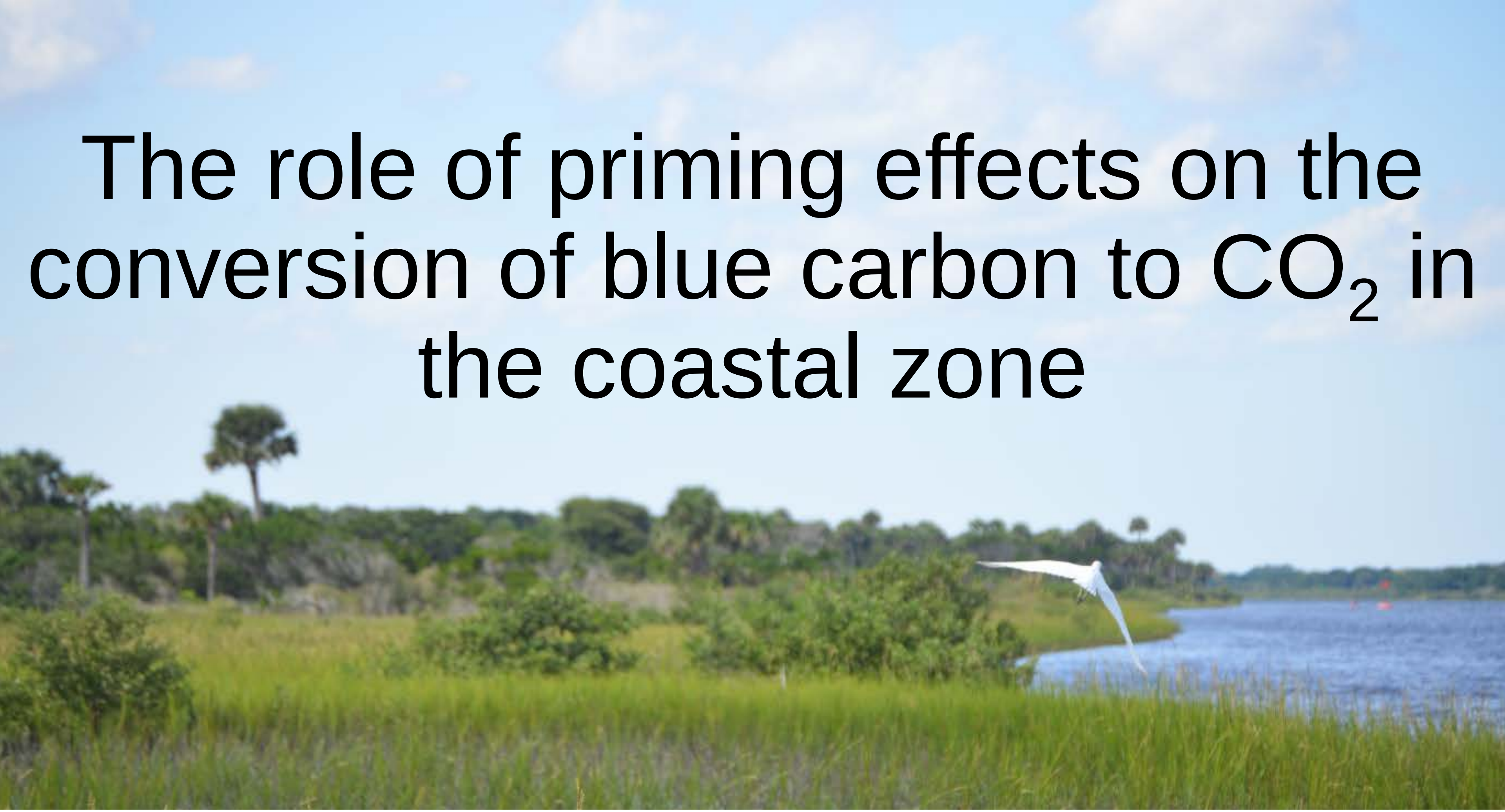


The role of priming effects on the conversion of blue carbon to CO_2 in the coastal zone

Elise Morrison

N. Ward, A. Arellano, Y. Liu, A. Rivas-Ubach, A. Ogram, T. Osborne, D. Vaughn, T.S. Bianchi

Outline

- Introduction
- Research Questions
- Methods
    - Experimental design
- Results
    - FT-ICR MS
    - Metagenomics
- Conclusions
- Future Directions

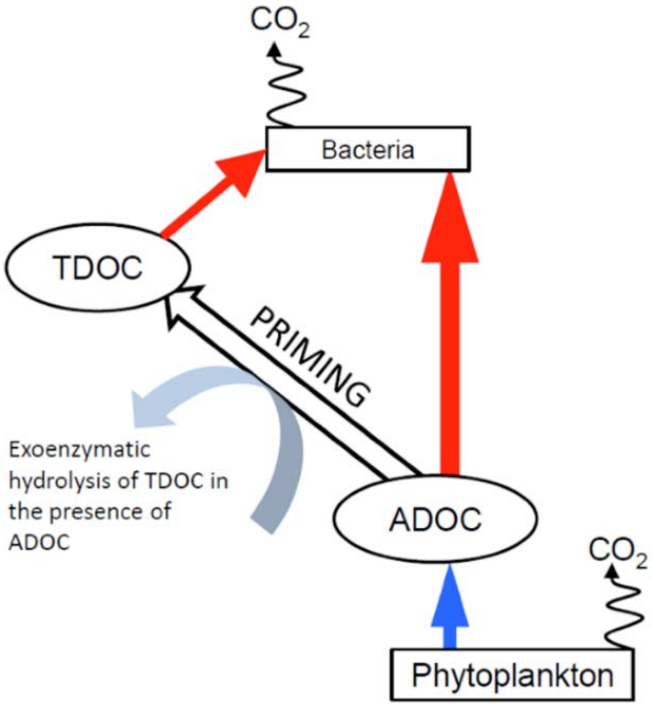
Priming

Enhanced degradation of “recalcitrant” organic matter in the presence of “labile” organic matter

Many potential mechanisms

Microbially mediated – not reported in sterile conditions

No consensus in aquatic systems



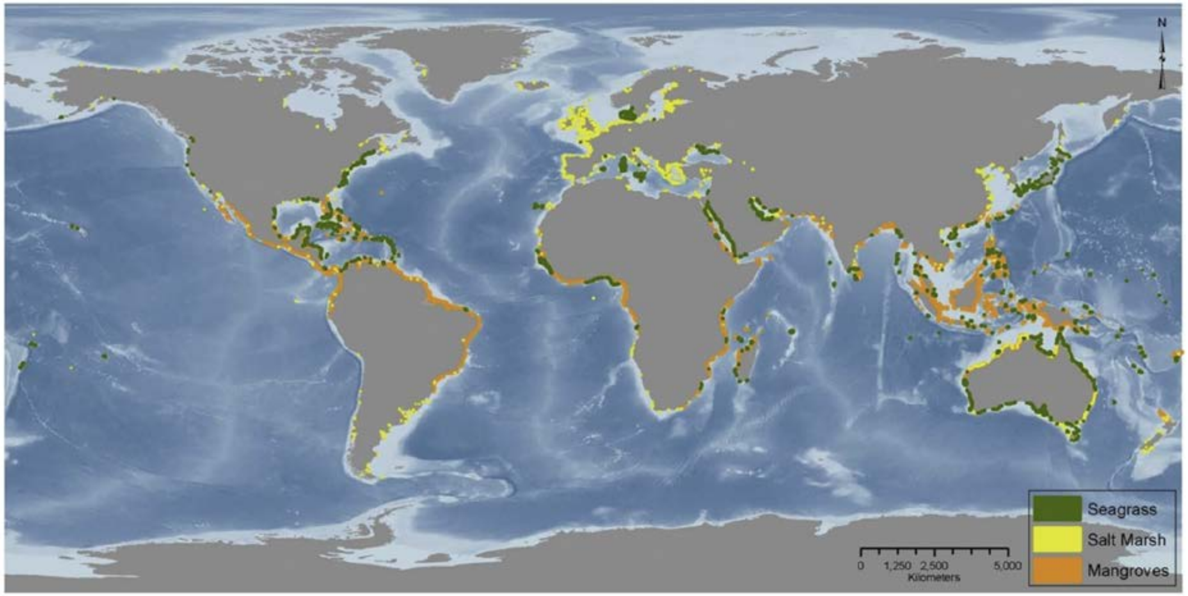
From T.S. Bianchi (2015)

Priming and blue carbon

Exposure of peat in south Florida

From T.S. Bianchi

Global distribution of blue carbon habitats



From Pendleton et al. 2012

Key questions

What happens when blue carbon is exported to coastal waters?

Will there be enhanced decomposition of peat-derived DOM (P-DOM) in the presence of algal-derived DOM (A-DOM)?

If so, what molecular and microbial changes will occur?

Methods: laboratory incubations

Four treatments established with filtered seawater

Seawater (SW)
Seawater + algal leachate (SWA)
Seawater + peat leachate (SWP)
Seawater + peat + algal leachate (SWPA)

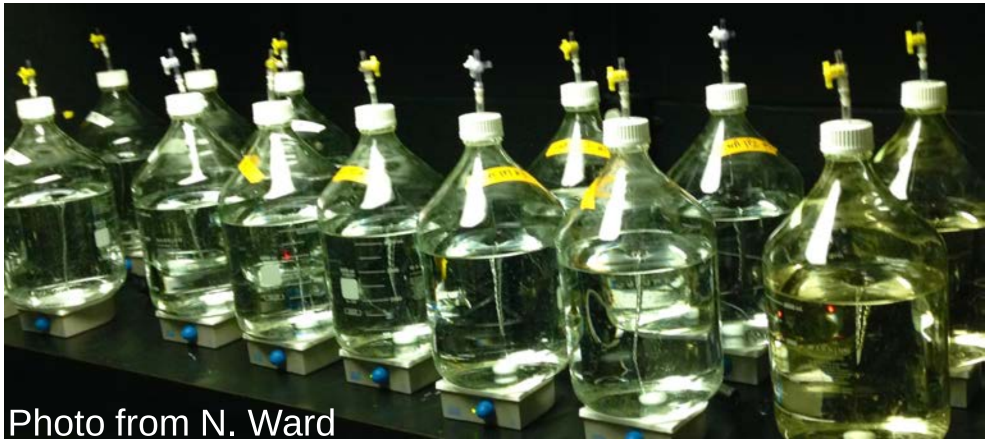
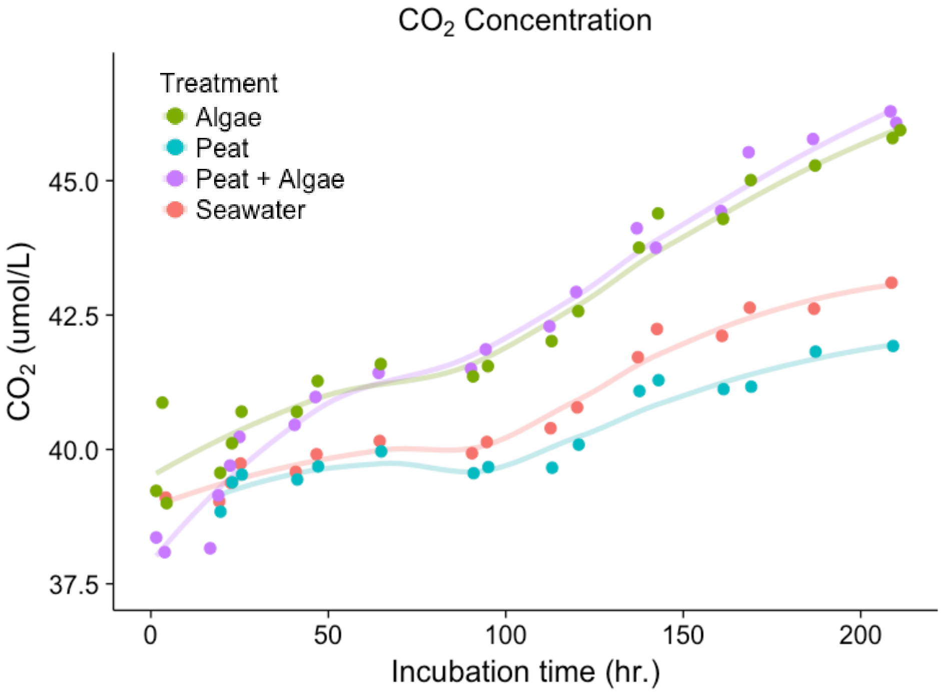


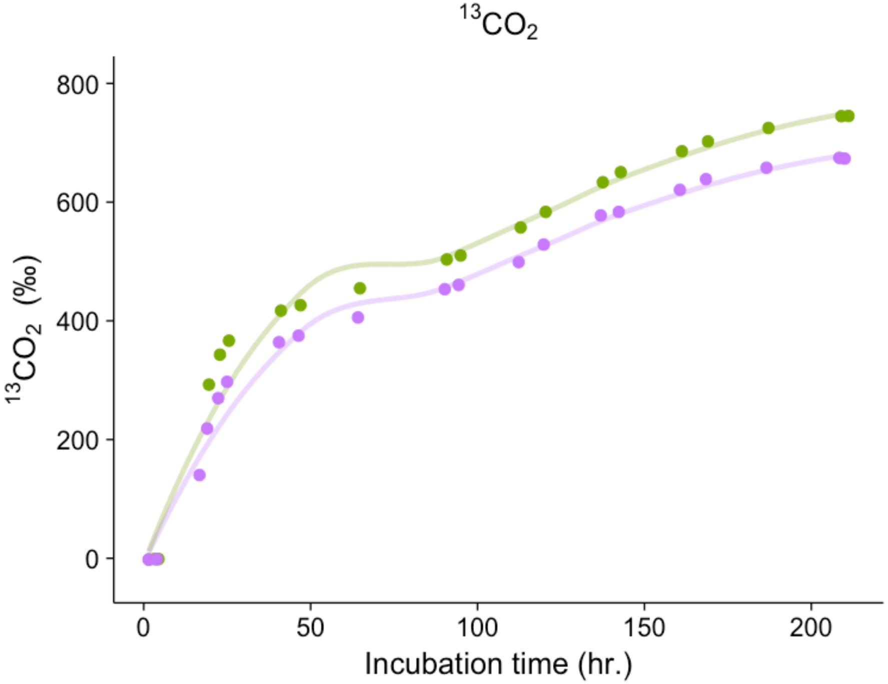
Photo from N. Ward

Analyzed for:

CO_2 and $^{13}CO_2$
Molecular formulae (FT-ICR-MS)
Metagenomics
DOC, TDN
CDOM optical measurements

Greater peat conversion to CO_2 with P+A



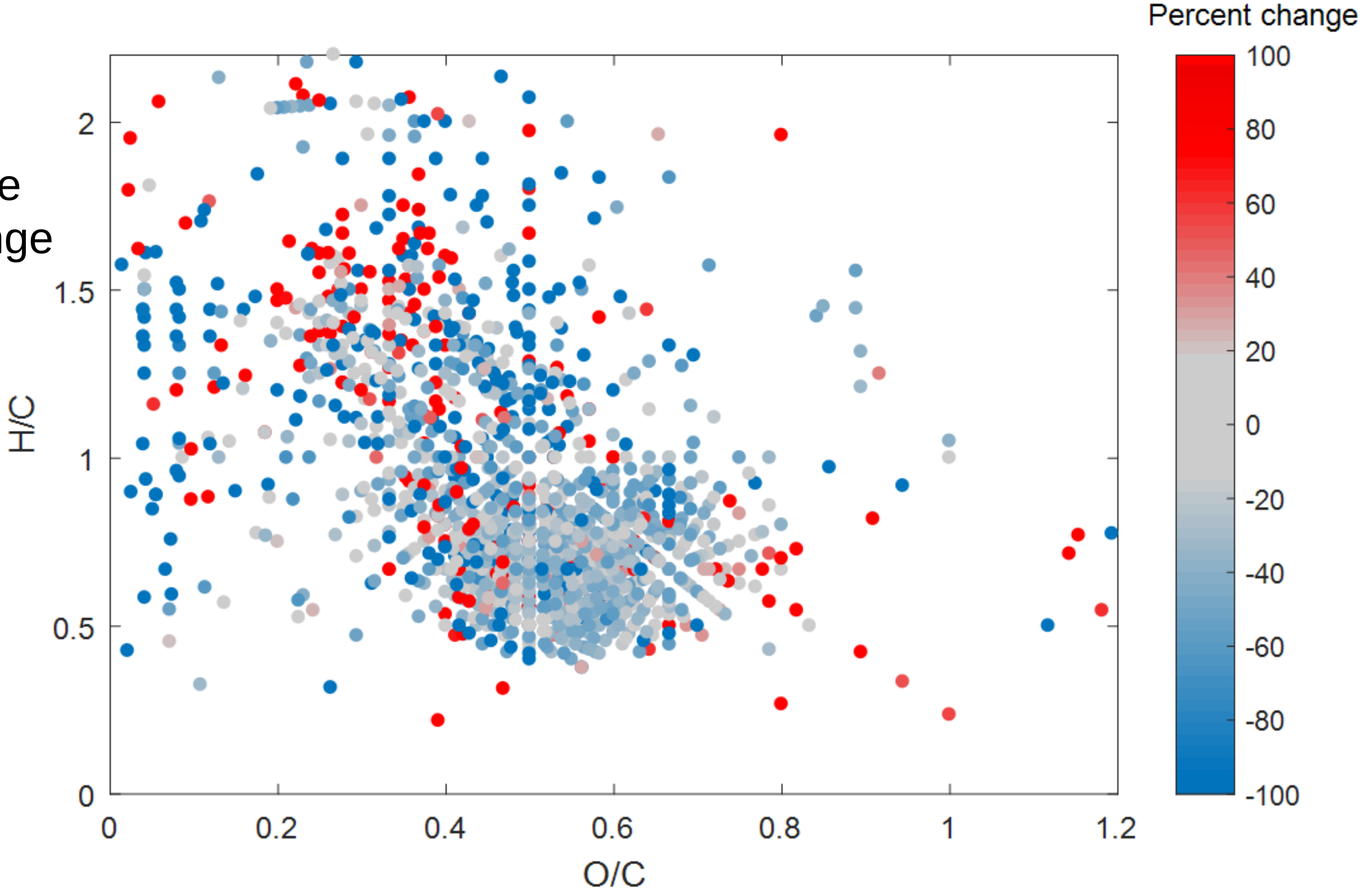


31% increase in respiration in P+A treatment, relative to P treatment

Data from N. Ward, PNNL

Peat DOM changes over time

At time point 2:
Red: significant increase
Blue: significant decrease
Grey: no significant change



Y. Liu, Texas A&M

Degraded DOM differs by treatment

Averaged features for each treatment

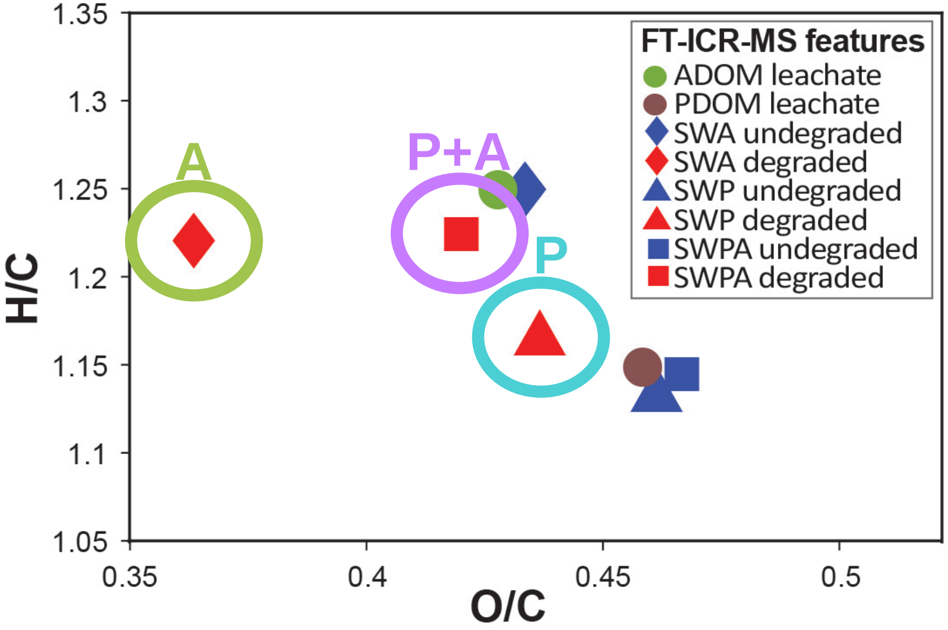
Un-degraded: present at the beginning and end of the incubation

Degraded: present only at the beginning of the incubation

Un-degraded signatures match their respective leachates

Each treatment has a distinct degradation signature

van Krevelen diagram (FT-ICR-MS data)



A. Rivas-Ubach, PNNL

Metagenomics

Shotgun metagenomic sequencing
Sequenced at the Joint Genome Institute
Illumina HiSeq 2500

To evaluate microbial:
- community composition
- potential function

JOINT GENOME INSTITUTE
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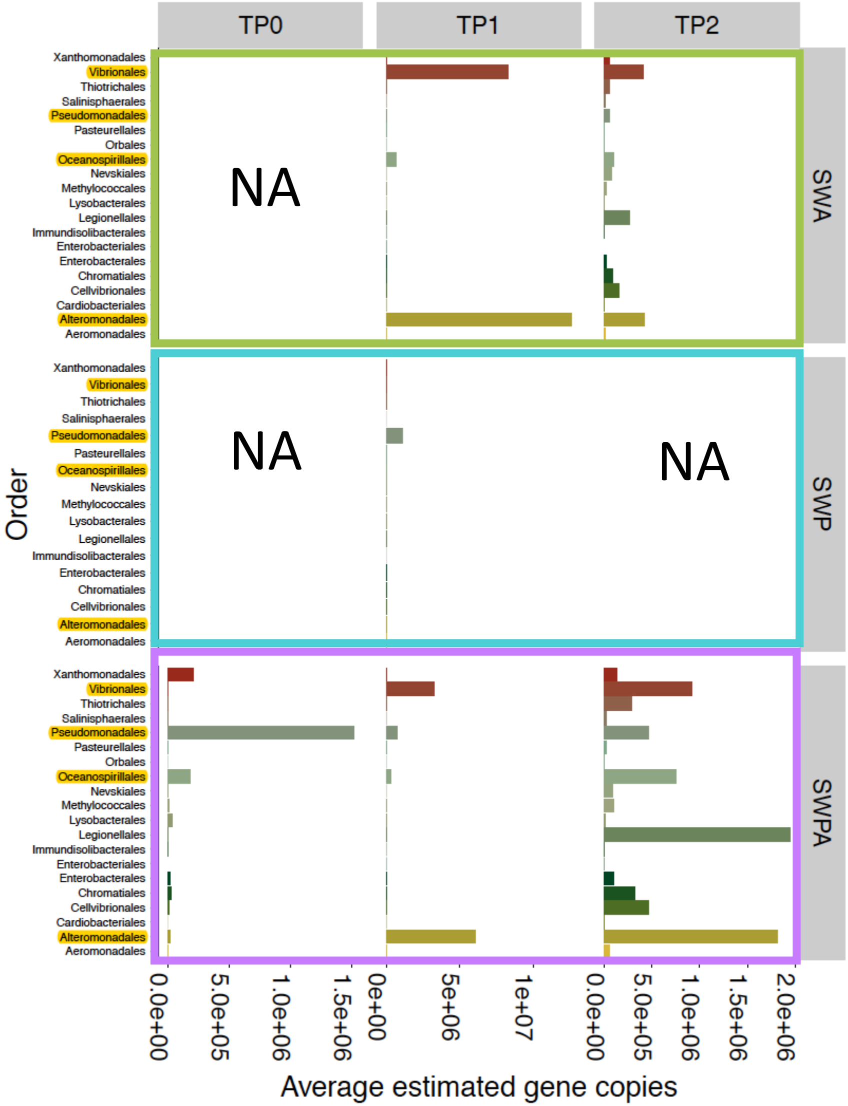
Microbial communities more diverse with P+A

Gammaproteobacteria most abundant class

Previously described DOM degraders (Poretsky et al. 2010)

Alteromonadales
Vibrionales
Pseudomonadales
Oceanospirillales

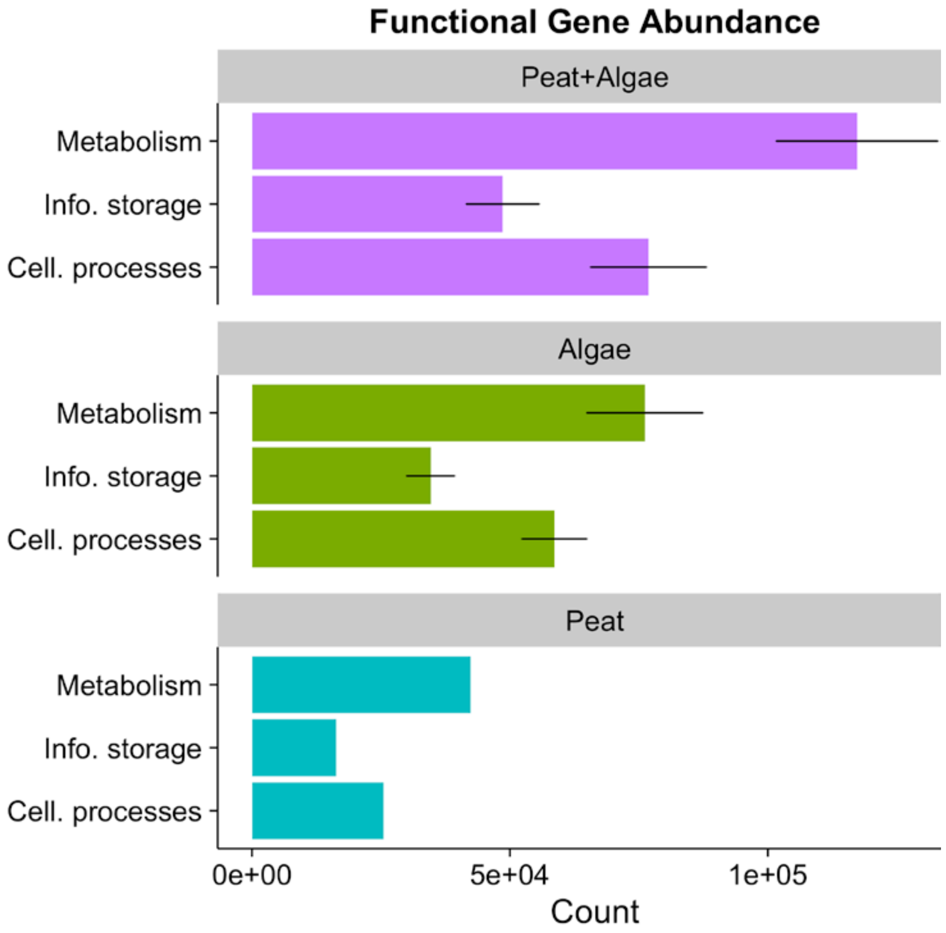


Functional gene abundance increases with P+A

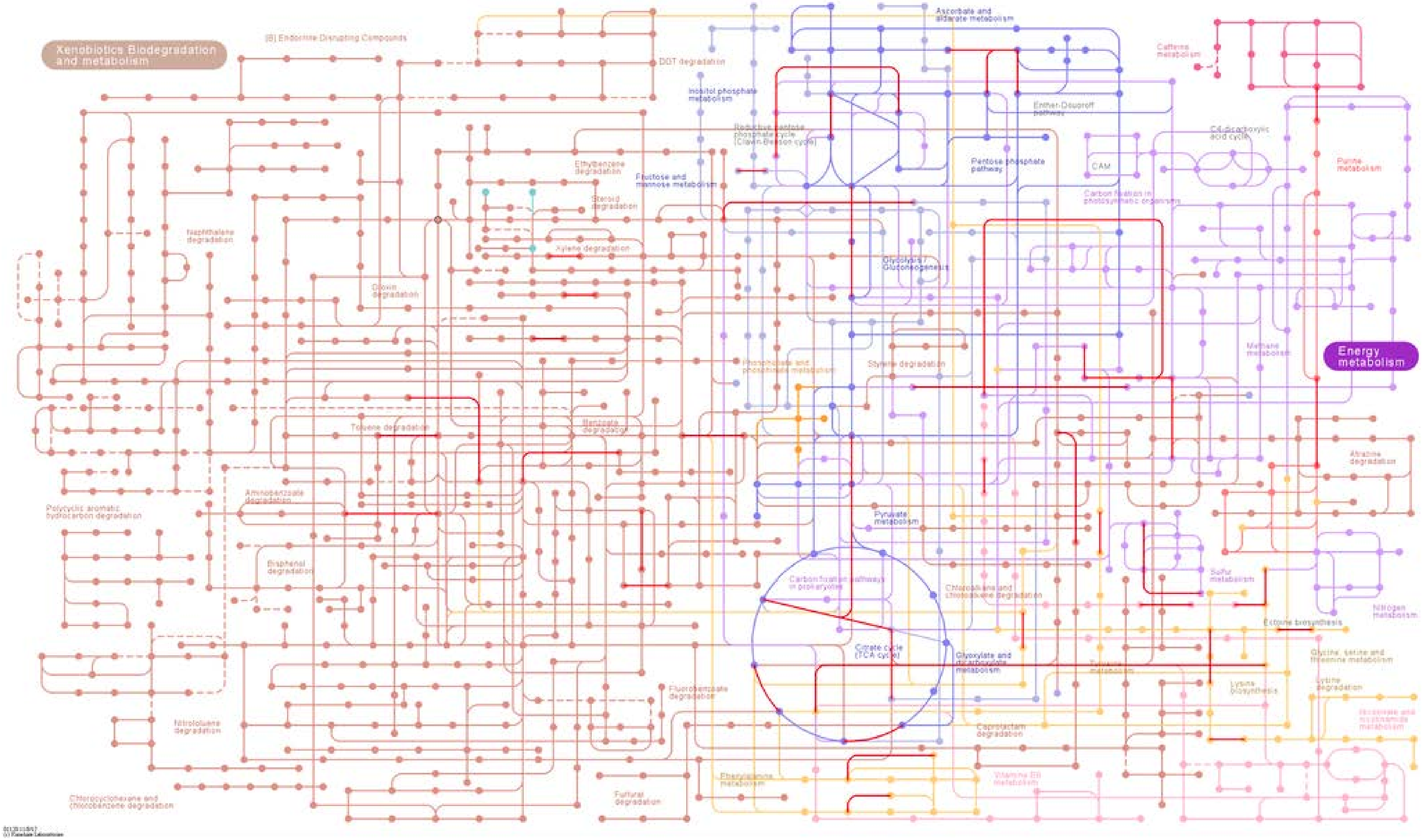
Peat + Algae treatment:

Greatest abundance for all functional categories

Metabolic processes most abundant category



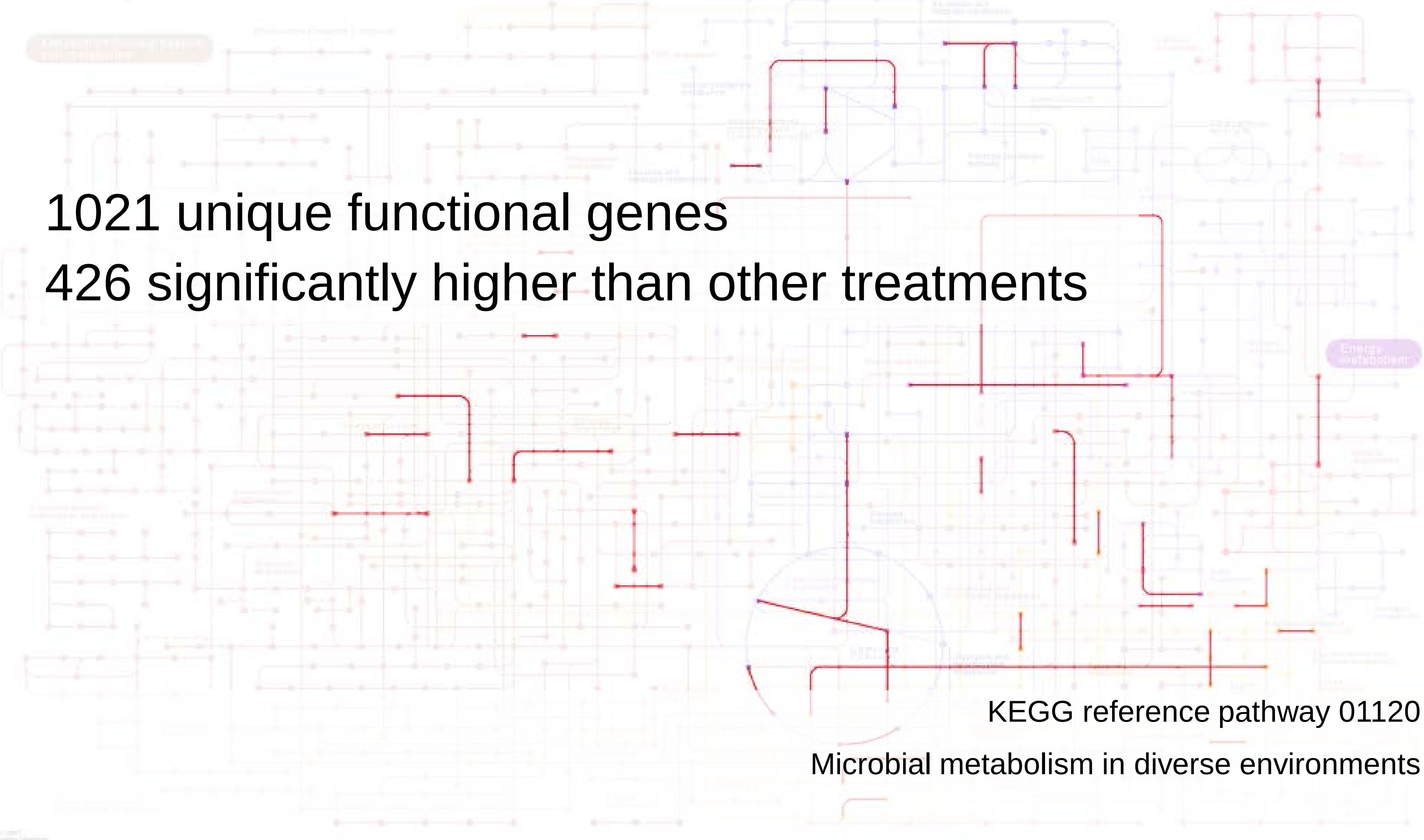
Reference pathway: microbial metabolism in diverse environments



Unique functional genes in P+A treatment

1021 unique functional genes

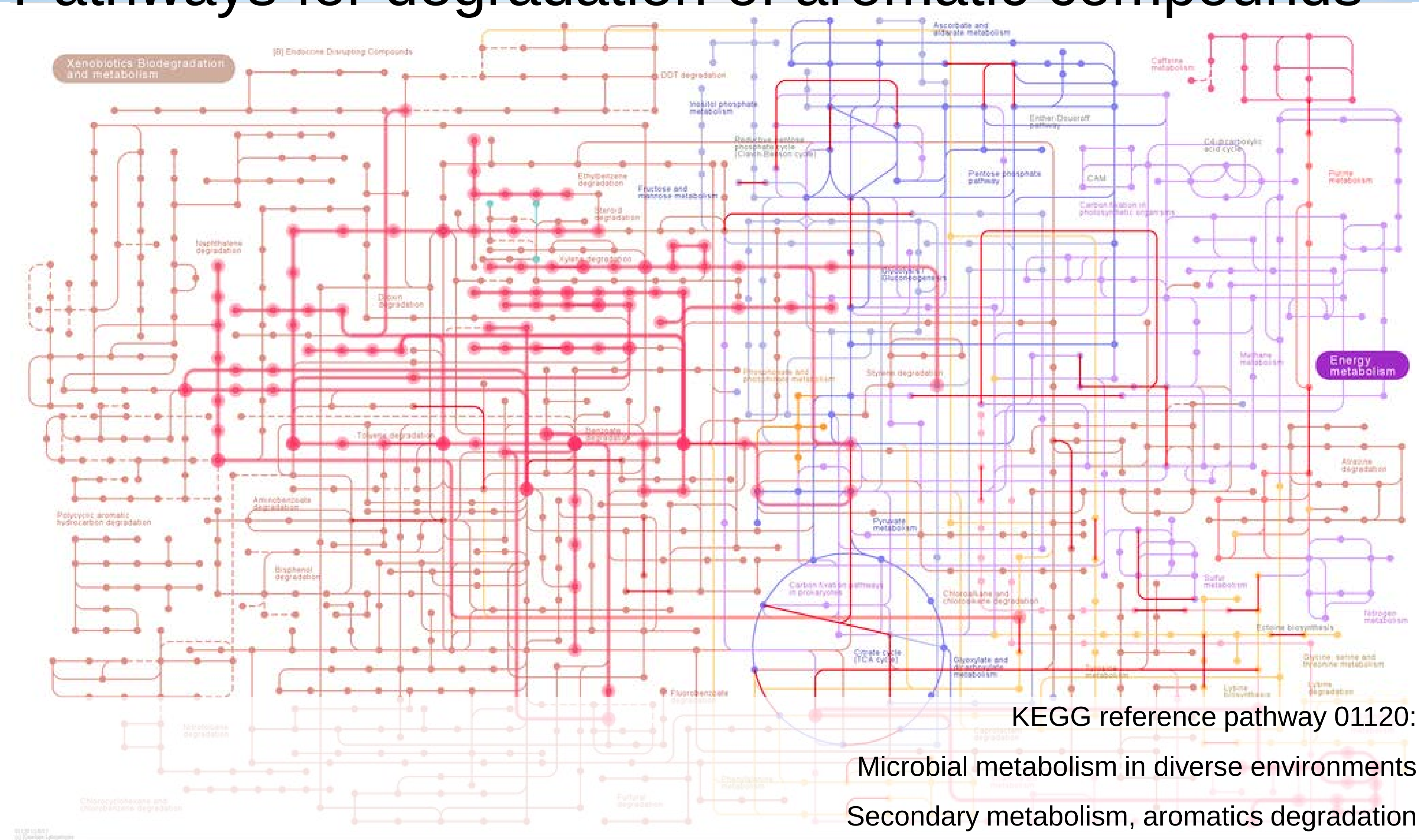
426 significantly higher than other treatments



KEGG reference pathway 01120

Microbial metabolism in diverse environments

Pathways for degradation of aromatic compounds



KEGG reference pathway 01120:

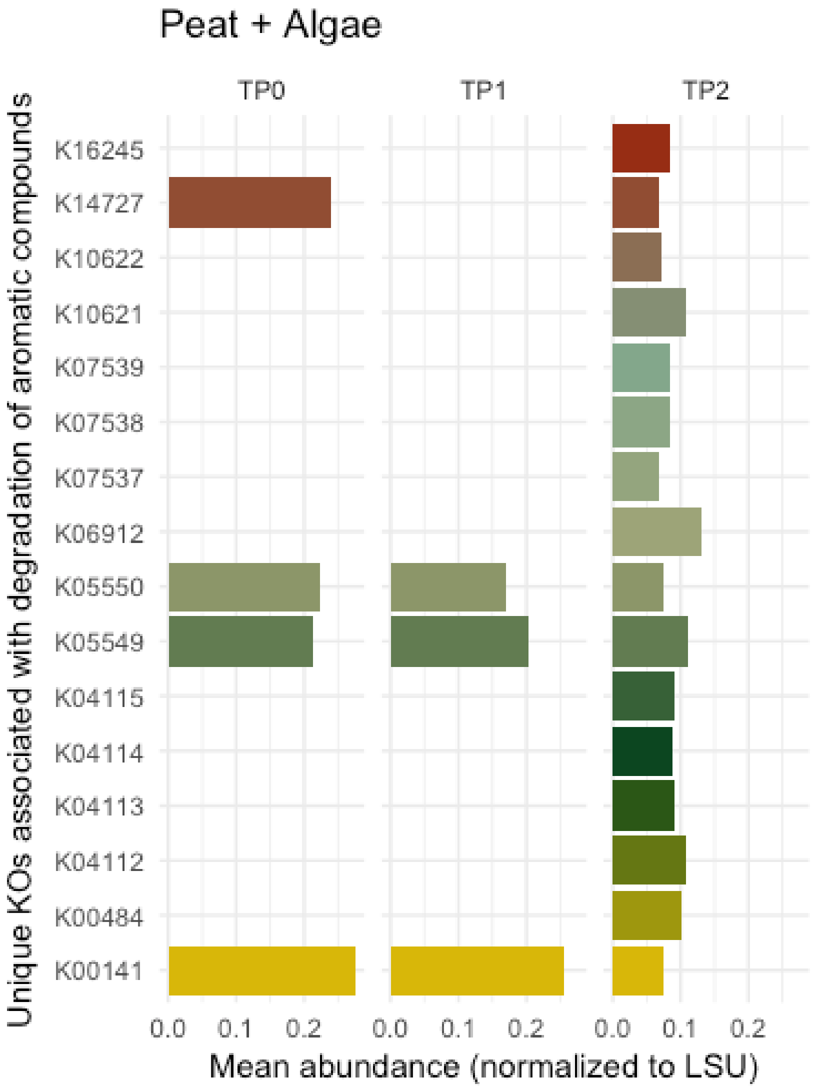
Microbial metabolism in diverse environments

Secondary metabolism, aromatics degradation

Functional gene diversity increases over time

Genes associated with degradation of aromatic compounds

Unique to P+A treatment



Conclusions

When peat was incubated with algae:

- Increased CO_2 production
- 31% greater conversion of peat to CO_2
- Increased microbial diversity
- *Gammaproteobacterial* DOM-degraders identified
- Increased functional genes, particularly for metabolism

Suggests enhanced conversion of peat DOM to CO_2 with algal DOM

Implications

If blue C habitats are lost, previously sequestered blue C may be at risk of conversion to CO_2, particularly in eutrophic zones.

Further work is needed to understand the mechanisms, rates, and prevalence of this issue.

Future Directions

Conduct an additional incubation to analyze transcripts and metabolites

Establish other treatments to investigate the role of:

- Different blue carbon DOM sources
- Nutrient availability
- Mixed vs. homogeneous microbial communities

Acknowledgements

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Thank you!

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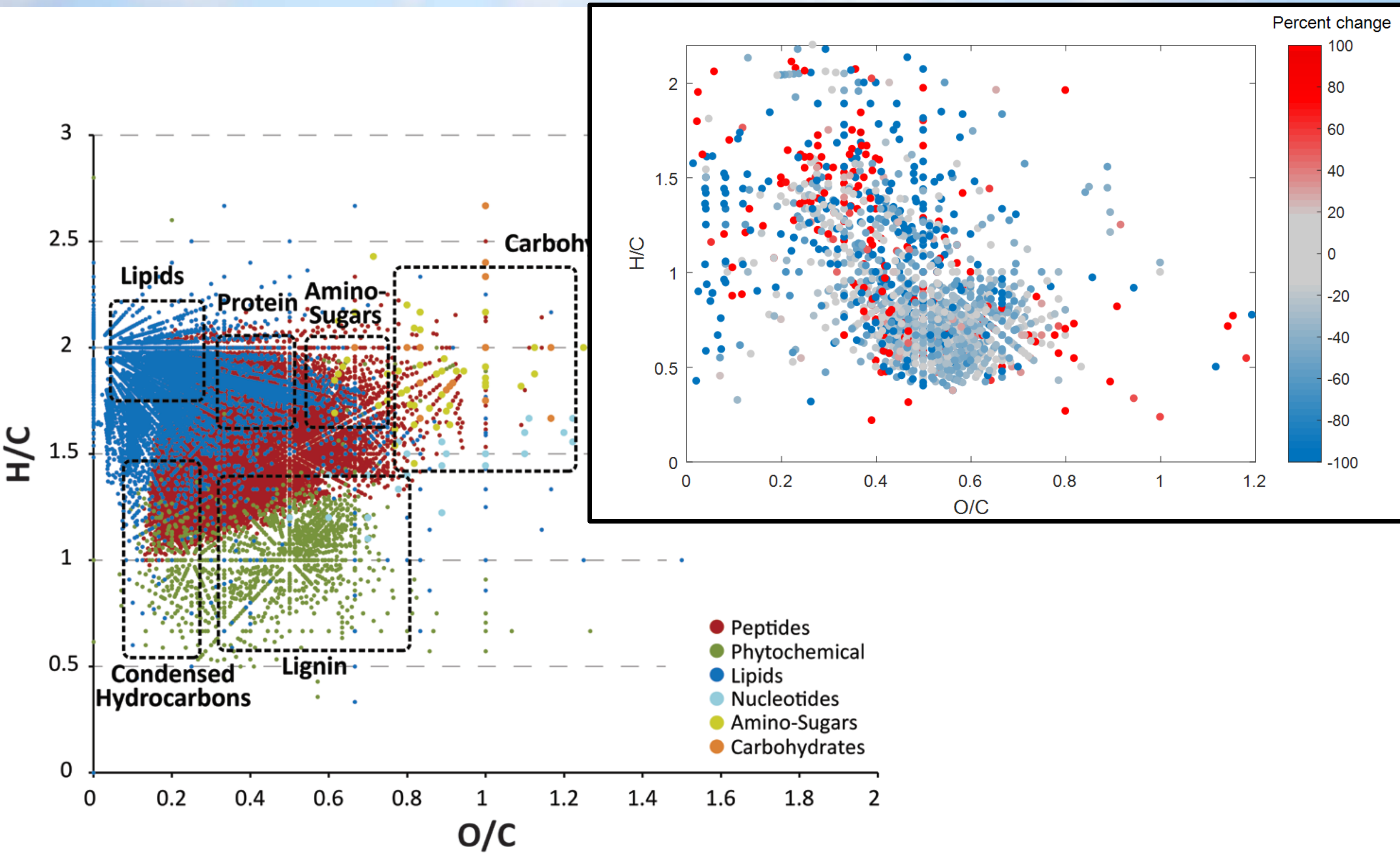

Lipids
Protein
Amino-Sugars
Carboh
Condensed Hydrocarbons
Lignin
H/C
O/C
3
2.5
2
1.5
1
0.5
0
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2
● Peptides
● Phytochemical
● Lipids
● Nucleotides
● Amino-Sugars
● Carbohydrates
Percent change
100
80
60
40
20
0
-20
-40
-60
-80
-100
H/C
O/C
2
1.5
1
0.5
0
0
0.2
0.4
0.6
0.8
1
1.2

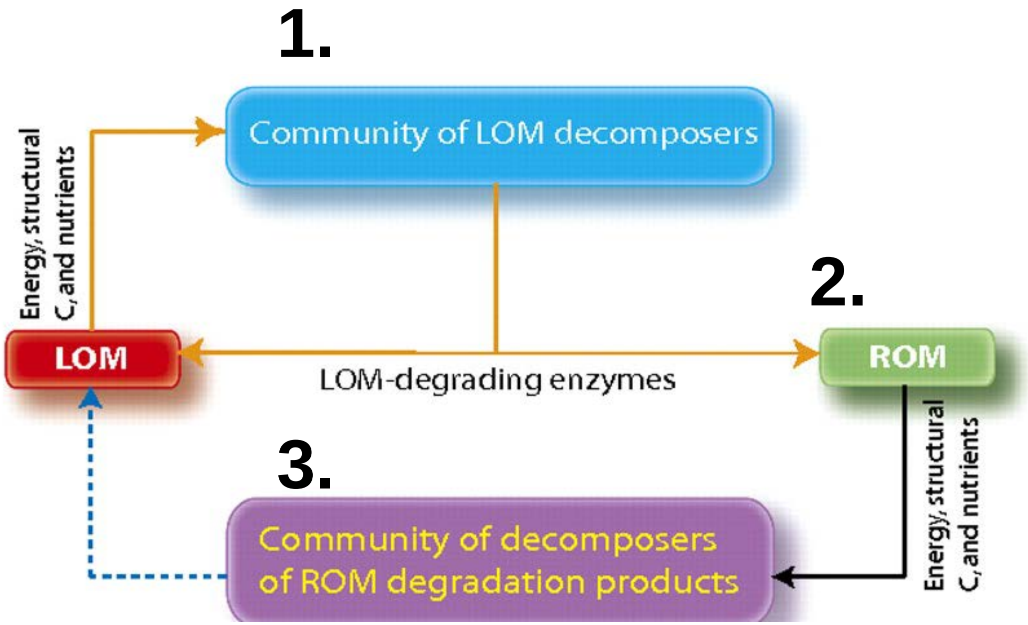
Potential Mechanisms: I

Could be co-metabolism:

1. LOM may stimulate LOM decomposer enzyme production

2. Enzymes can also degrade ROM

3. LOM degraders cannot use ROM degradation products, but another community can



From T.S. Bianchi (2011)
Guenet et al. (2010)

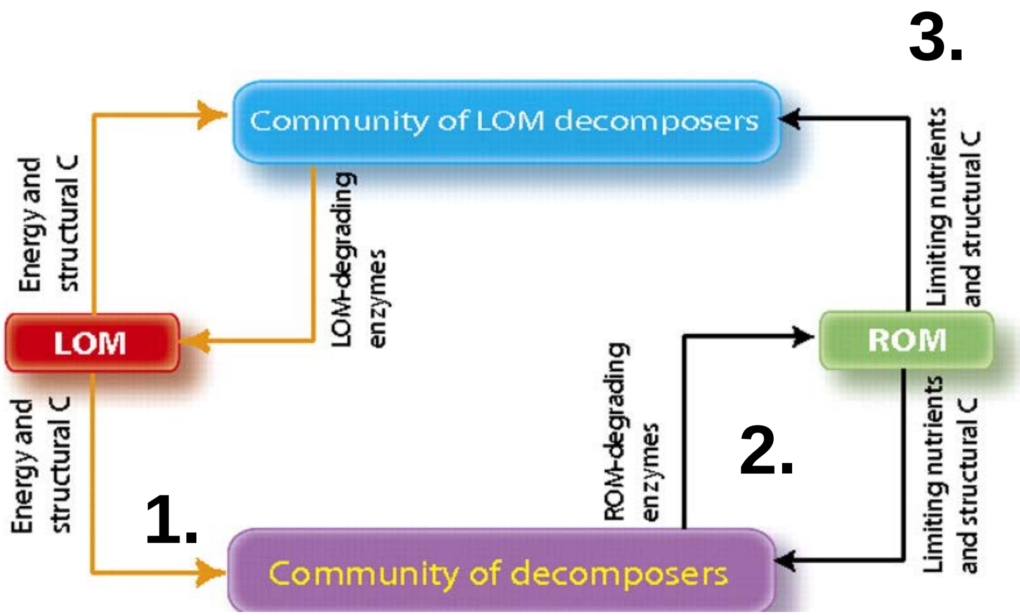
Potential Mechanisms: II

Could be an interaction between two populations:

1. LOM degradation products stimulate ROM decomposers

2. ROM decomposers release ROM degrading enzymes

3. ROM decomposition products are used by both ROM and LOM degrading communities

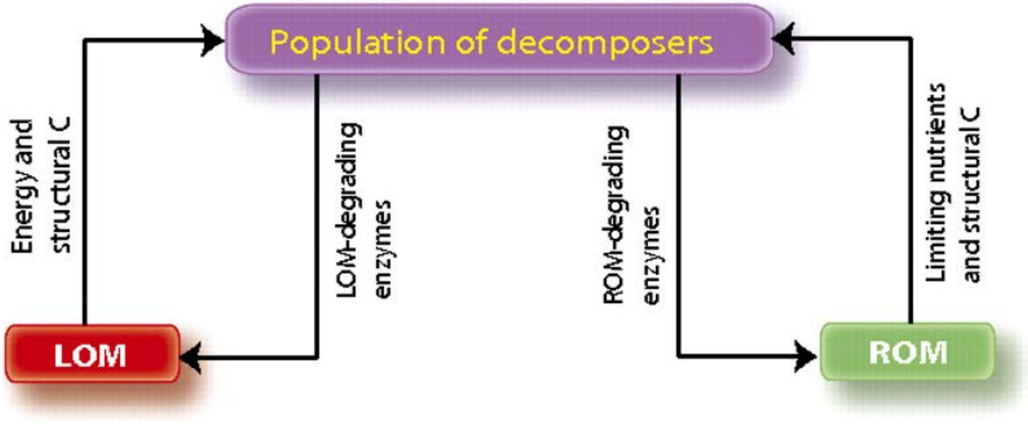


From T.S. Bianchi (2011)
Guenet et al. (2010)

Potential Mechanisms: III

Could be the activity of a homogeneous community

Capable of degrading ROM when LOM is available as an energy source

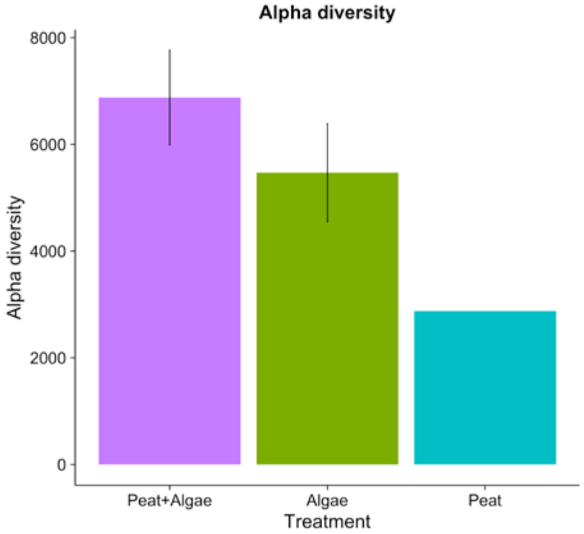


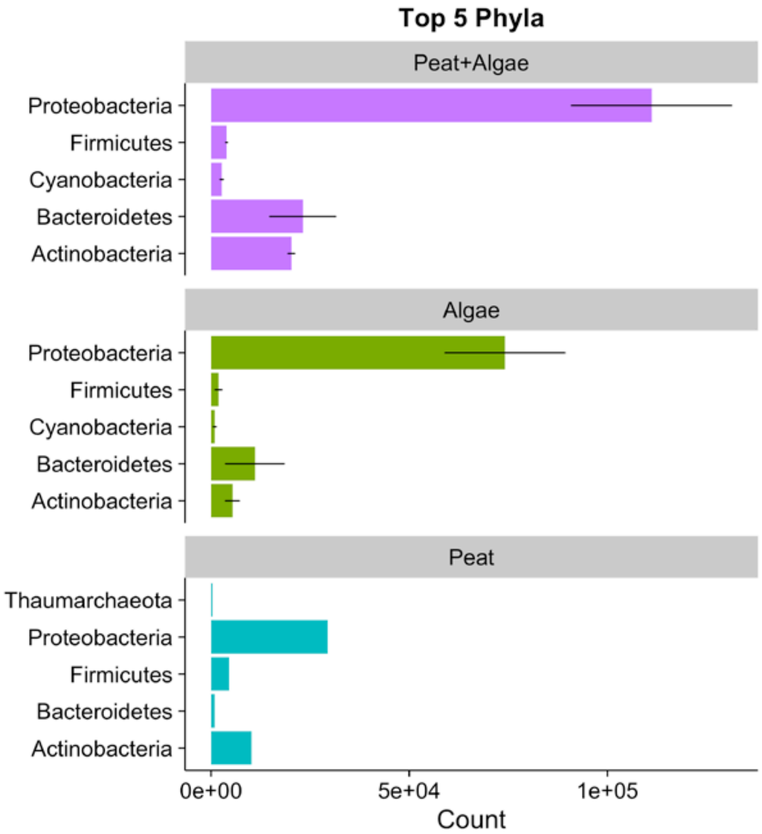
From T.S. Bianchi (2011)
Guenet et al. (2010)

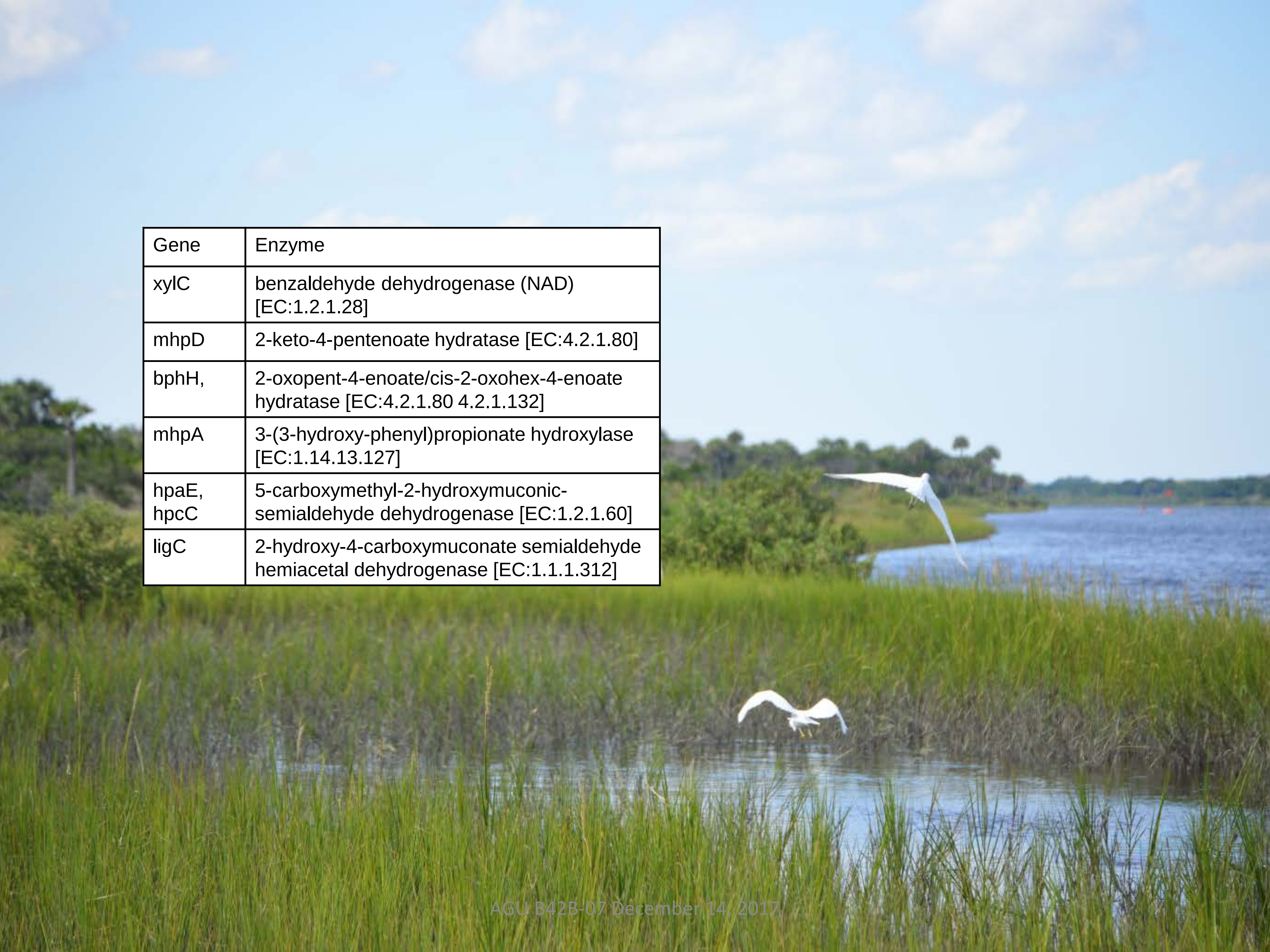
Microbial communities more diverse in P+A

Peat + Algae treatment:

Greatest alpha diversity
Greatest abundance of top 5 phyla







Gene	Enzyme
xylC	benzaldehyde dehydrogenase (NAD) [EC:1.2.1.28]
mhpD	2-keto-4-pentenoate hydratase [EC:4.2.1.80]
bphH,	2-oxopent-4-enoate/cis-2-oxohex-4-enoate hydratase [EC:4.2.1.80 4.2.1.132]
mhpA	3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.127]
hpaE, hpcC	5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase [EC:1.2.1.60]
ligC	2-hydroxy-4-carboxymuconate semialdehyde hemiacetal dehydrogenase [EC:1.1.1.312]