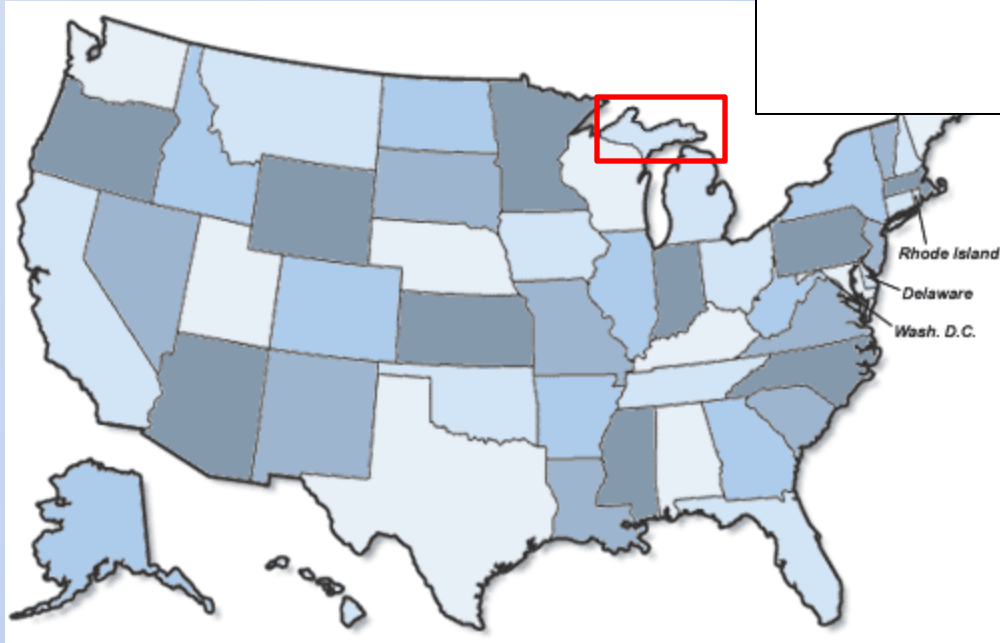


ombrotrophic

minerotrophic

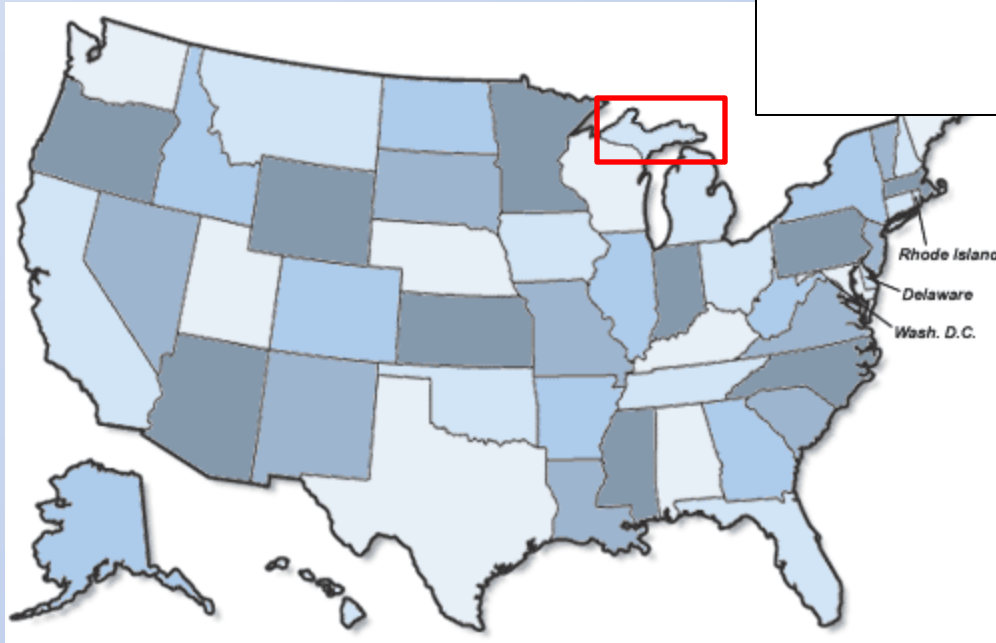
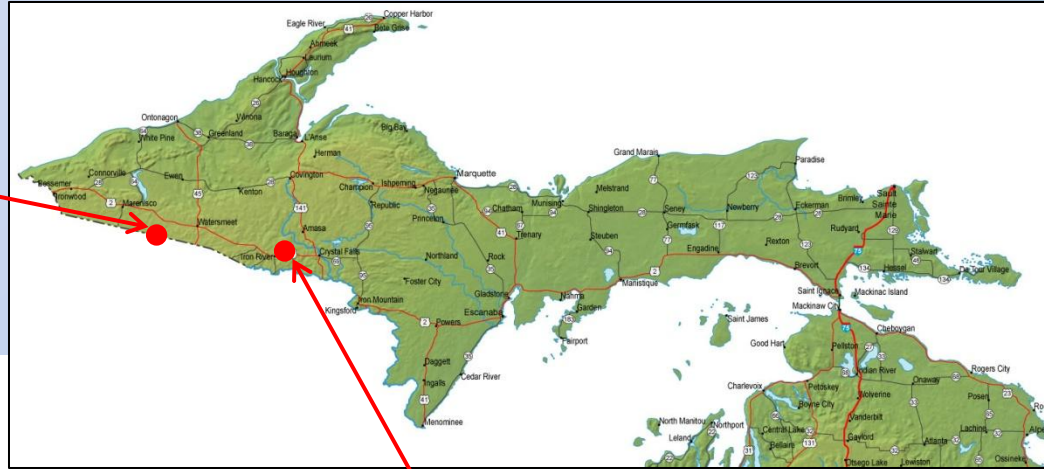


Study Sites



Study Sites

University of Notre Dame
Environmental Research
Center (UNDERC)



Crystal Falls, MI
(most ombrotrophic site)

Study Sites

ombrotrophic

- Bog
- Bog
- Poor Fen
- Intermediate Fen
- Cedar Swamp
- Rich Fen

minerotrophic



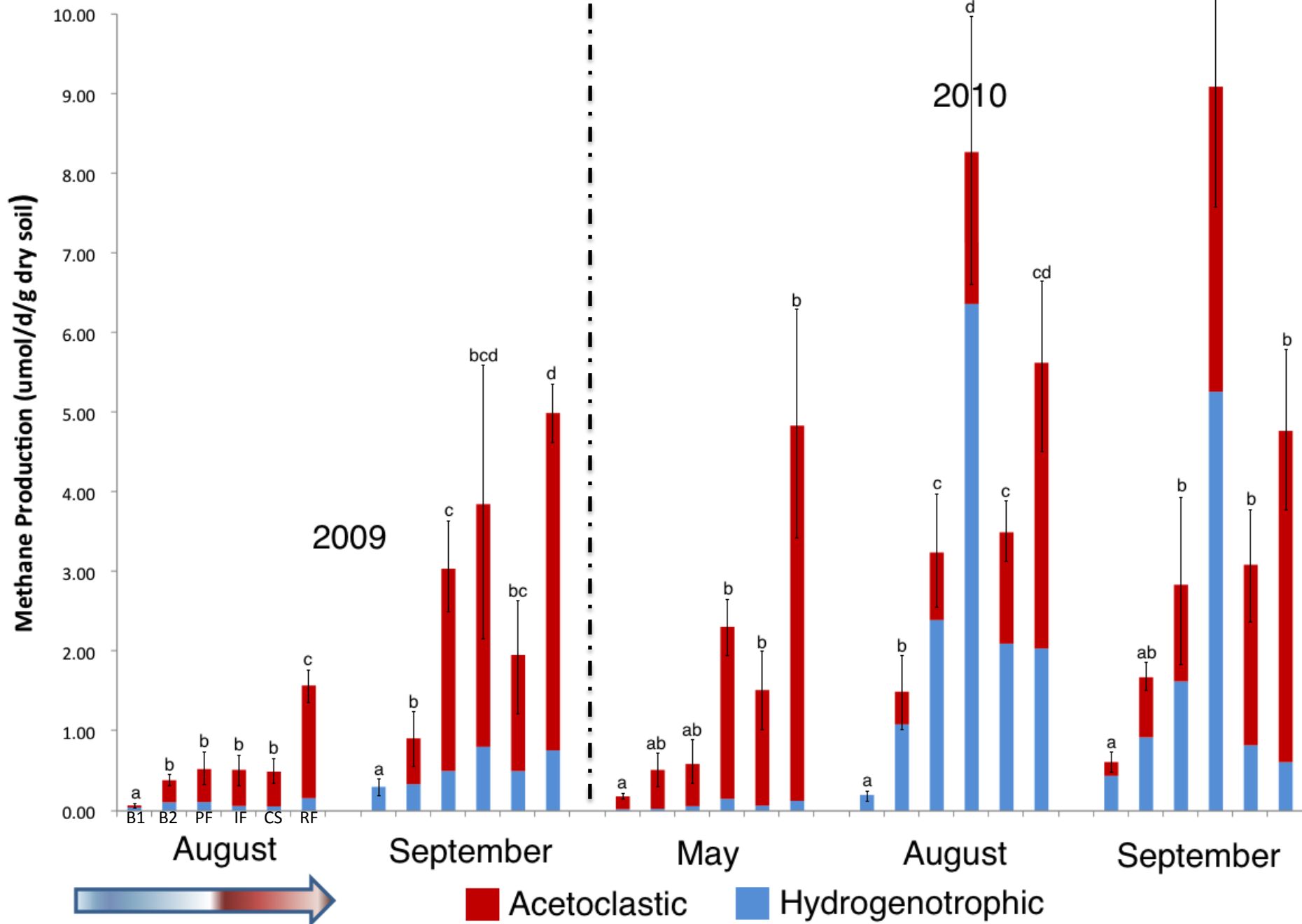
Study Sites

Sampling:

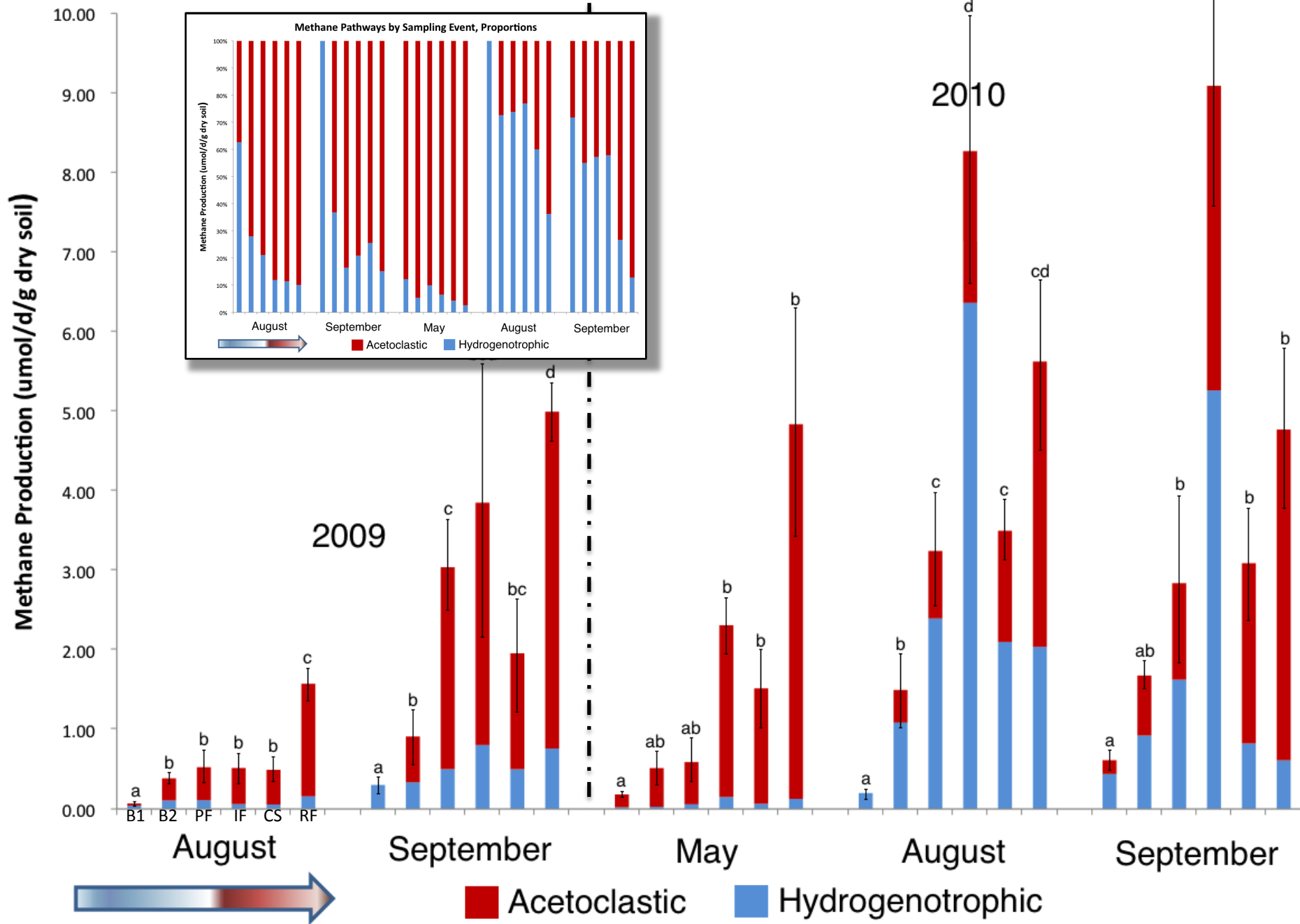
- 5 events (two in 2009, three in 2010)
- 5 replicate samples from each site
- Samples incubated at average in situ temperature with ^{14}C -labeled bicarbonate tracer



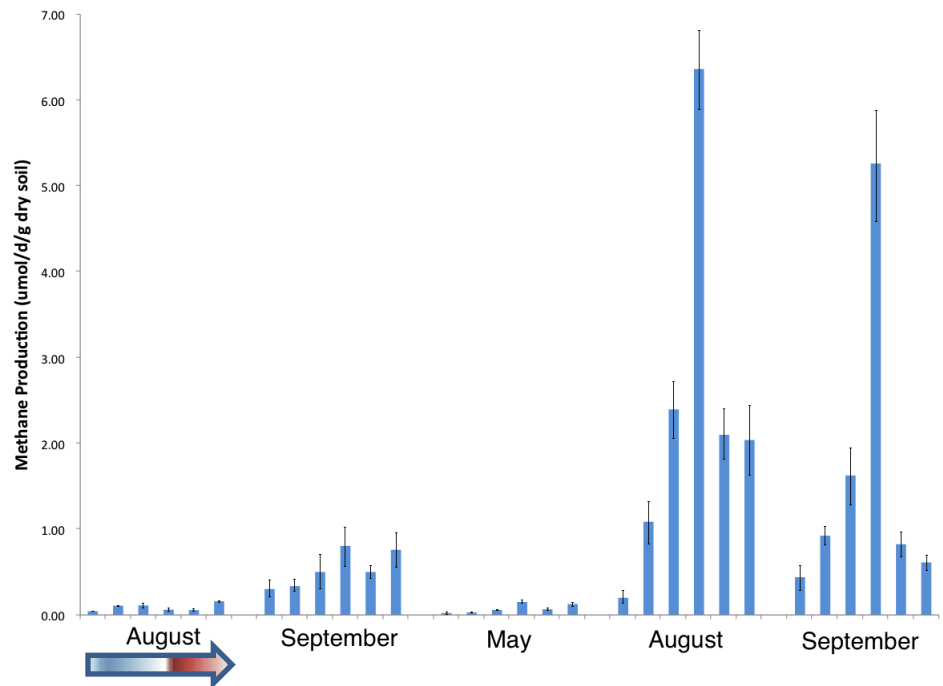
Methane Pathways by Sampling Event



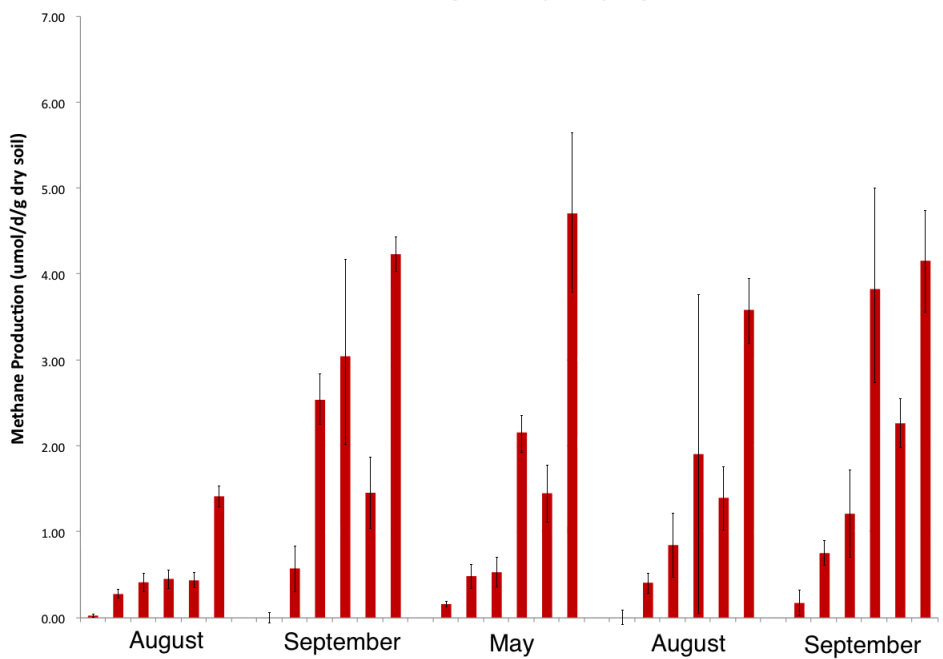
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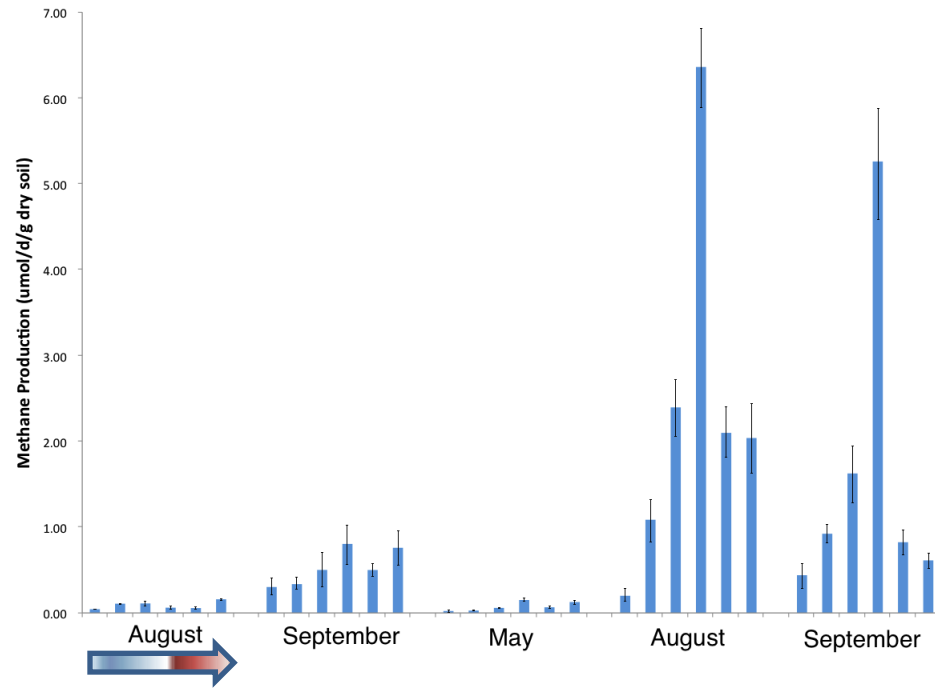
Hydrogenotrophic Methanogenesis by Sampling Event



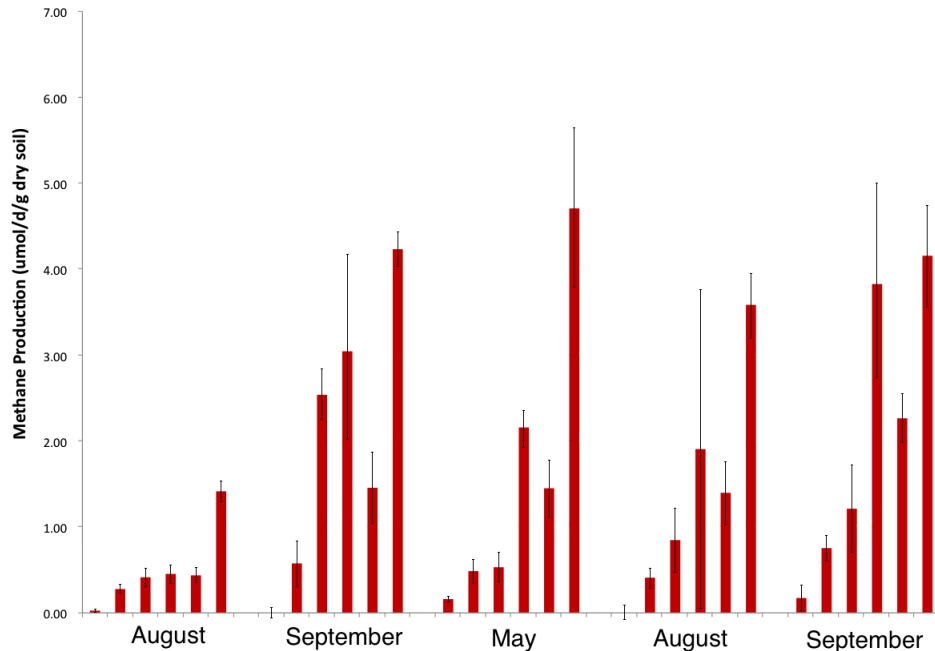
Acetoclastic Methanogenesis by Sampling Event



Hydrogenotrophic Methanogenesis by Sampling Event



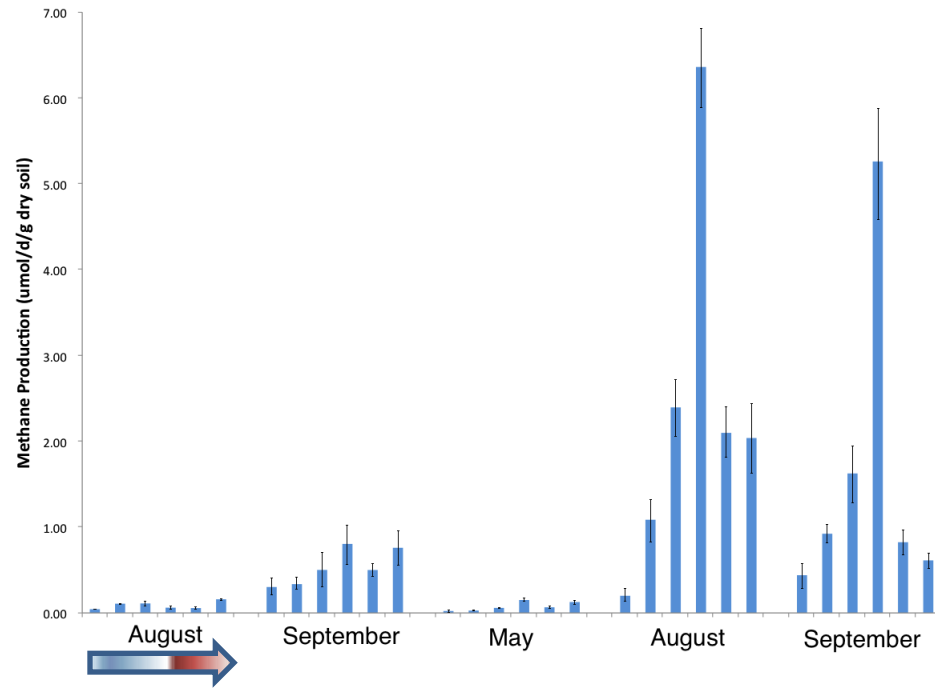
Acetoclastic Methanogenesis by Sampling Event



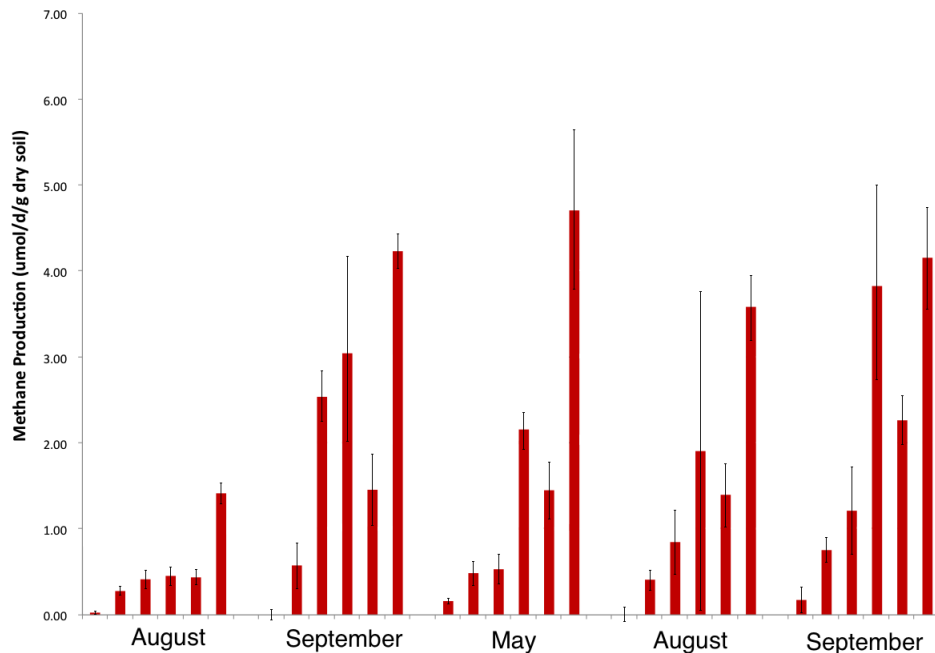
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- however, acetoclastic methanogenesis did not significantly vary with season in any site!

Hydrogenotrophic Methanogenesis by Sampling Event



Acetoclastic Methanogenesis by Sampling Event

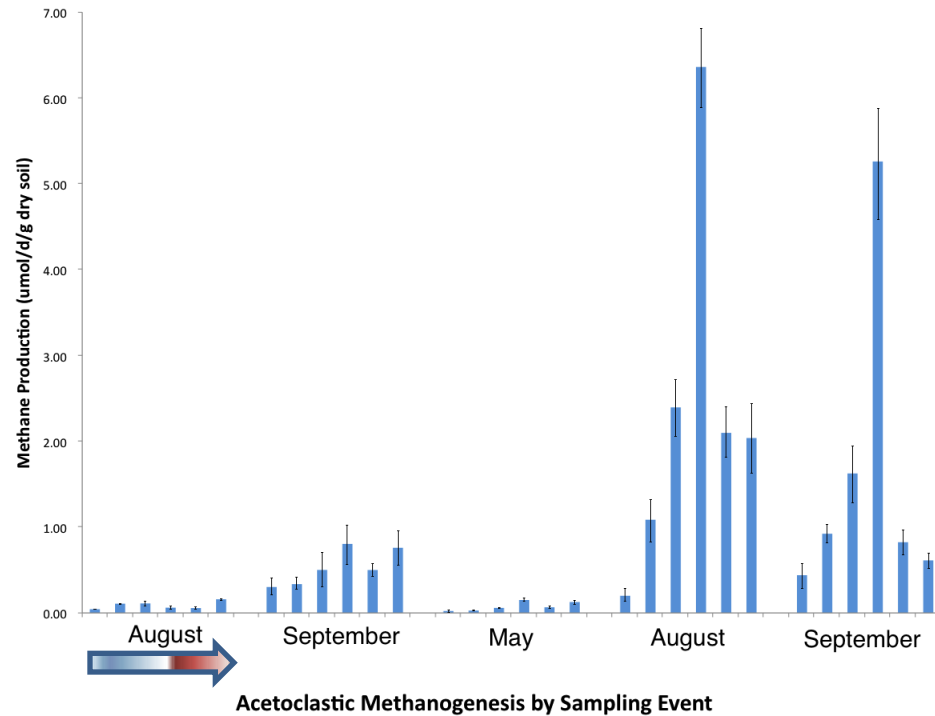


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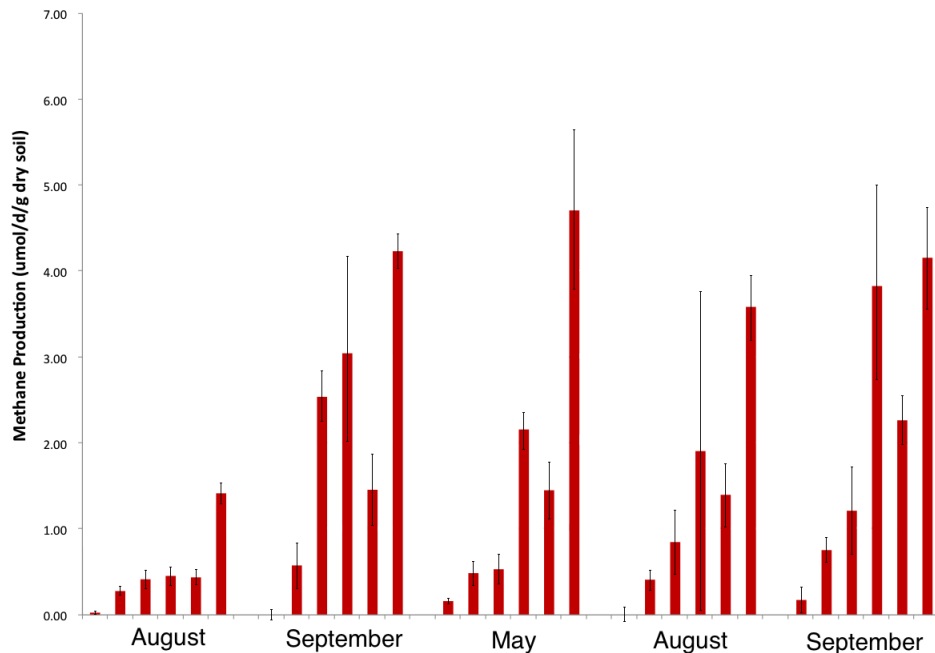
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Hydrogenotrophic Methanogenesis by Sampling Event



Acetoclastic Methanogenesis by Sampling Event

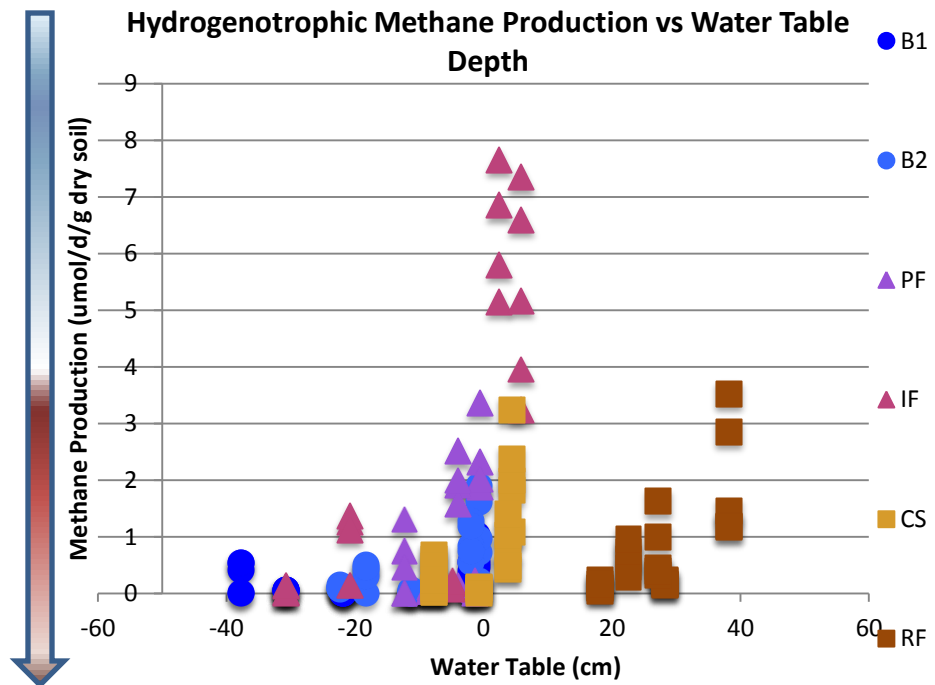
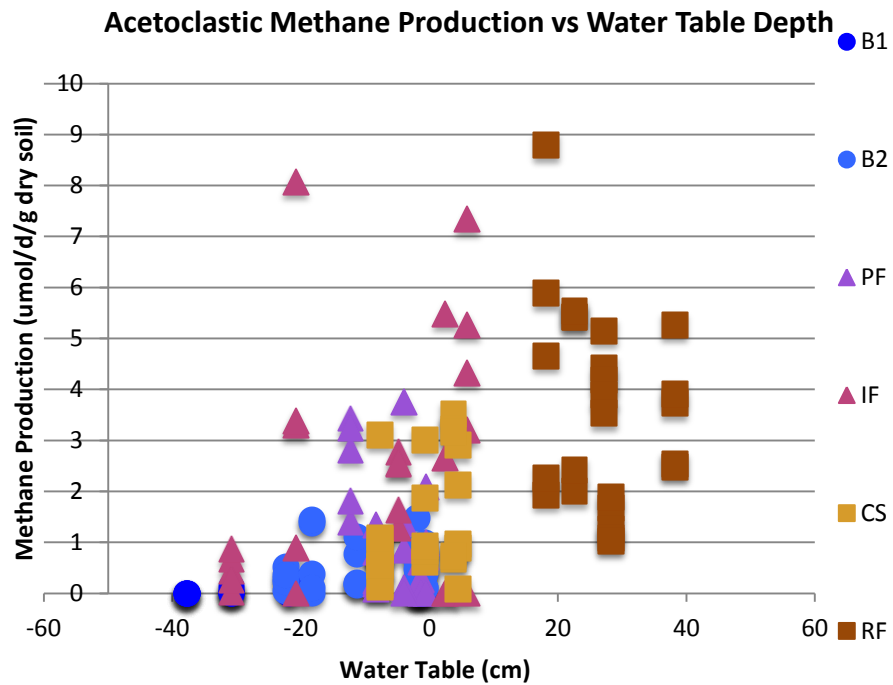


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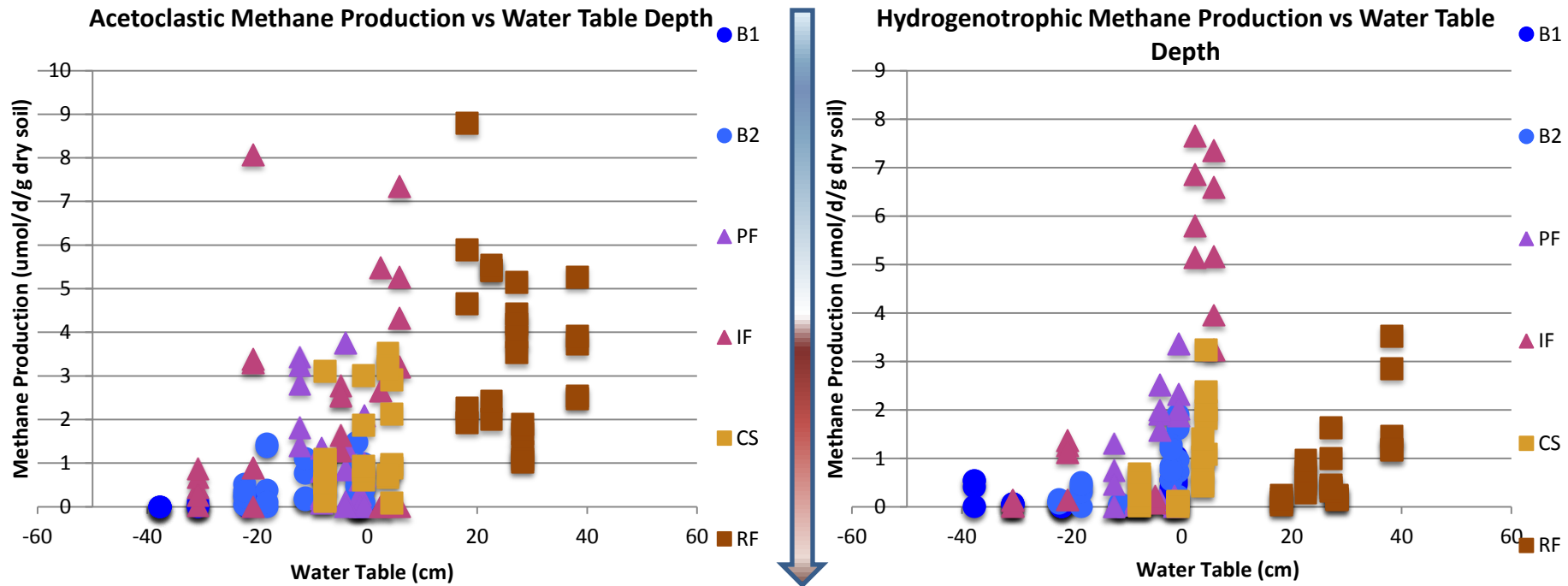
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- what could account for this inter-annual variability in hydrogenotrophic methanogenesis?



Water table depth appears to **strongly** effect hydrogenotrophic methanogenesis



Pathways Summary

- Acetoclastic methanogenesis varied primarily with gradient position, and did not vary significantly between years or (generally) throughout the growing season

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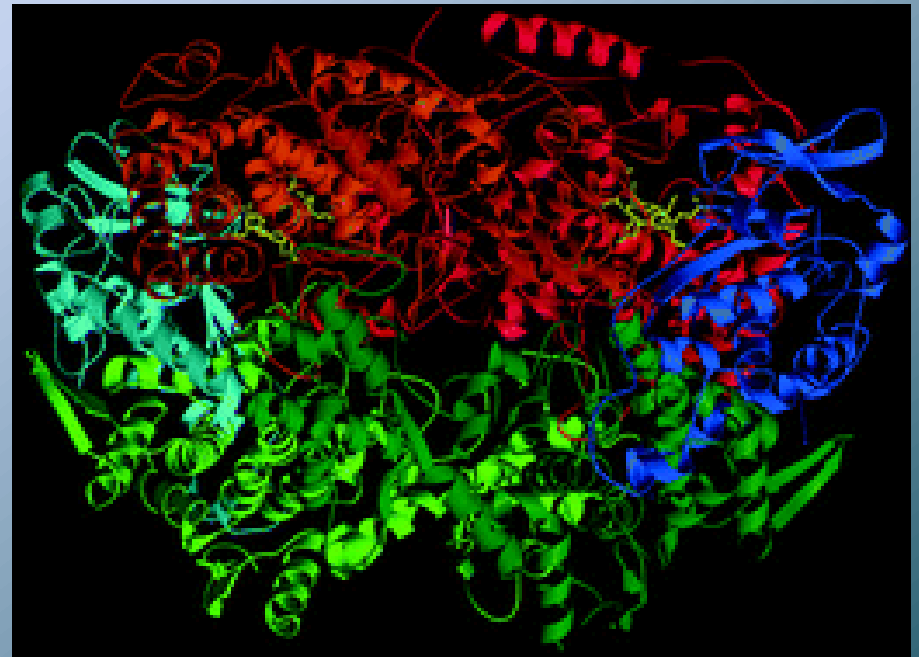
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- Hydrogenotrophic methanogenesis, on the other hand, varied tremendously between 2009 and 2010, becoming dominant in nearly every site in the latter year, which was unusually wet
- Could the substantially different spatial and temporal dynamics of the two pathways be explained by the phylogenetically distinct methanogens carrying them out?

Community Structure Analysis: *mcrA*, functional gene marker about town

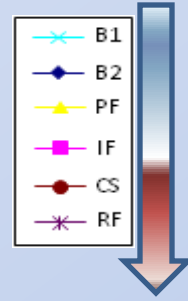
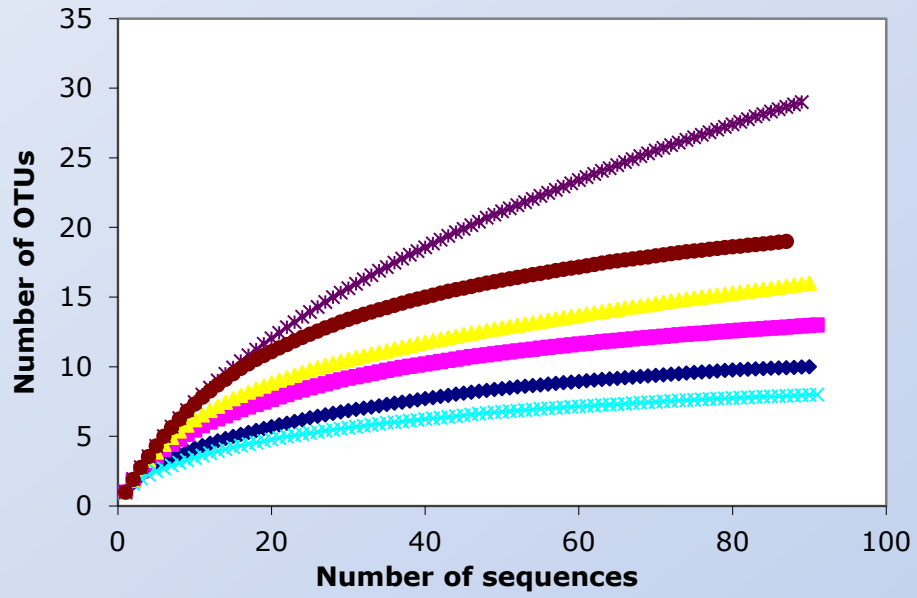
- *mcrA* is a gene that codes the alpha-subunit of methyl coenzyme-M reductase (MCR), which catalyzes the terminal step of methanogenesis in *all methanogens*
- Only one copy per genome, simplifying quantification



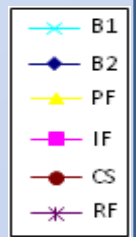
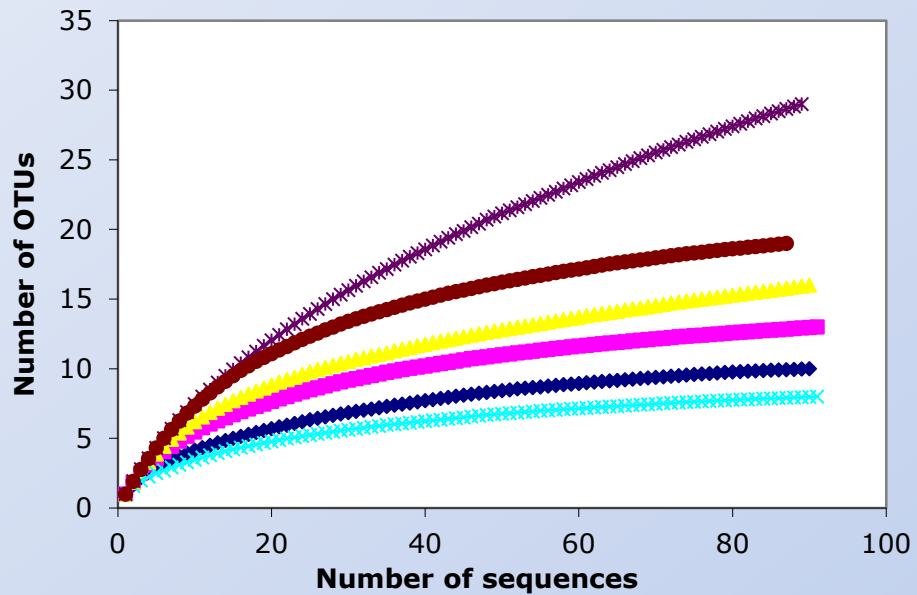
Preliminary Community Data

- DNA was extracted from one core from each site taken in May 2010
- *mcrA* was amplified from each core using PCR, and the PCR amplicons were cloned and sequenced via Sanger sequencing
- the resulting sequence libraries were trimmed, aligned, and binned into operational taxonomic units (putative genera) using the MOTHUR microbial genomics software package

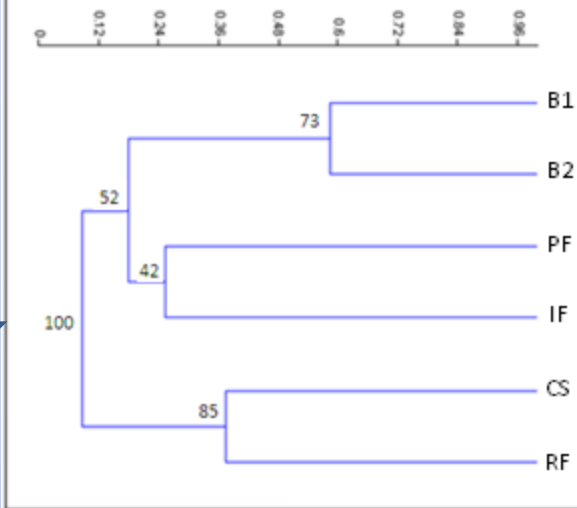
Collector's Curves, Genera



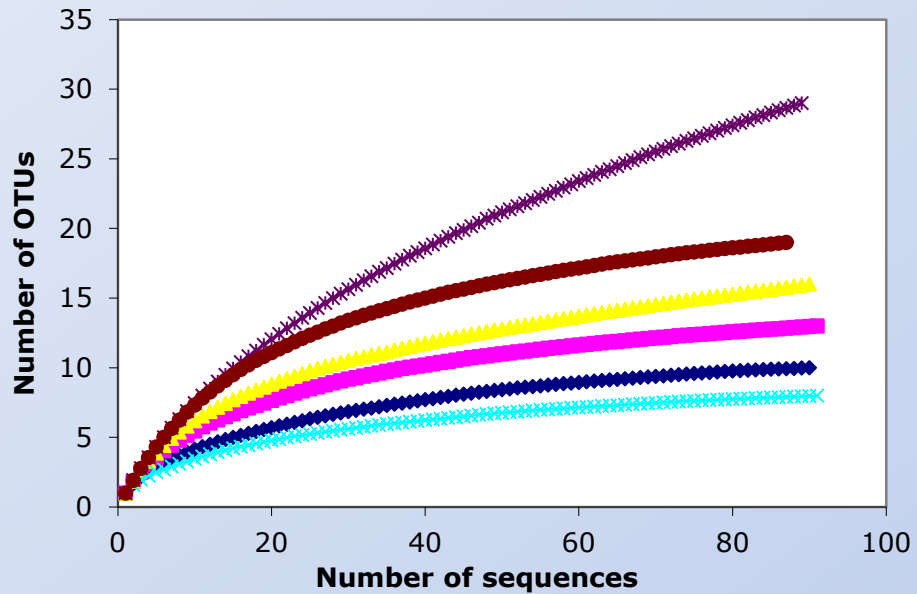
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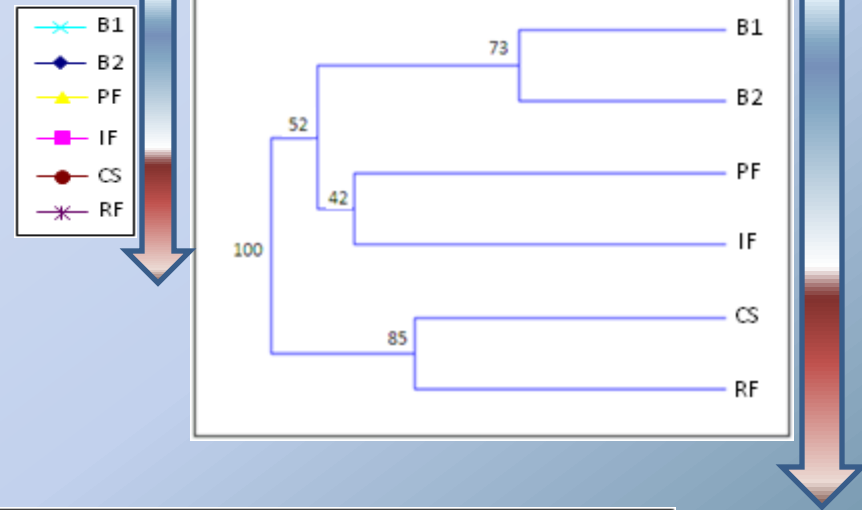
Bray-Curtis Cluster Analysis



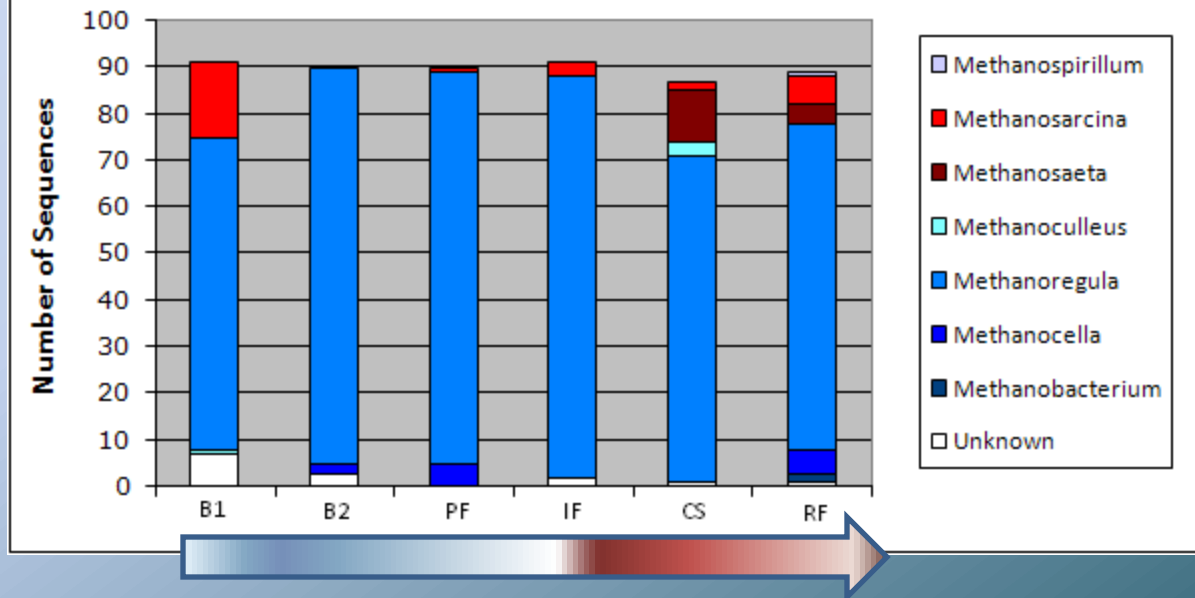
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Bray-Curtis Cluster Analysis



Community Composition by Site, Genera



Community Conclusions

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- This difference appears to be driven by the ombrotrophic-minerotrophic gradient
- *All communities dominated by putative hydrogenotrophs*

Structure and Function

- The interannual variability in methanogenesis within the peatland sites appears to be driven by changes in hydrogenotrophic methanogenesis rates

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- Putative hydrogenotrophs are dominant in all May 2010 community samples
- Acetoclastic methanogenesis correlate very strongly to gradient position, while hydrogenotrophic methanogenesis does not

Hypotheses

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- H2: Hydrogenotrophic methanogenesis in northern peatlands is primarily driven by dynamic or opportunistic changes in hydrogenotroph community activity by season, resulting in a strong temporal pattern of rate variation

Future Directions

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- Thoroughly sample the *mcrA* DNA of each site during all seasons, to determine if the total communities remain stable throughout the growing season (H1) using high-throughput sequencing (454 pyrosequencing)

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- Use SEM and NMS to compare effects of community and hydrogeomorphic context on the two pathways (H1)
- Thoroughly sample *mcrA* mRNA from each site and sampling event, to determine if the transcriptional activity of functional methanogen groups fluctuates in sync with the rates of their associated pathways (H2)

Acknowledgements

Jason Keller

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Nate Eisenhut

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Evan Jones

National Science Foundation

Society of Wetland Scientists

The Wetland Foundation

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Fellowship in Biology

