Impacts of dynamic soil redox on tropical soil microbiomes and biogeochemical transformations

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BERKELEY LAB

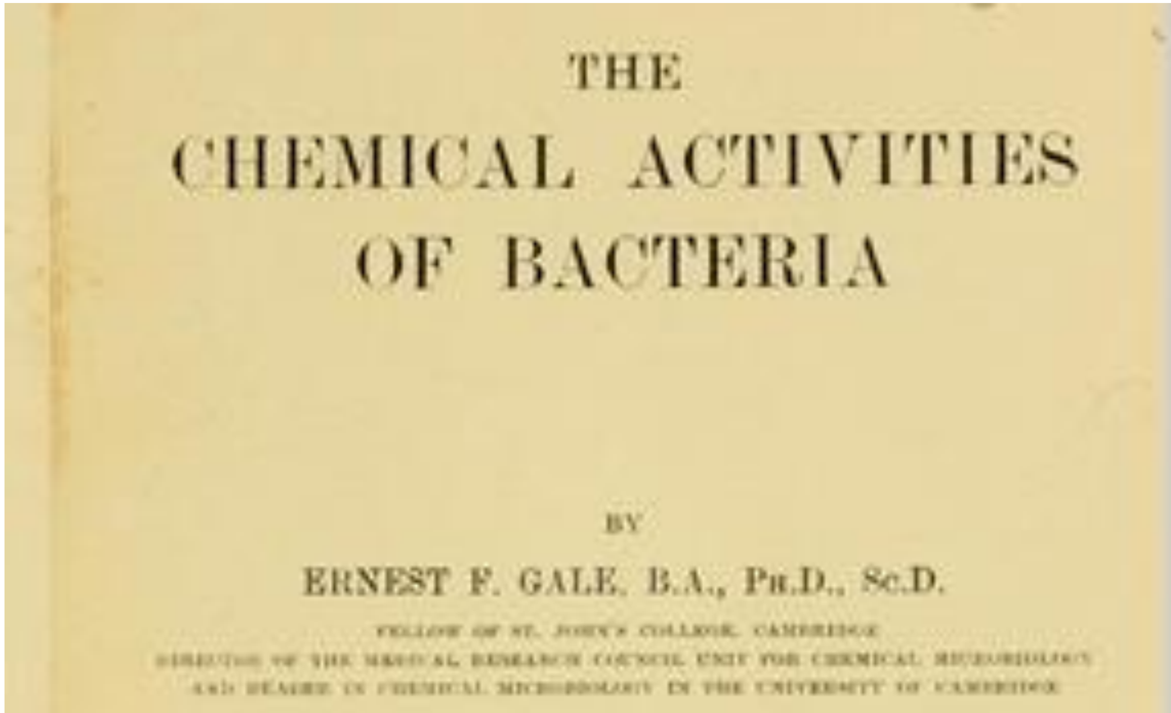
U.S. DEPARTMENT OF ENERGY

Paradigms

- Upland soils…dominated by aerobic processes
- Redox stratification… ‘*a wetland thing*’
- Microbes… obligate anaerobes, obligate aerobes
- Methanogens… oxygen = toxic
- Aerobic respiration…leads to high CO_2 fluxes
- Carbon accumulates…when its anoxic
- Well controlled experiments…avoid oscillation

But what if we’re wrong? (even just a little)

REDOX: Oxidation (loss of e-) & Reduction (gain of e-)


THE
CHEMICAL ACTIVITIES
OF BACTERIA

BY

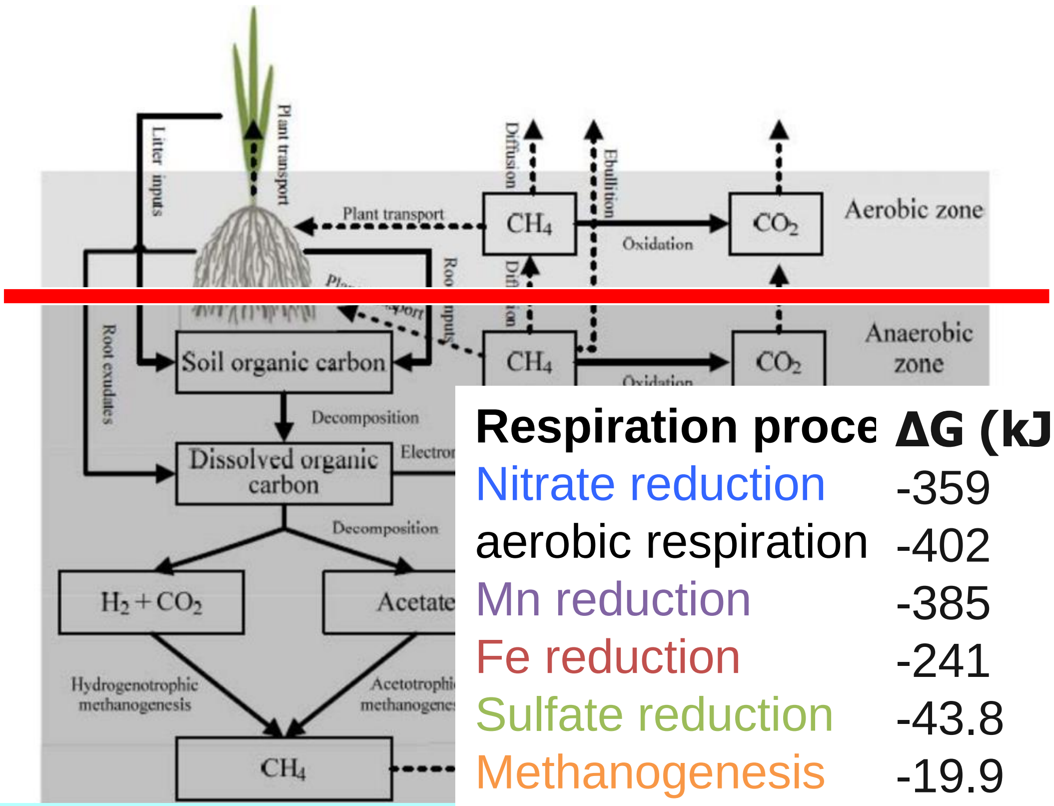
ERNEST F. GALE, B.A., Ph.D., Sc.D.

"it is probably not unscientific to suggest the somewhere or other some organism exists which can, under suitable conditions, oxidize any substance which is theoretically capable of being oxidized"

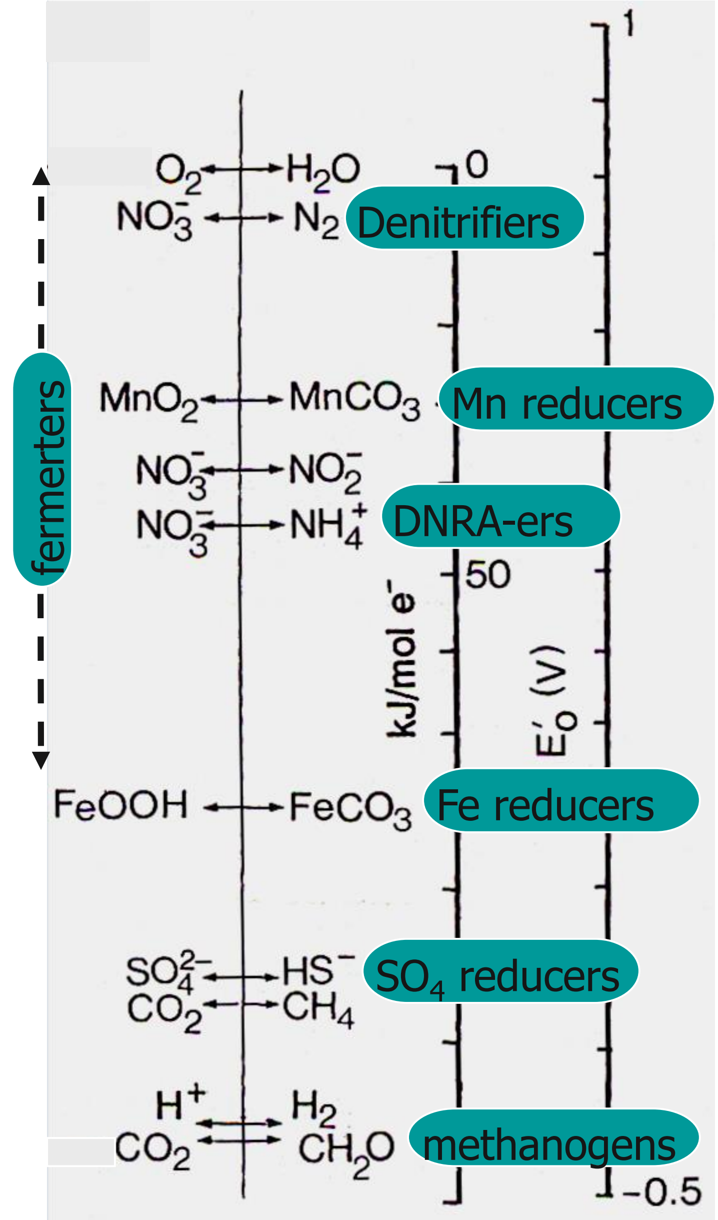
–E.F. Gale 1952

Terminal electron acceptors

Thermodynamics tells us microbes should use terminal electron acceptors sequentially, according to the 'redox ladder'…



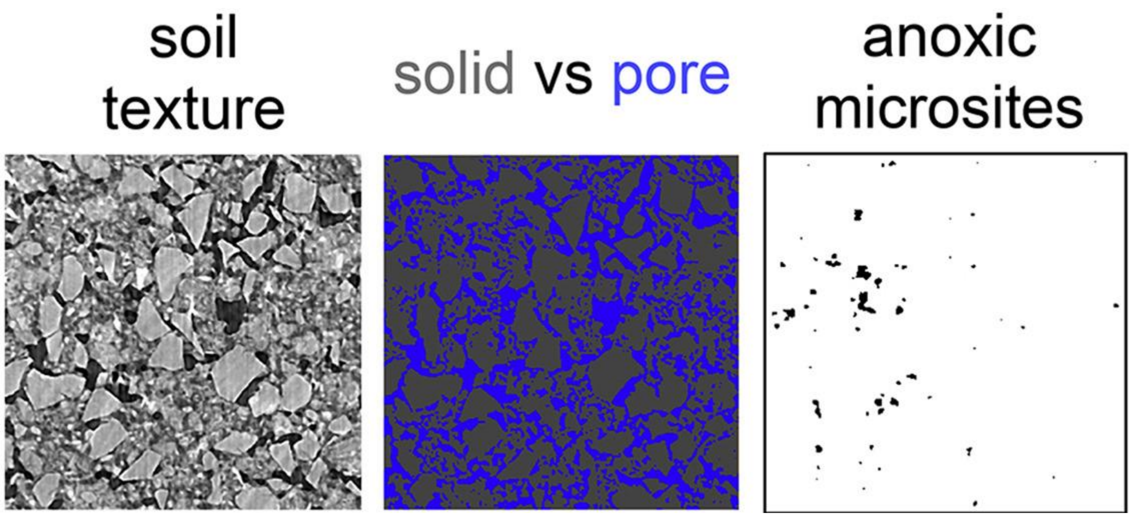
Respiration proce	ΔG (kJ)
Nitrate reduction	-359
aerobic respiration	-402
Mn reduction	-385
Fe reduction	-241
Sulfate reduction	-43.8
Methanogenesis	-19.9



But is this the right conceptualization?

Redox patterns are dynamic in space

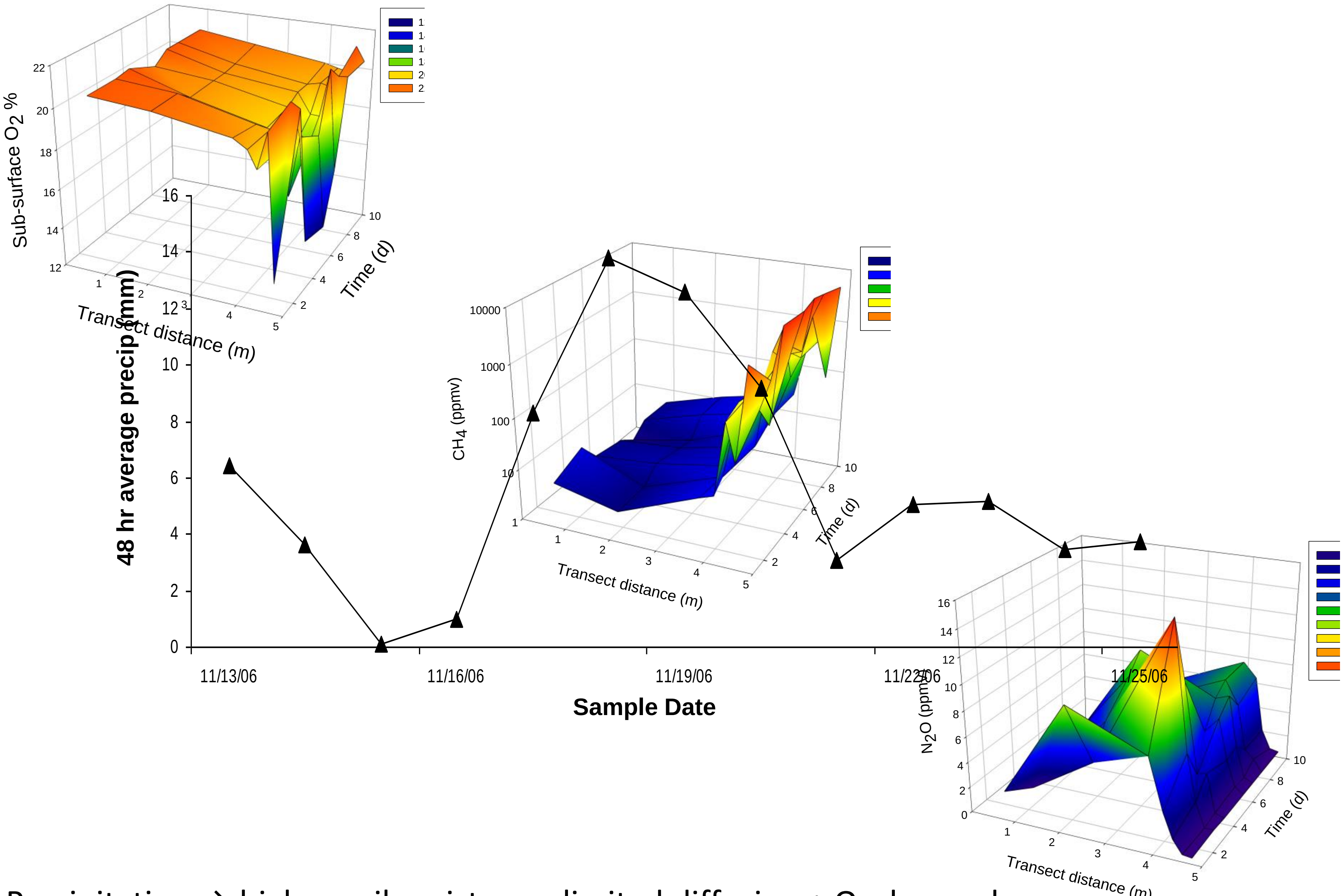
- In deep soils
- In surface soil microsites
  (Sexstone et al. 1985)
- In the rhizosphere
  (Keiluweit et al. 2015; Richter et al 2007)



Keiluweit et al. (2018)

Planar optode, microtomography

Redox patterns are also dynamic in time & space



Precipitation → higher soil moisture = limited diffusion + O_1 demand = low pE

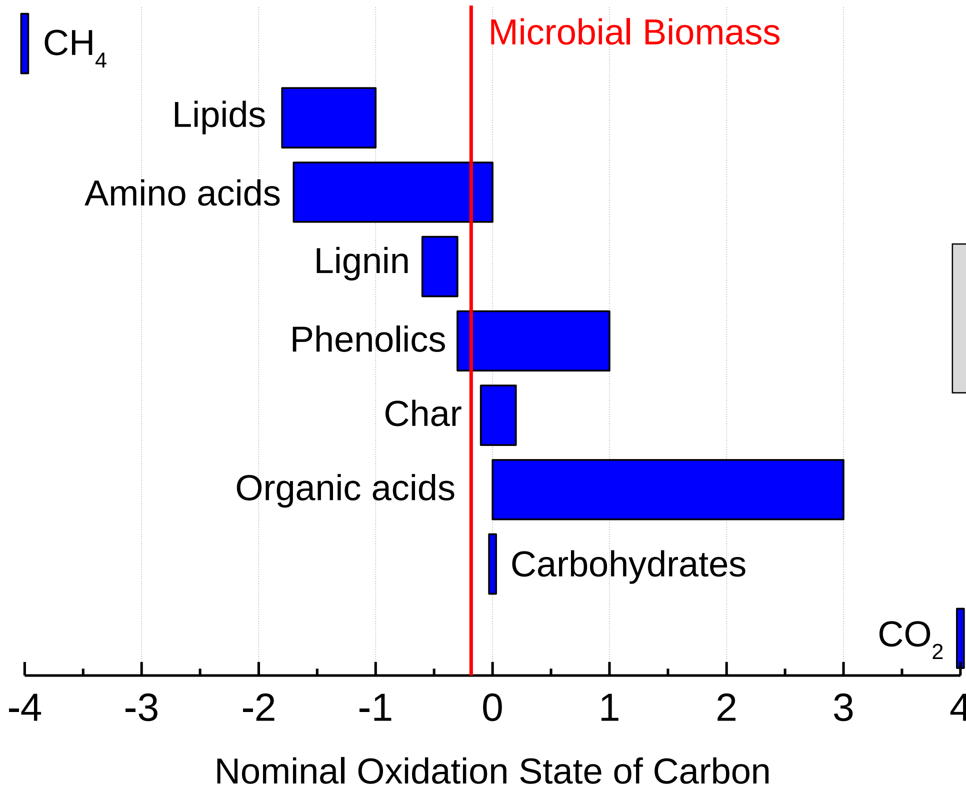
Pett-Ridge (2005)

Electron donors

Energy storage in organic compounds

“High energy”

reduced C
(electron rich)



oxidized C
(electron – poor)

“Low energy”

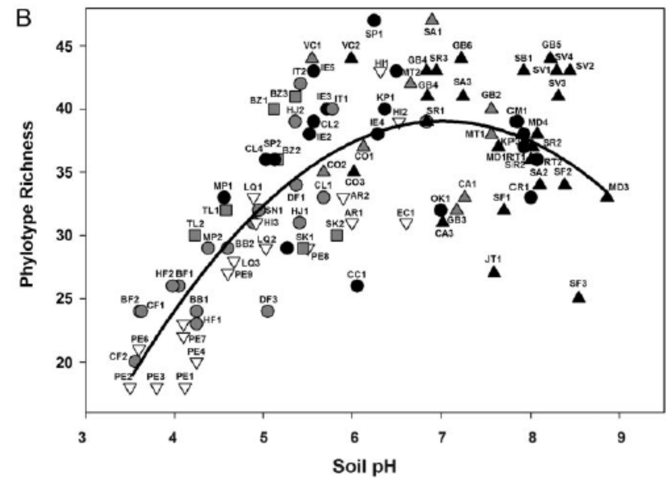
“NOSC”

LaRowe and Van Cappellen (2011)

The organization of global microbial communities is linked to substrate & redox traits

The diversity and biogeography of soil bacterial communities

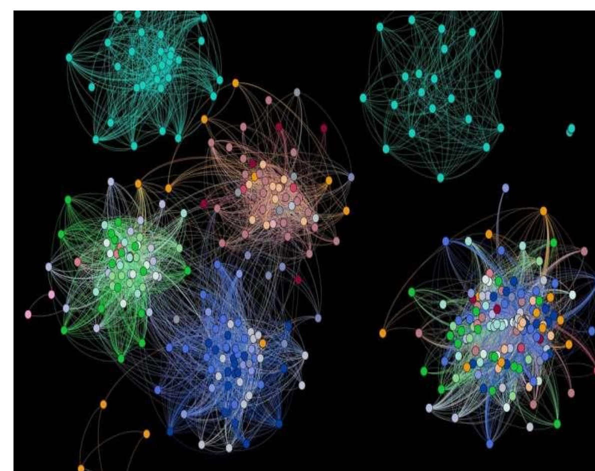
Noah Fierer*† and Robert B. Jackson*‡



Redox traits characterize the organization of global microbial communities

Salvador Ramírez-Flandes, Bernardo González, and Osvaldo Ulloa

PNAS February 26, 2019 116 (9) 3630-3635; first published February 11, 2019 https://doi.org/10.1073/pnas.1817554116

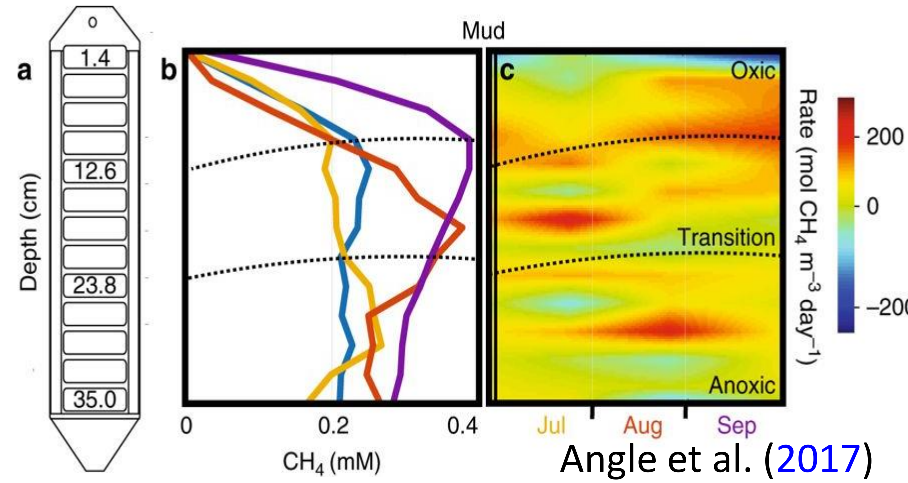


Network of oxidoreductase and taxonomic genes from 247 microbial metagenomes. Nodes=metagenomes, colored by biome.

Metagenomes of uncultured microbes—illustrate taxa who ‘break the rules’

- ‘Strict’ anaerobes—methanogens

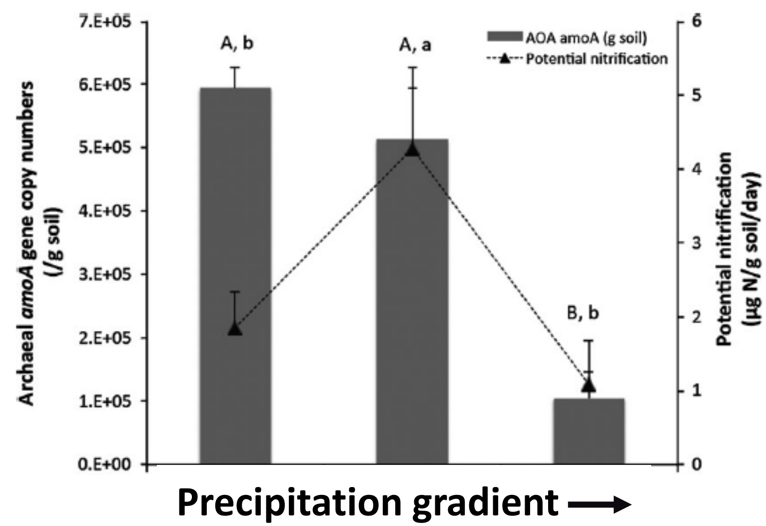
BUT…*Candidatus* Methanothrix paradoxum



Angle et al. (2017)

- ‘Strict’ aerobes—ammonia oxidizers

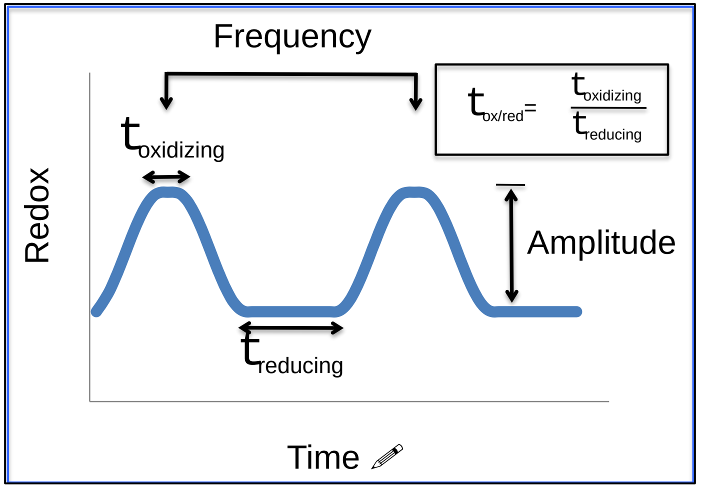
BUT… Nitrososphaera 7.2 and Nitrosotalea 1.1



Pett-Ridge et al. (2013)

The micro-ecological dimension of redox fluctuation

- Unlike T, H_2O, pH, or mineralogy… soil O_2/pE is one of the few environmental drivers that oscillates on a timestep faster than microbial populations can respond (via growth)



IF τ_{Ox} or τ_{red} << T (turnover time)

THEN populations must adapt via:

- Avoidance (refugia)
- Tolerance (superoxide dismutase, polyphosphate storage)
- Flexible metabolism (alternative e- acceptors)

Knowledge Gap

Need to improve understanding of **dynamic** soil redox conditions as a driver of Fe, C, nutrient transformations

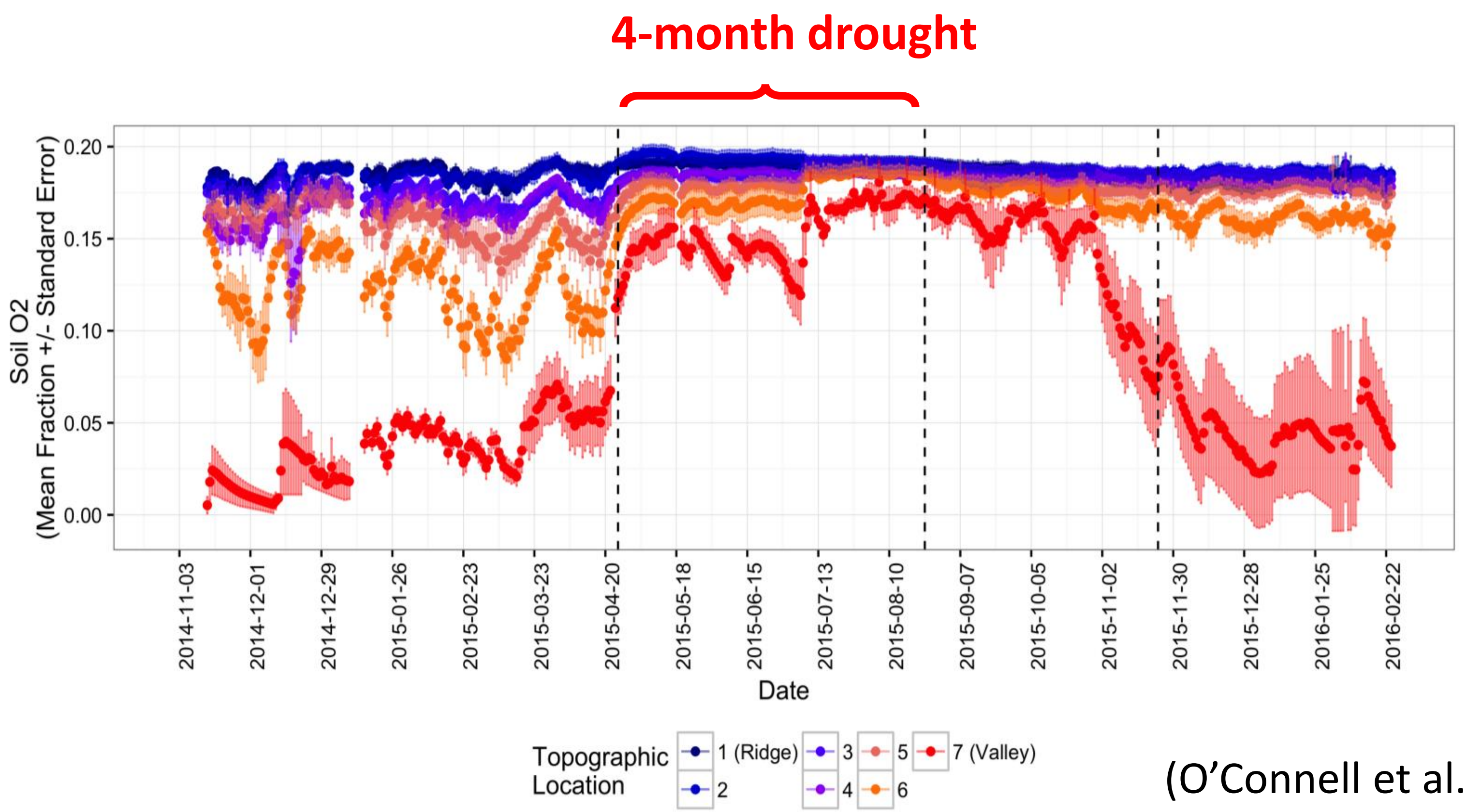
Objectives

Measure how shifts in soil oxygen/pE patterns affect

- Fe-oxide mineral crystallinity
- composition of metabolic products
- fate of complex C substrates
- soil respiration
- microbial community structure

Luquillo Critical Zone Observatory, Puerto Rico

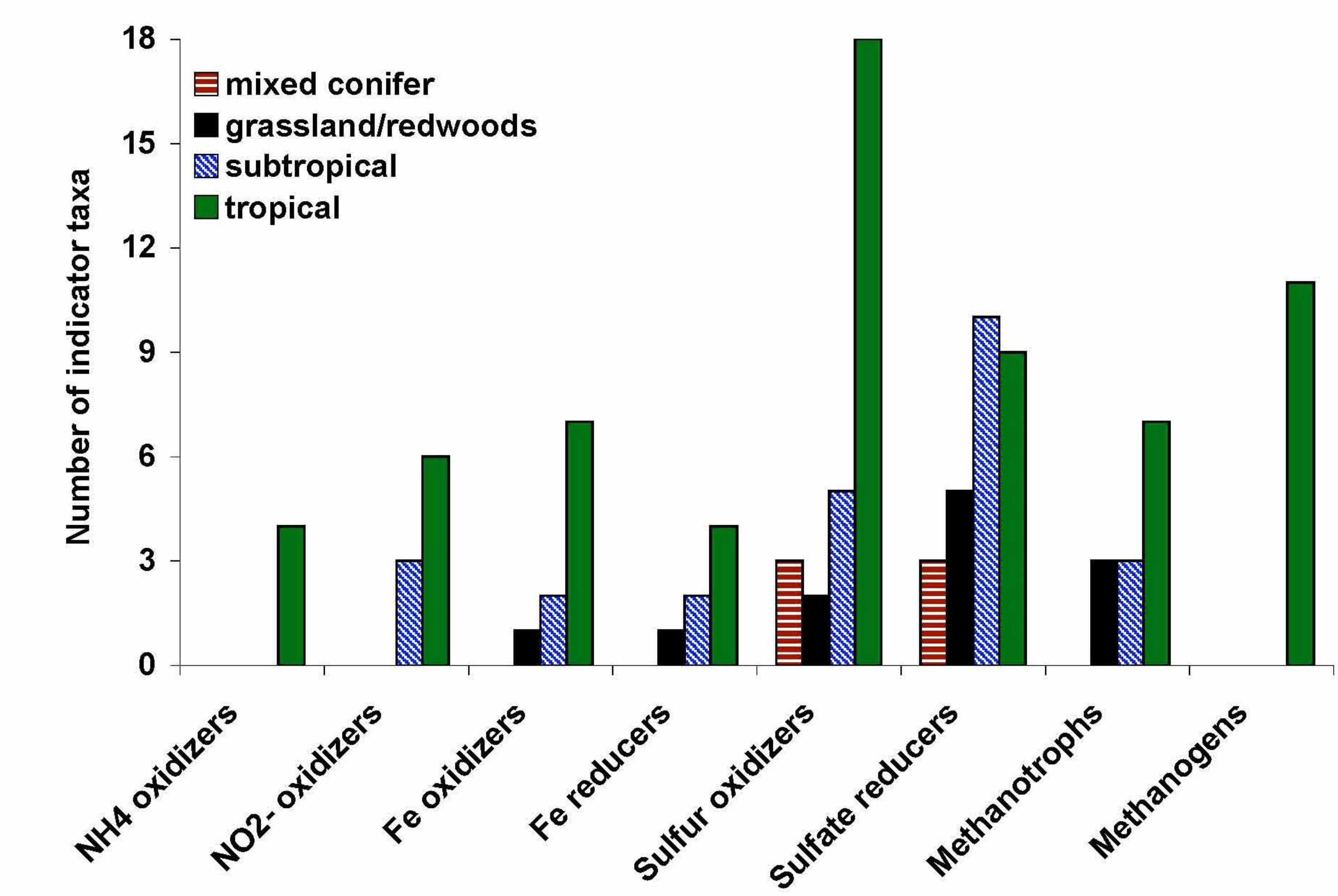
Climate changes are already altering the predominant redox regime of soils in the Luquillo CZO



(O'Connell et al., 2018)

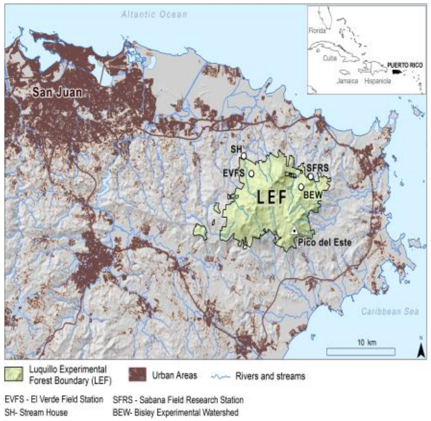
- Redox fluctuations in these upland tropical forest soils are <u>spatially and temporally</u> heterogeneous
- Redox oscillations affect Fe-C-P-N cycles

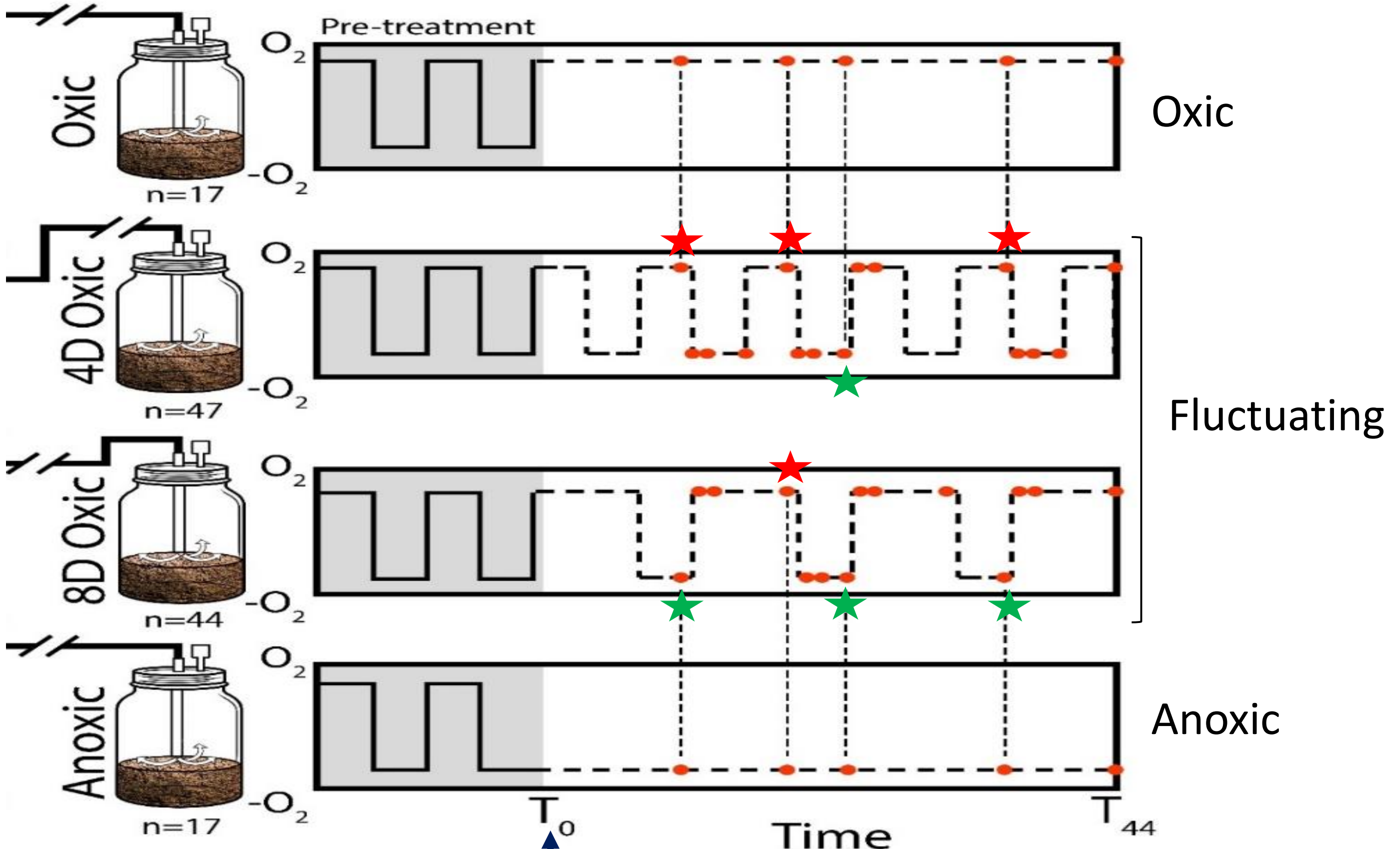
Tropical soils have diverse microbial functional capacity



(Dubinsky et al. unpublished)

Soil manipulation experiment—effects of redox patterns on microbial communities and their functionality



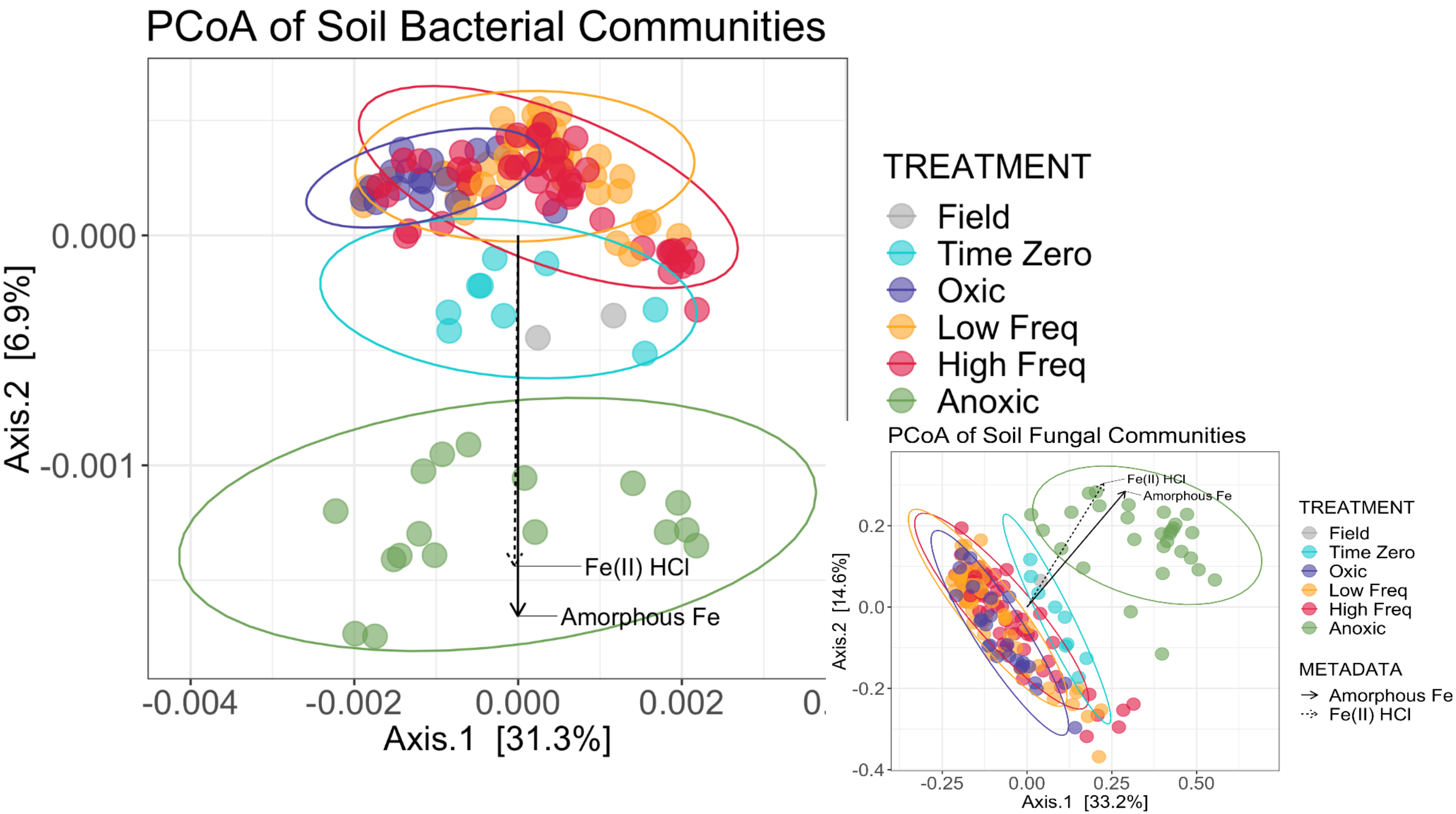


(^{13}C plant litter added to a subset of microcosms)

★ Oxic to anoxic
★ Anoxic to oxic

The 'Great Redox Experiment'

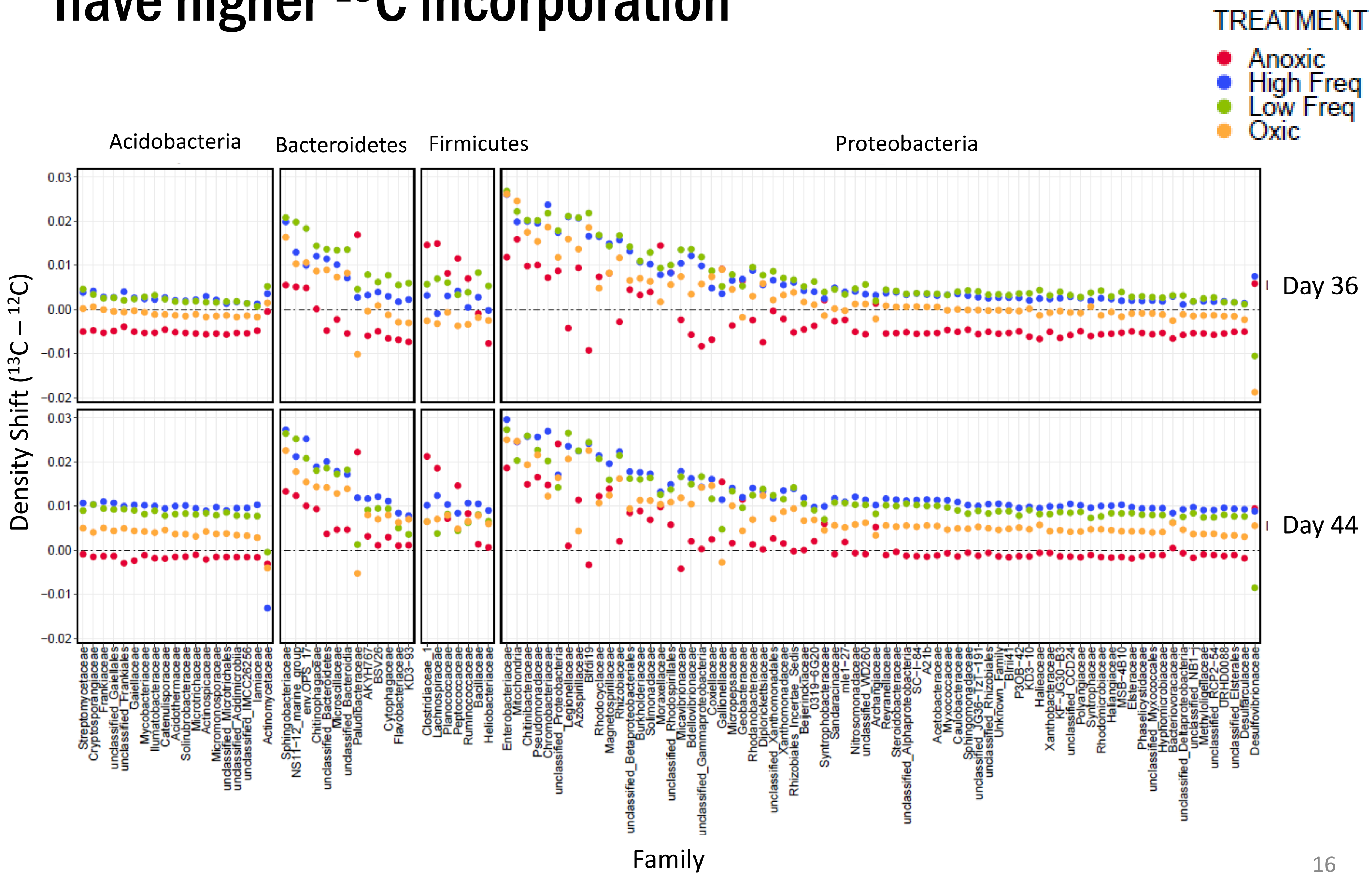
Oxic and oscillating redox communities are barely distinguishable; anoxic soils develop a unique cohort



N.B. vast majority of OTUs were not impacted by redox

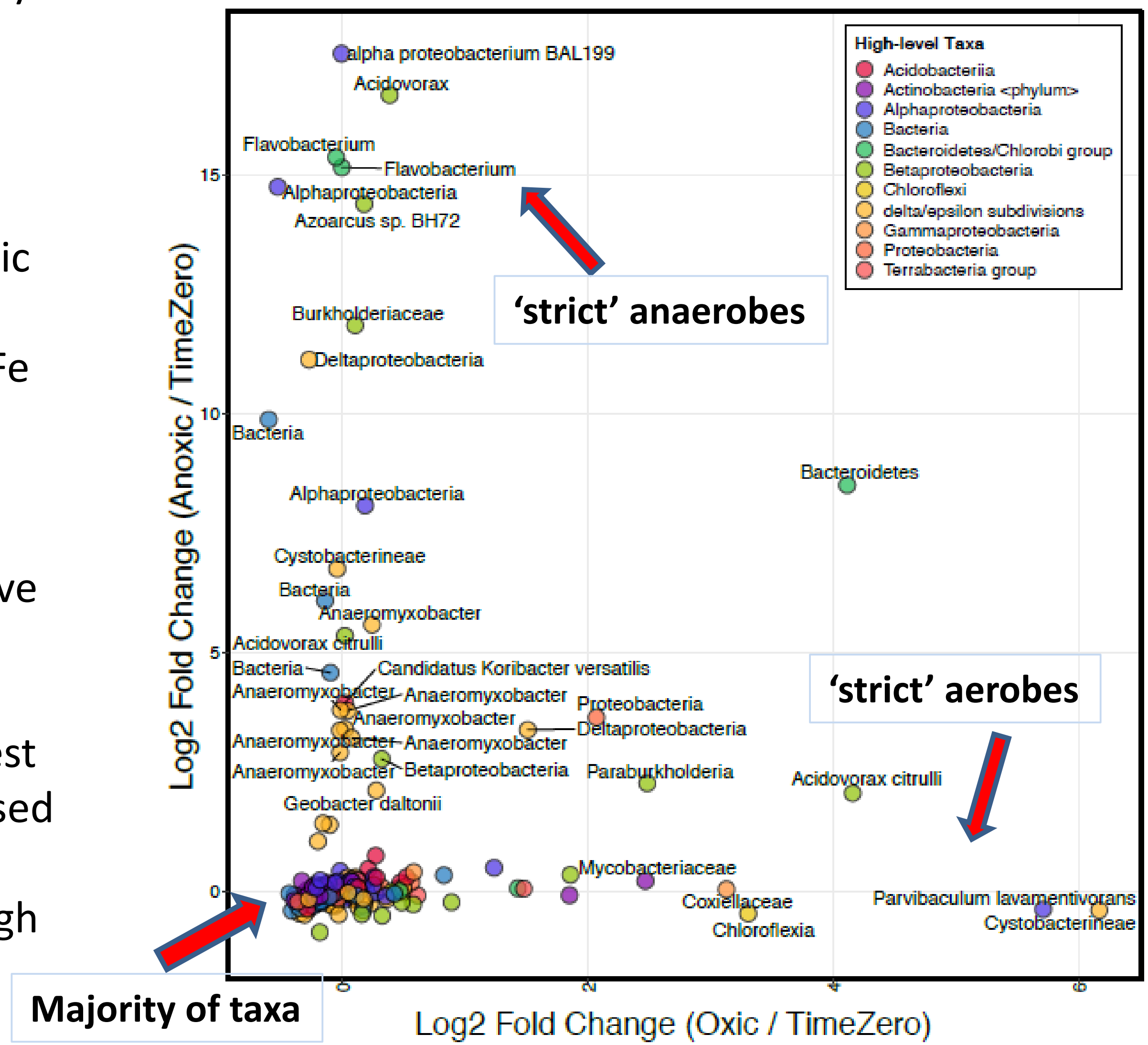
Campbell et al. (in prep)

^{13}C stable isotope probing (SIP): fluctuating soil OTUs have higher ^{13}C incorporation

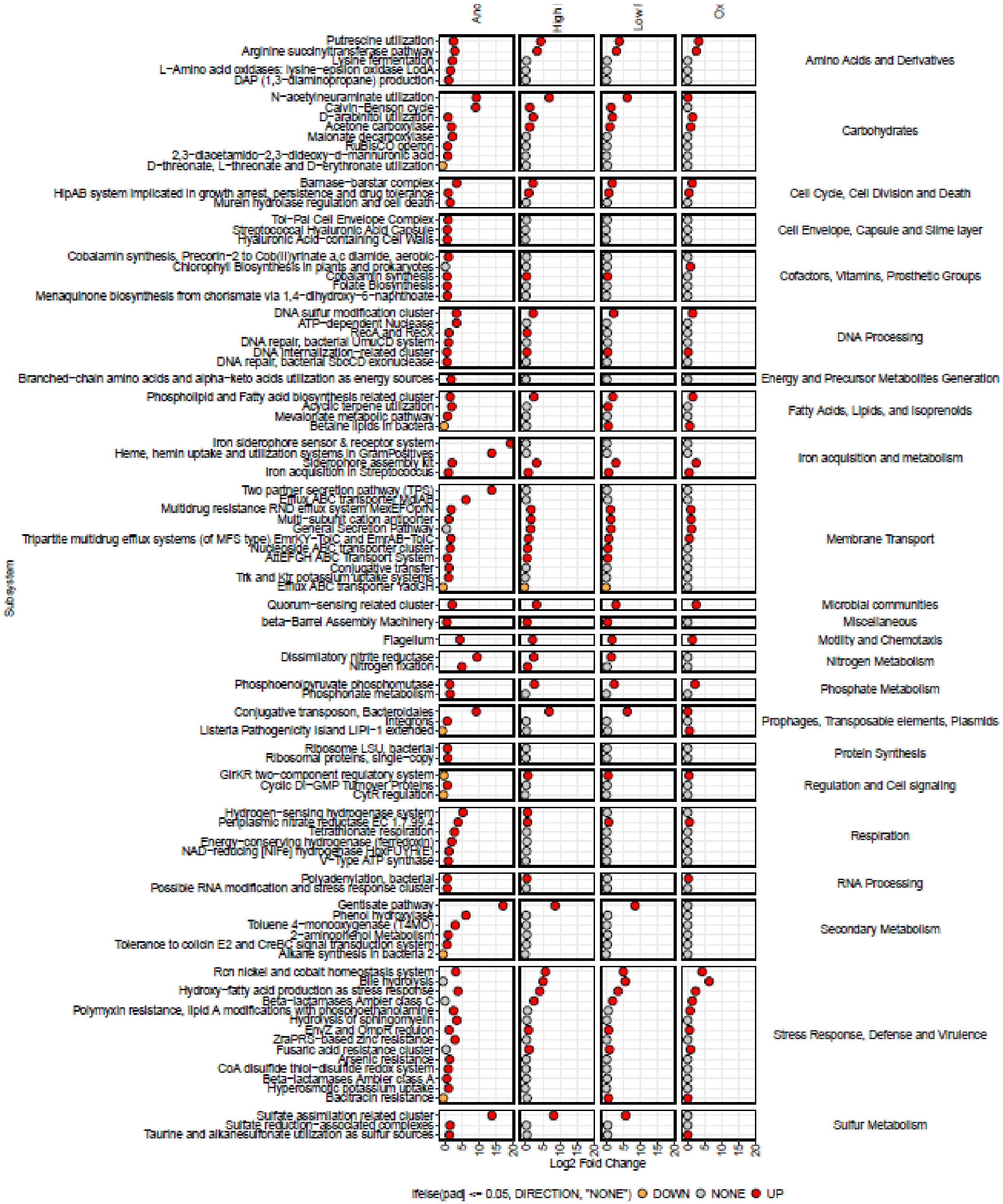


^{13}C SIP metagenomes, many novel viral sequences

- 326 medium/high quality bins (MAGs) from ^{13}C enriched DNA fractions
- largest changes in the static anoxic vs static oxic
- strong response in the Fe reducer community
- found 460 viral OTUs, ¼ were unique to the active fraction (^{13}C).
- Viral richness was highest in oxic samples, decreased with O_2 availability (oxic>low frequency>high frequency>anoxic)



Enriched Metabolic Subsystems (rel to time zero)



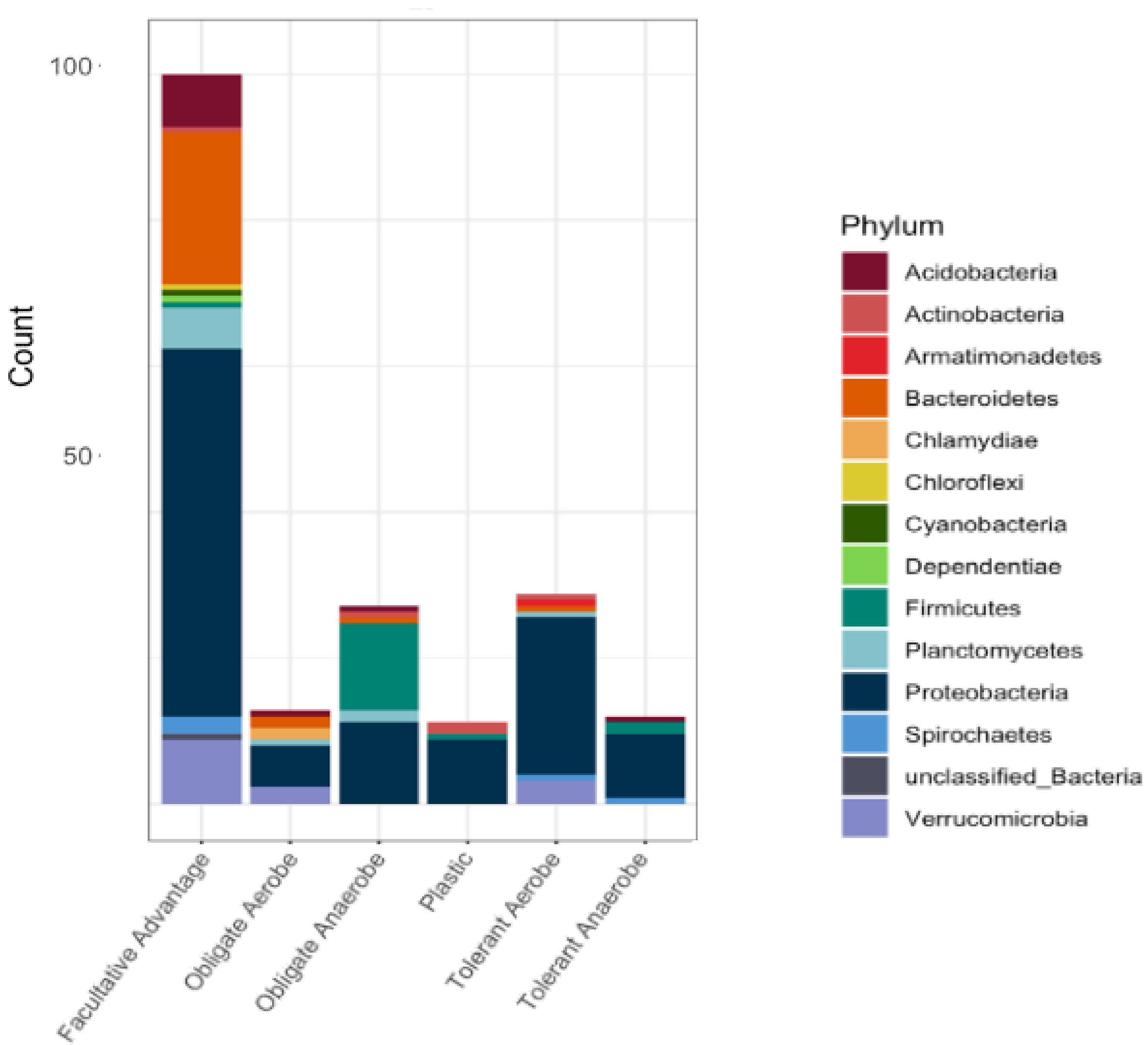
Metabolic subsystems from genomes of ^{13}C enriched organisms

Iron acquisition and metabolism

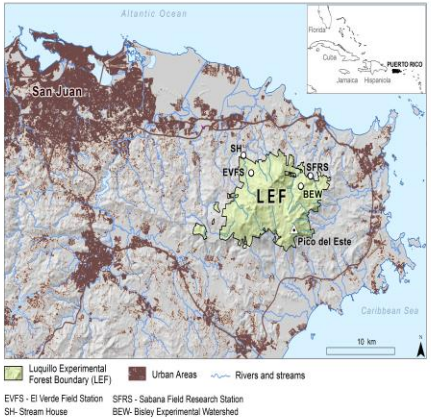
Stress Response, Defense, Virulence

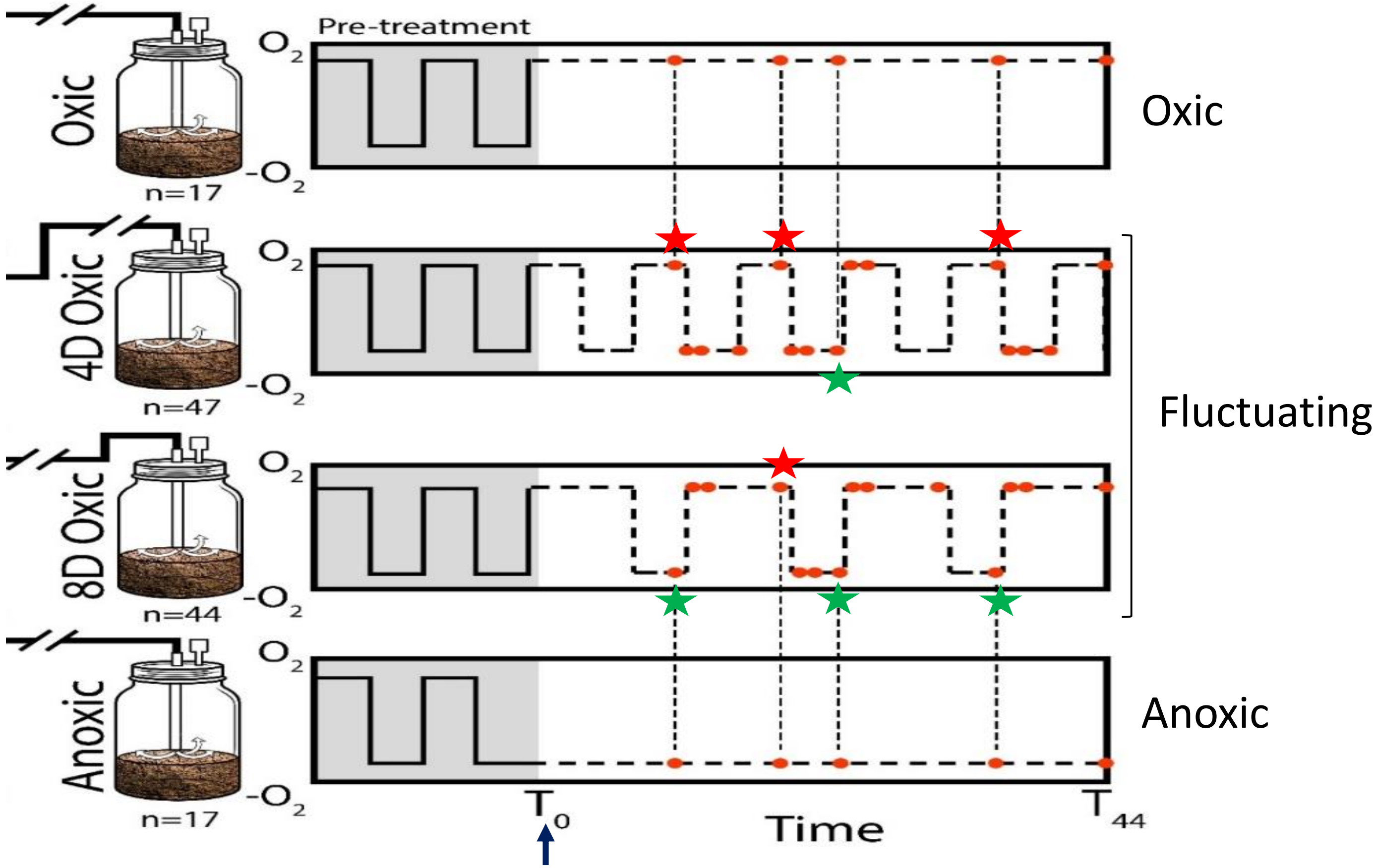
Microbial strategies to ‘cope’ with soil redox status

OTUs change with time, primarily due to metabolic tolerance …..NOT plasticity



Soil manipulation experiment—effects of redox patterns on soil biogeochemistry





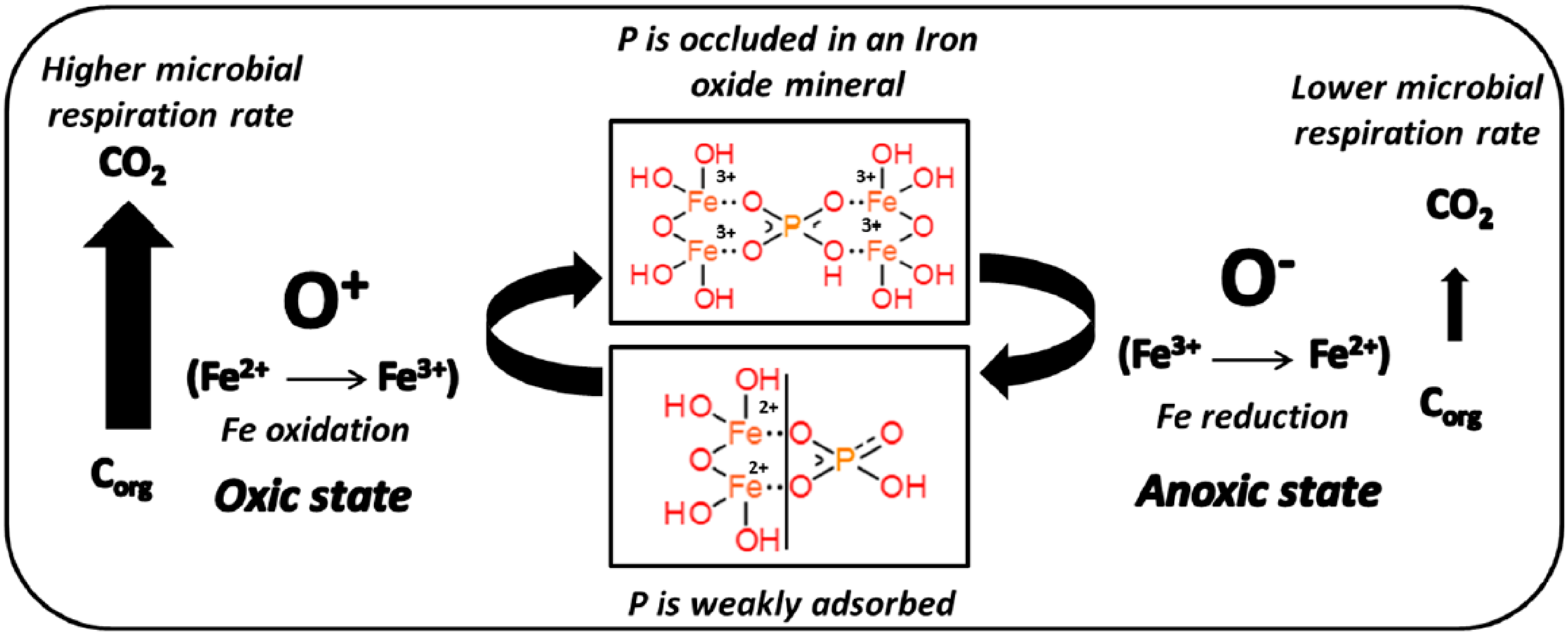
(^{13}C plant litter added to a subset of microcosms)

★ Oxic to anoxic

★ Anoxic to oxic

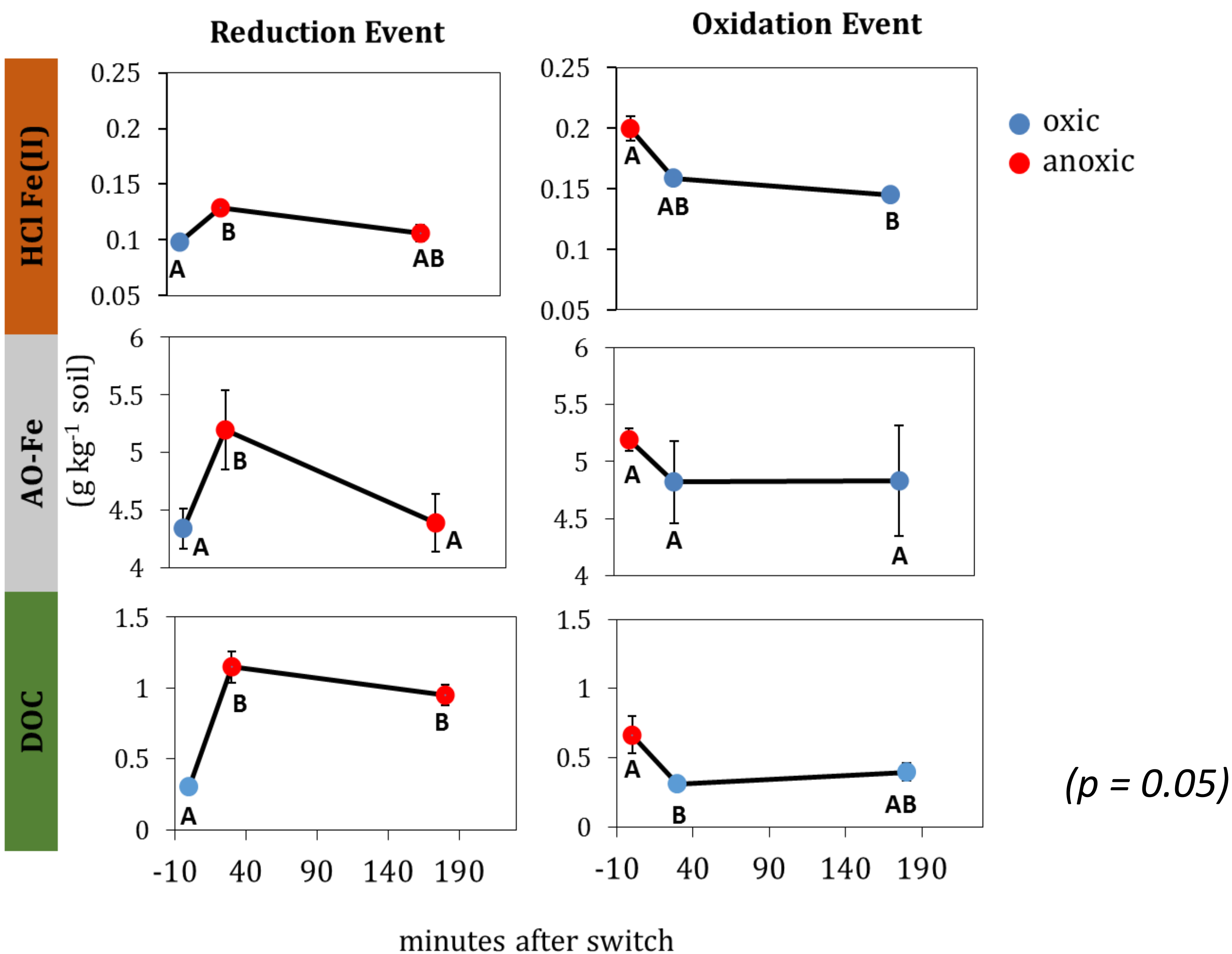
The 'Great Redox Experiment'

Expectations…(based on the literature)



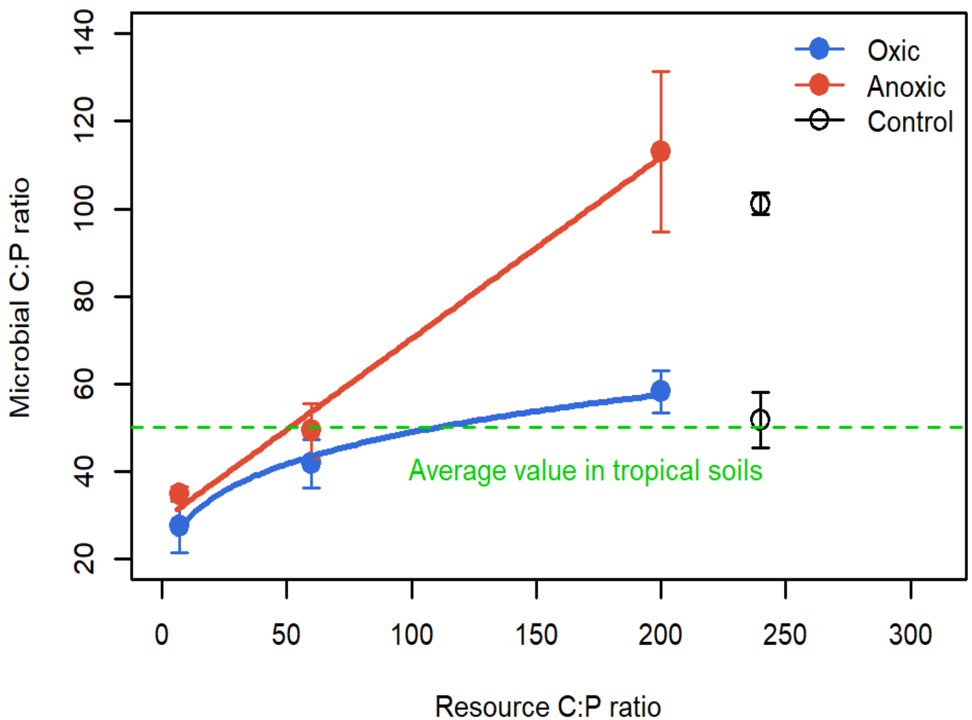
Gross et al., *Soil Systems* 2018

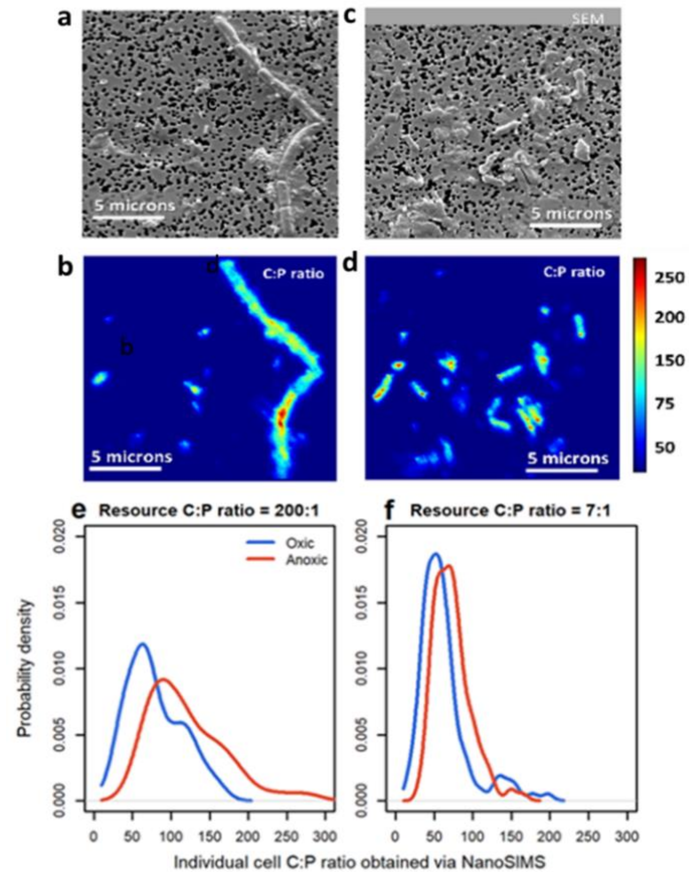
Rapid changes in Fe(II), amorphous Fe and DOC were observed when redox conditions switched



Bhattacharyya et al., *ES&T* 2018; Lin et al. *JGR Biogeosciences* 2018

Anoxia constrains carbon use efficiency and microbial capacity for P uptake

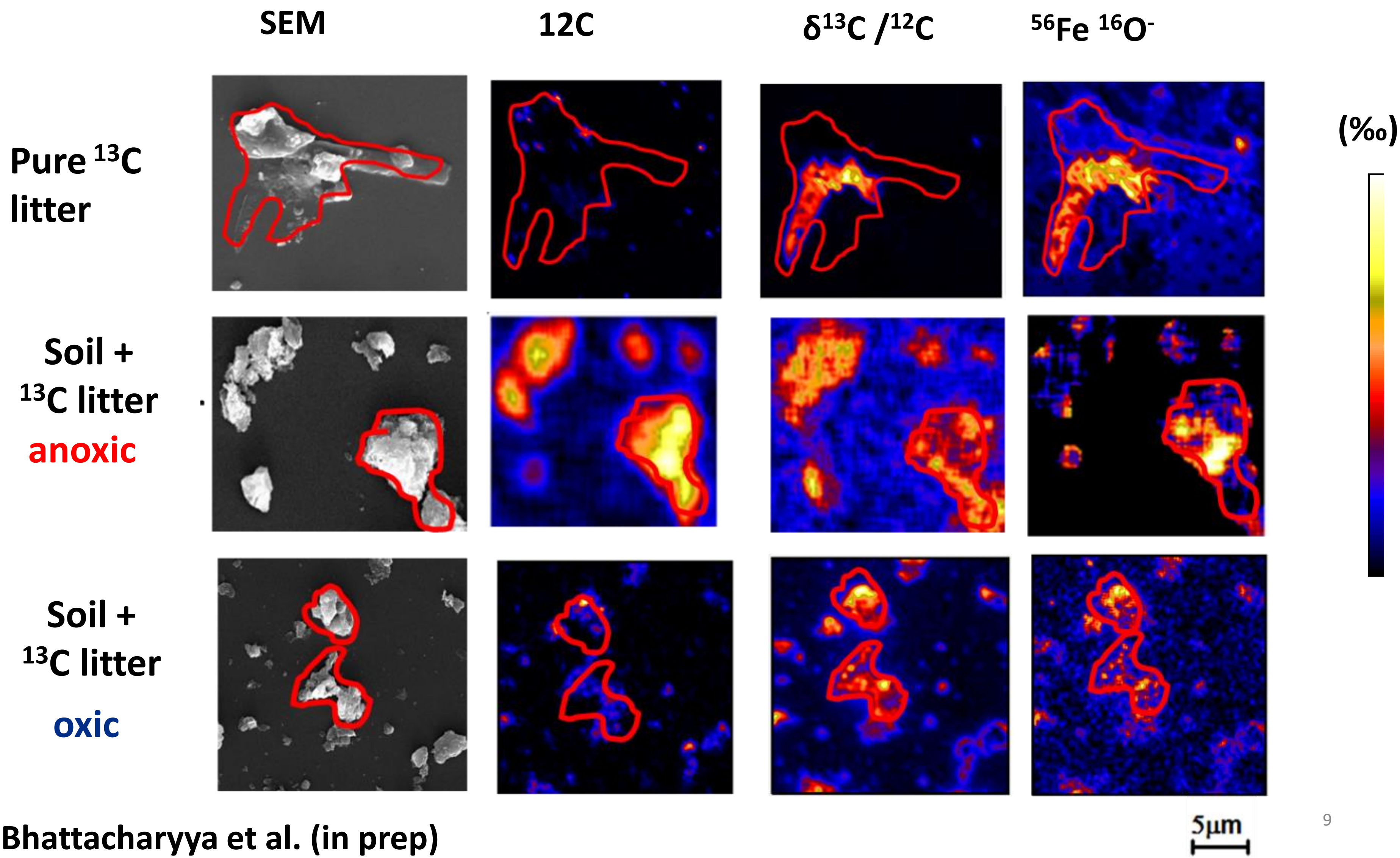




Mean C:P ratios of microbial biomass in LEF soils incubated with oxic or anoxic conditions (10 d) and then amended with glucose and potassium phosphate at different C:P ratios.

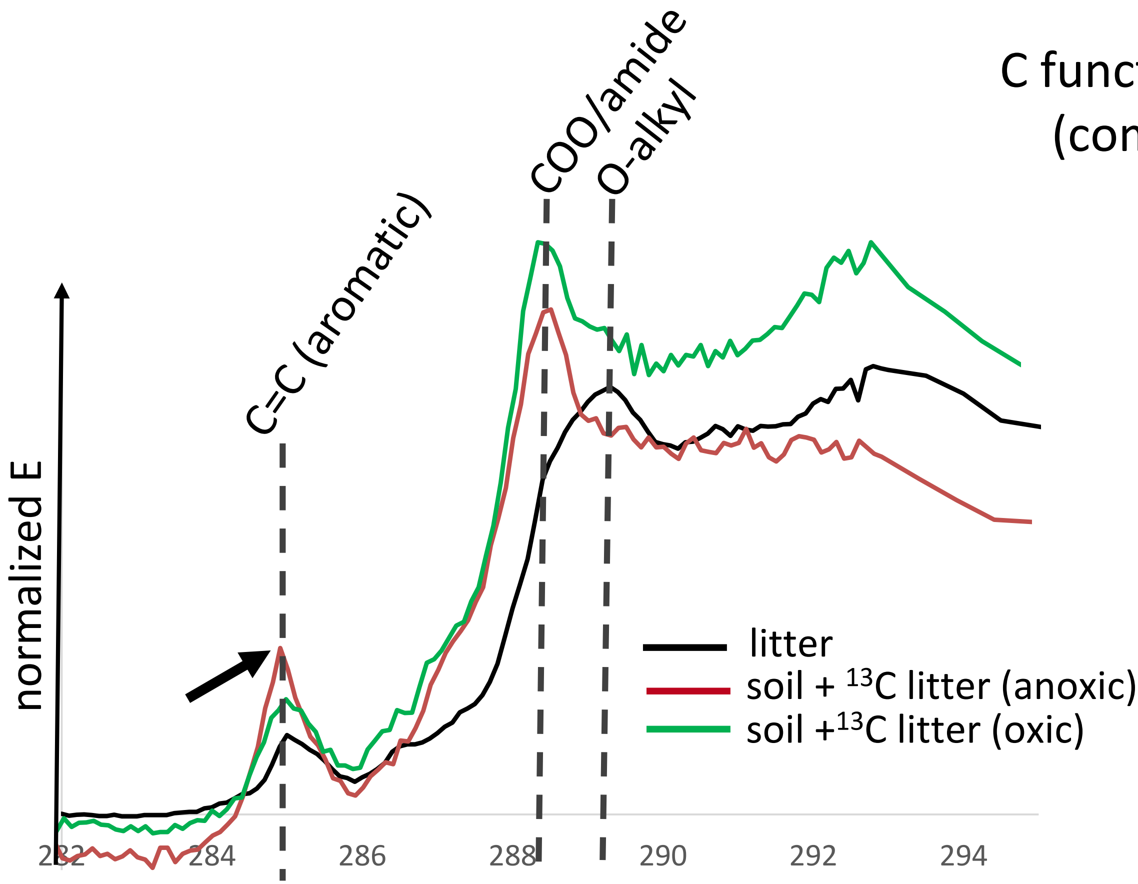
Gross, Lin et al. ***Ecology*** **(in press)**

^{13}C enriched organic matter is associated with iron oxide surfaces



Bhattacharyya et al. (in prep)

Aromatic components are 'left behind' in anoxic soils



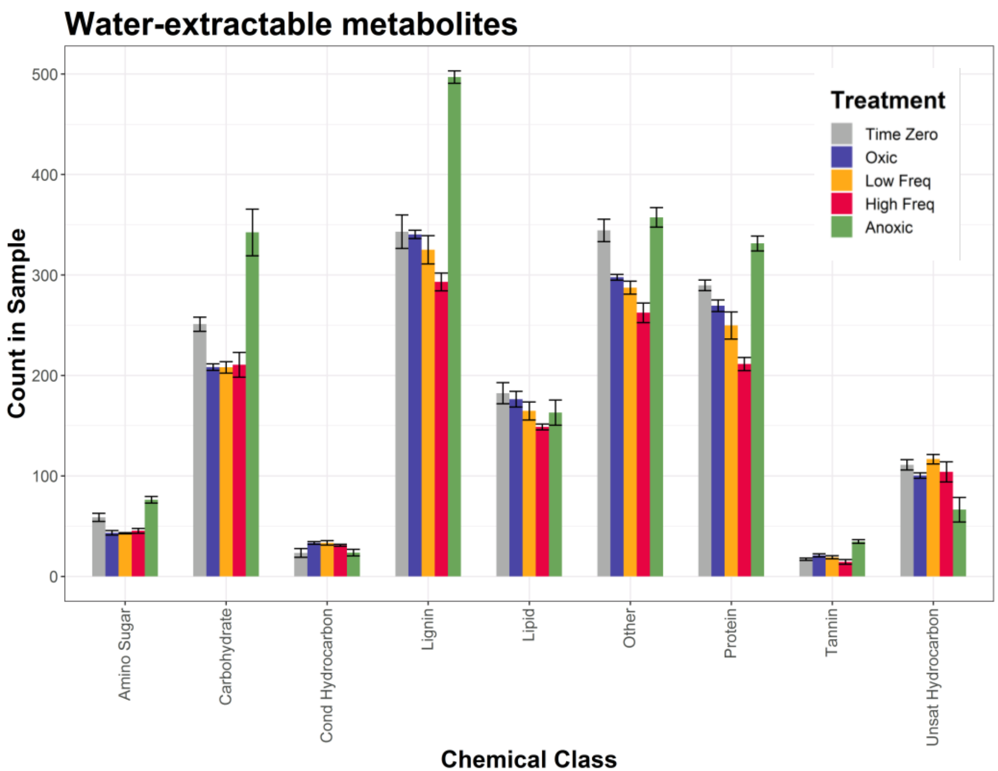
C 1s NEXAFS

C functional groups of ^{13}C hotspots (combined STXM/NEXAFS and nanoSIMS)

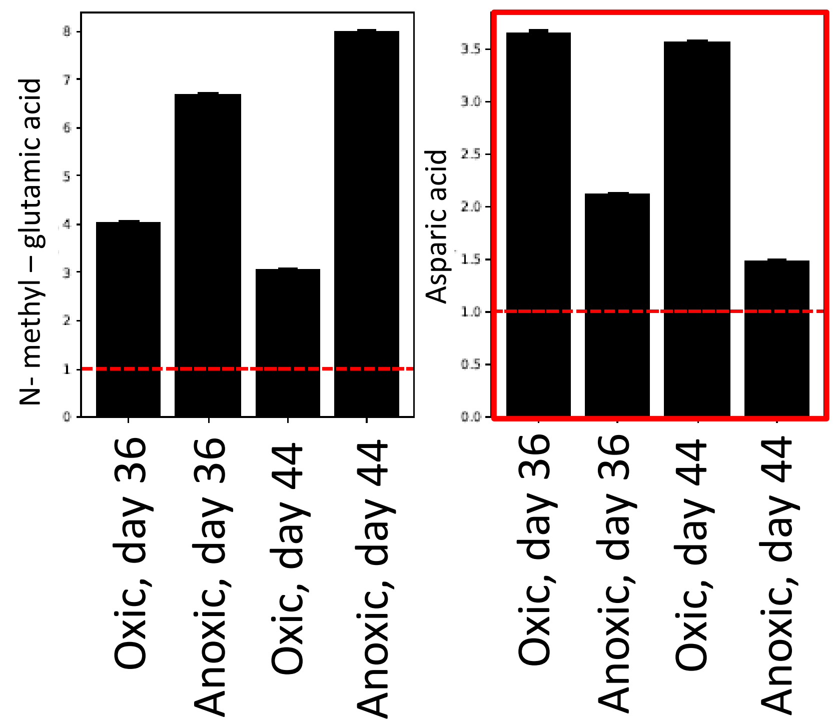
- Composition of C remaining from added ^{13}C litter differs in oxic vs. anoxic soils
- Anoxic soils show an accumulation of aromatic components
- O-alkyl residues were more common in oxic soils

Redox impacts on soil metabolites—most transformation observed for flux/oxic treatments

FTICR-MS (EMSL)

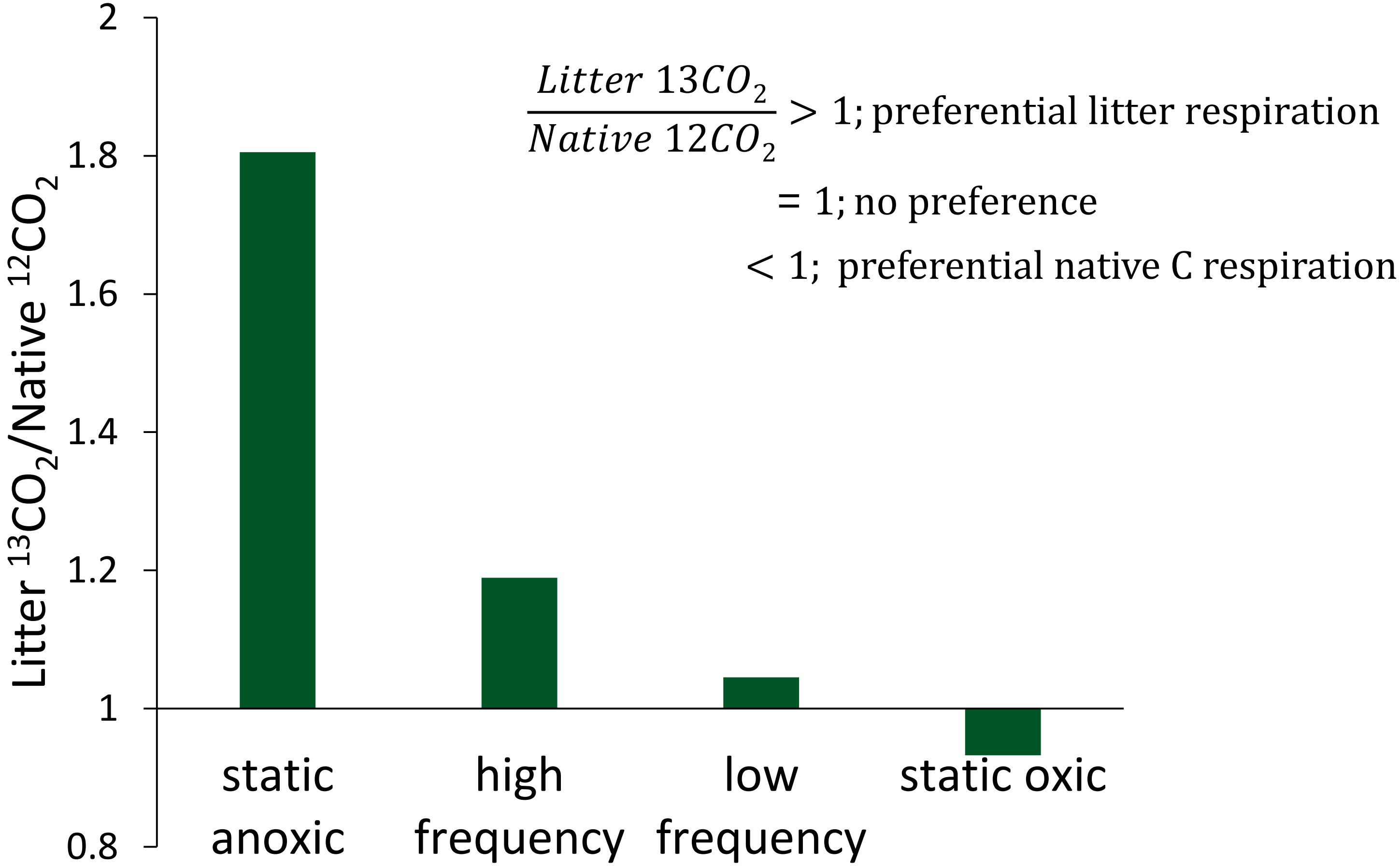


LC-MS-MS (JGI)



Campbell et al. (in prep)

Fresh litter enables rapid anoxic respiration; decomposition of pre-existing SOM is limited by [O_2] availability



- Ratio of fresh litter/native OM soil CO_2 fluxes.
- Relatively more 'fresh' litter was metabolized and respired under anoxic conditions, whereas more (pre-existing) soil-derived C was respired in oxic conditions.

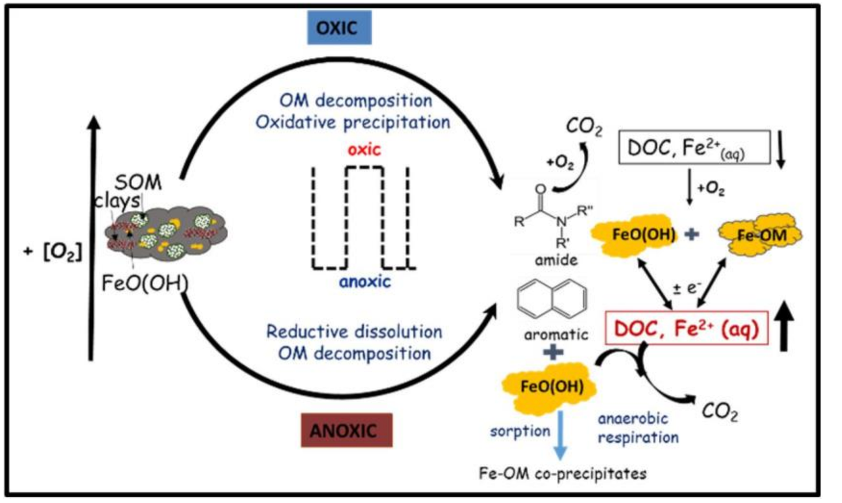
Bhattacharyya et al. *in prep;* Lin et al. *in prep.*

Messages to take away

In upland soils, rapid redox depletion is driven by precipitation-borne influxes of labile C, which drive O_2 consumption, CO_2 and H_2 production.

In Fe oxide rich tropical soils, oscillation between crystalline and amorphous forms provides brief pulses of DOC, which are rapidly consumed.

Oscillation promotes rapid microbial use of fresh C. Average soil O_2 is a poor predictor of BGC fluxes.

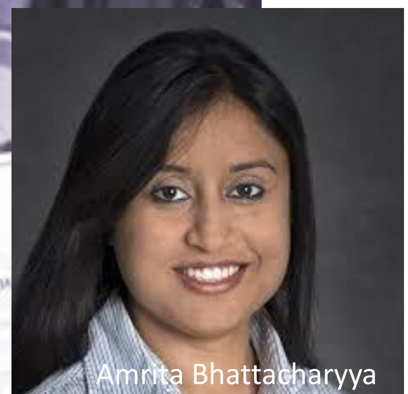


Multi-day shifts in soil redox status do not dramatically restructure the bacterial communities. Instead, taxa appear tolerant of redox changes, which play different ‘chords’ on a background microbial ‘keyboard’*.

Next Steps…

TRACE
Tropical Responses to
Altered Climate Experiment

<u>Their</u> next steps…



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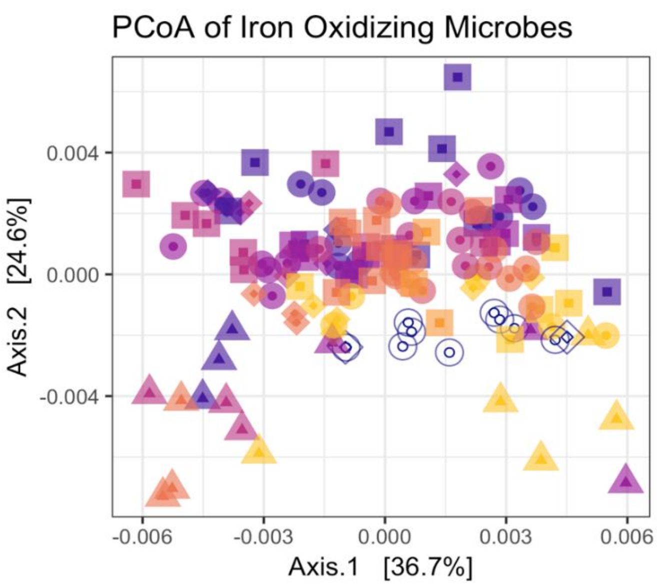
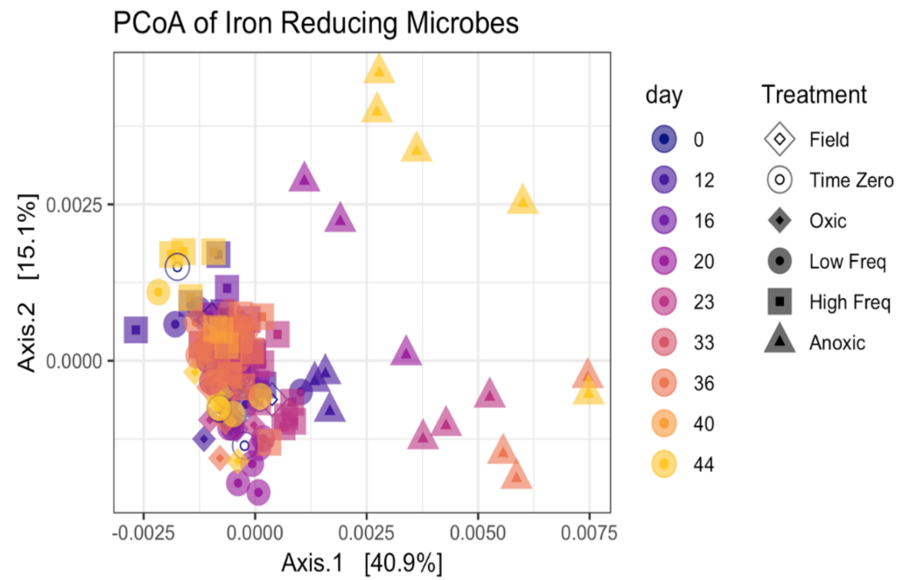
Composition of iron cycling microbes is impacted by soil redox—stronger response in the reducer community



Sphaerotilus spp.
Rhodomicrobium spp.
Pseudomonas spp.
Dechloromonas spp.
Chromobacterium spp.



Klebsiella spp.
Geothrix spp.
Geobacter spp.
Desulfovibrio spp.
Desulfosporosinus spp.
Desulfitobacterium spp.
Bacillus spp.
Anaeromyxobacter spp.
Acidocella spp.
Acidiphilium spp.