The microbial ecology of soil carbon across scales

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Florida CO$_2$ experiment
\[ \uparrow \text{CO}_2 \rightarrow \uparrow \text{C storage?} \]
Ambient CO₂  Elevated CO₂

- aboveground litter
- fine root
- coarse root
- soil

Hungate et al., New Phytologist, 2013
$\uparrow \text{CO}_2 \rightarrow \uparrow \text{C storage?}$
Ambient CO₂ Elevated CO₂

aboveground litter
fine root
coarse root

soil

Hungate et al., New Phytologist, 2013
Soil Carbon, Light fraction, g C m⁻²

Ambient CO₂ → soil carbon

Carney, Hungate, Drake & Megonigal,
PNAS, 2007; Hungate et al. New Phytologist, 2013b
Soil organic matter → CO₂ → soil organic matter
Soil organic matter
$^{13}\text{C}\text{-glucose}$
$^{13}$C-glucose

$^{13}$C-methane

$^{13}$C-carbon dioxide

$^{18}$O-H$_2$O
low GC $\rightarrow$ high GC

low $\rightarrow$ high

density
uses glucose for growth
grows, but not with glucose
Mau et al., 2015, ISME
↑sugar $\rightarrow$ ↑Priming

Microbial biodiversity
Mau et al., in review, ISME
Proportion of 16S gene copy number

**Arthrobacter**

- $^{16}$O-$\text{H}_2\text{O}$
- $^{18}$O-$\text{H}_2\text{O}$

Values:
- $^{16}$O-$\text{H}_2\text{O}$: 1.68<br>$^{18}$O-$\text{H}_2\text{O}$: 1.70

Graph shows the proportion of 16S gene copy number with data points at 1.68 and 1.70 for $^{16}$O-$\text{H}_2\text{O}$ and $^{18}$O-$\text{H}_2\text{O}$ respectively.
For each density fraction, $k$, estimate abundance of taxon, $i$, for each sample, $j$, as the product of relative abundance of $i$ in total assemblage, $f$

$$y_{ijk} = p_{ijk} \cdot f_{jk}$$

Sum across density fractions for each taxon, $i$

$$y_{ij} = \sum_{k=1}^{K} y_{ijk}$$

Calculate the weighted average density for each taxon

$$W_{ij} = \sum_{k=1}^{K} x_{jk} \cdot \left( \frac{y_{ijk}}{y_{ij}} \right)$$

Increase in weighted average density with isotope uptake $\sim$ increase in molecular weight of the labeled DNA ($M_{LABi}$)

$$M_{LABi} = \left( \frac{Z_i}{W_{LIGHTi}} + 1 \right) \cdot M_{LIGHTi}$$

Calculate atom fraction excess isotope composition, $A$, for each taxon, $i$

$$A_{OXYGENi} = \frac{M_{LABi} - M_{LIGHTi}}{M_{HEAVYMAXi} - M_{LIGHTi}} \cdot (1 - 0.002000429)$$
Week 1
Slope = 1.71
r = 0.84

Week 6
Slope = 0.85
r = 0.76

Dominant Phyla
- Acidobacteria
- Actinobacteria
- Chloroflexi
- Firmicutes
- Gemmatimonadetes
- Proteobacteria
- TM7

Relative Abundance
- 0.02
- 0.04
- 0.06

Morrissey et al., in review
### Equation

\[
N_{\text{TOTAL}i} = N_{\text{LIGHT}i} + N_{\text{HEAVY}i}
\]

\[
N_{\text{LIGHT}i} = N_{\text{TOTAL}i} \left( \frac{M_{\text{HEAVY}i} - M_{\text{LAB}i}}{M_{\text{HEAVY}i} - M_{\text{LIGHT}i}} \right)
\]

\[
d_i = \ln \left( \frac{N_{\text{LIGHT}i}}{N_{\text{LIGHT}i0}} \right) \cdot \frac{1}{t}
\]

\[
b_i = \ln \left( \frac{N_{\text{TOTAL}i}}{N_{\text{LIGHT}i}} \right) \cdot \frac{1}{t}
\]

\[
d_i + b_i = r_i
\]

### Translation

- **Total organisms =** labeled organisms plus unlabeled organisms
- **Unlabeled organisms =** total organisms x proportion unlabeled
- **Mortality is how fast unlabeled organisms disappear**
- **Birth or reproduction is how fast new labeled organisms appear**
- **birth + death = net growth (r)**

Ben Koch et al., in prep
Normal distribution of growth rate

Growth Rate, \( r \), (day\(^{-1} \))

Net growth rate rank (by genera)

Ben Koch et al. in prep
Organic Carbon

CO₂
Organic Carbon

Biosynthesis

CO$_2$
pyruvate
Pyruvate dehydrogenase catalyzes the conversion of pyruvate into Acetyl coenzyme A (Acetyl CoA), which then enters the Krebs cycle. The reaction is as follows:

\[ \text{Pyruvate} \rightarrow \text{Acetyl CoA} \]

This step is a key point in glycolysis where the three-carbon pyruvate molecule is converted into a two-carbon molecule, allowing for the entry into the citric acid cycle for further energy production.
Isocitrate
\[ \text{H}_2\text{C}-\text{COO}^- \]
\[ \text{H}-\text{C}-\text{COO}^- \]
\[ \text{HO}-\text{C}-\text{COO}^- \]
\[ \text{H} \]

Isocitrate dehydrogenase

\[ \text{CO}_2 + \]
\[ \text{H}_2\text{C}-\text{COO}^- \]
\[ \text{H}-\text{C}-\text{H} \]
\[ \text{O=O}-\text{C}-\text{COO}^- \]

\( \alpha \)-ketoglutarate

Glycolysis

Krebs cycle
\[ \alpha\text{-ketoglutarate} \]
\[ \begin{array}{c}
\text{H}_2\text{C}−\text{COO}^− \\
\text{H}−\text{C}−\text{H}
\end{array} \]
\[ \text{O=H}−\text{COO}^− \]

\[ \text{dehydrogenase} \]

\[ \alpha\text{-ketoglutarate} \]
\[ \begin{array}{c}
\text{H}_2\text{C}−\text{COO}^− \\
\text{H}−\text{C}−\text{H}
\end{array} \]
\[ \text{O=H}−\text{S−CoA} \]

\[ \text{CO}_2 + \]

\[ \text{succinyl coenzyme-A} \]

Krebs cycle

glycolysis
Carbon use efficiency of microbial communities: stoichiometry, methodology and modelling

Abstract
Carbon use efficiency (CUE) is a fundamental parameter for ecological models based on the physiology of microorganisms. CUE determines energy and material flows to higher trophic levels, conversion of plant-produced carbon into microbial products and rates of ecosystem carbon storage. Thermodynamic calculations support a maximum CUE value of $\approx 0.60$ ($\text{CUE}_{\text{max}}$). Kinetic and stoichiometric constraints on microbial growth suggest that CUE in multi-resource limited natural systems should approach $\approx 0.3$. 

maximum CUE 0.6  actual CUE $\approx 0.3$
Accelerated microbial turnover but constant growth efficiency with warming in soil

Shannon B. Hagerty¹, Kees Jan van Groenigen¹,², Steven D. Allison³, Bruce A. Hungate¹,², Egbert Schwartz¹, George W. Koch¹,², Randall K. Kolka⁴ and Paul Dijkstra¹,²*
Mycorrhizal association as a primary control of the CO₂ fertilization effect

César Terrer,¹ Sara Vicca,² Bruce A. Hungate,³,⁴ Richard P. Phillips,⁵ I. Colin Prentice¹,⁶
Nitrogen availability
Mycorrhizal Type
\( \otimes \text{CO}_2 \)
Fumigation Technology
Precipitation
Ecosystem Type
Duration of experiment
Temperature
Vegetation Age

Sum of Akaike Weights

Terrer et al., 2016, Science
Arbuscular mycorrhizae
Ecto-mycorrhizae

% bimoass response to elevated CO$_2$

Terrer et al., 2016, Science
Effect of CO$_2$ on Soil C Accumulation (E-A, g C m$^{-2}$ y$^{-1}$)

Hungate et al., Global Change Biology 2009
2-pool model of soil C over time

\[
\text{Input } (I) \quad \xrightarrow{f} \quad \text{Fast C pool } (C_f) \quad \xrightarrow{(1-CUE) \cdot k_{\text{fast}}} \quad \text{CO}_2 \\
\xrightarrow{(1-f)} \quad \text{Slow C pool } (C_s) \quad \xrightarrow{k_{\text{slow}}} \quad \text{CO}_2
\]

Van Gestel et al., in review
\[ C_t = C_0 e^{-kt} + \frac{l}{k} (1 - e^{-kt}) \]
\[ C_t = C_0 e^{-kt} + \frac{1}{k} (1 - e^{-kt}) \]

van Groenigen, et al., 2014, *Science*
\[ C_t = C_0 e^{-kt} + \frac{l}{k} (1 - e^{-kt}) \]

\[ C_t = C_0 e^{-k_{\text{old}}t} + \frac{l}{k_{\text{new}}} (1 - e^{-k_{\text{new}}t}) \]
\[ C_t = C_0 e^{-k_{\text{old}} t} + \frac{I}{k_{\text{new}}} (1 - e^{-k_{\text{new}} t}) \]

effect of elevated CO₂, %

van Groenigen, et al., 2014, *Science*
Significant changes in the skin microbiome mediated by the sport of roller derby

James F. Meadow, Ashley C. Bateman, Keith M. Herkert, Timothy K. O’Connor, Jessica L. Green

PeerJ 1:e53 https://dx.doi.org/10.7717/peerj.53
Colonization of the human nose by *Staphylococcus aureus*: community predictors

Threshold densities predict *S. aureus* carriage

Liu et al., in review
Male Circumcision Significantly Reduces Prevalence and Load of Genital Anaerobic Bacteria


Circumcision → lower bacterial abundance, especially anaerobes