Warming rate drives microbial limitation and enzyme expression during peat decomposition

Patrick W. Inglett, Debjani Sihi*, and Kanika S. Inglett

Soil and Water Sciences Department
University of Florida, Gainesville FL

*Now at Oak Ridge National Laboratory, Oak Ridge TN
Decomposition Models
(Modified from Allison et al., 2010)

SOC - Soil organic C; DOC - Dissolved organic C; MBC - Microbial biomass C; CUE - C use efficiency; Vmax & Km - Enzyme kinetic parameters

Vmax, Km

SOC → DOC → MBC → CUE → CO₂ + CH₄

Enzymes

Warming

CUE, CO₂, CH₄

Warming Response

Thermal acclimation

SOC - Soil organic C; DOC - Dissolved organic C; MBC - Microbial biomass C; CUE - C use efficiency; Vmax & Km - Enzyme kinetic parameters
Objective

• Determine effect of warming rate on enzyme kinetic parameters for C, N, P related enzymes in contrasting soils

Hypotheses

– 1: Changes in Vmax/Km would be less in slow warming treatment than in rapid
– 2: Observed changes in Vmax/Km would be reflective of microbial nutrient stoichiometry
Methods
Inglett and Reddy, 2006
Sihi et al., 2016, 2017
Methods: Warming

Parameters Monitored
- CO₂, CH₄ (Continuous)
- Enzyme $V_{\text{max}}$ & $K_m$ (Mult. Pts)
- Microbial Biomass C/N/P (Mult. Pts)

<table>
<thead>
<tr>
<th>Enzymes analyzed</th>
<th>Abbreviations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enzyme Group</td>
<td>Enzyme Name</td>
</tr>
<tr>
<td>C acquisition enzyme</td>
<td>β-D-glucosidase</td>
</tr>
<tr>
<td></td>
<td>β-D-xylanidase</td>
</tr>
<tr>
<td>N acquisition enzyme</td>
<td>Leucine aminopeptidase</td>
</tr>
<tr>
<td></td>
<td>N-Acetyl-β-D glucosaminidase</td>
</tr>
<tr>
<td>P acquisition enzyme</td>
<td>Phosphomonoesterase</td>
</tr>
<tr>
<td></td>
<td>Phosphodiesterase</td>
</tr>
</tbody>
</table>
Warming Rate Effect

CO$_2$ + CH$_4$ (µg g$^{-1}$ day$^{-1}$)

F1-high nutrient

U3-low nutrient

C use efficiency (%)

Microbial biomass C (mg kg$^{-1}$)

Days

Sihi et al., 2017
C Acquisition Enzymes

**BG V_max**
- **High nutrient-F1**: step, ramp, control
- **Low nutrient-U3**: step, ramp, control

**XYL V_max**
- **High nutrient-F1**: step, ramp, control
- **Low nutrient-U3**: step, ramp, control

**BG K_m**
- **High nutrient-F1**: control, ramp, step
- **Low nutrient-U3**: control, ramp, step

**XYL K_m**
- **High nutrient-F1**: control, ramp, step
- **Low nutrient-U3**: control, ramp, step
N Acquisition Enzymes

**LAP**
- **Vmax** (μmol g⁻¹ hr⁻¹)
  - **Km** (μM)
- **Vmax** over time (Days)
  - **step**
  - **ramp**
  - **control**
- **Km** over time (Days)
  - **High nutrient-F1**
  - **Low nutrient-U3**

**NAG**
- **Vmax** (μmol g⁻¹ hr⁻¹)
- **Km** (μM L⁻¹)
- **Vmax** over time (Days)
- **Km** over time (Days)
**Microbial Biomass Stoichiometry**

<table>
<thead>
<tr>
<th></th>
<th>Init./Contr.</th>
<th>Step/Fast</th>
<th>Ramp/Slow</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>C:N</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N-Limited Site</td>
<td>12.3</td>
<td>6.5</td>
<td>11.5</td>
</tr>
<tr>
<td>P-Limited Site</td>
<td>7.3</td>
<td>3.9</td>
<td>8.8</td>
</tr>
<tr>
<td><strong>C:P</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N-Limited Site</td>
<td>37</td>
<td>13</td>
<td>46</td>
</tr>
<tr>
<td>P-Limited Site</td>
<td>73</td>
<td>27</td>
<td>105</td>
</tr>
<tr>
<td><strong>N:P</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N-Limited Site</td>
<td>3</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>P-Limited Site</td>
<td>10</td>
<td>7</td>
<td>12</td>
</tr>
</tbody>
</table>
Enzyme Ratios vs. Biomass & Dissolved Pool

(a) y = -0.12ln(x) + 0.58
R² = 0.70, p=0.0002

(b) y = -0.26ln(x) + 0.84
R² = 0.49, p<0.0001

(c) y = -1.13ln(x) + 4.7
R² = 0.86, p<0.0001

(d) y = -0.80ln(x) + 3.7
R² = 0.91, p<0.0001

(e) y = -3.02ln(x) + 6.83
R² = 0.95, p<0.0001

(f) y = -1.99ln(x) + 5.29
R² = 0.98, p<0.0001

(g) y = -0.13ln(x) + 0.51
R² = 0.68, p=0.0004

(h) y = -0.52ln(x) + 1.09
R² = 0.45, p<0.0001

(i) y = -0.87ln(x) + 2.81
R² = 0.31, p<0.0001

(j) y = -0.49ln(x) + 2.83
R² = 0.41, p<0.0001

(k) y = -5.38ln(x) + 8.84
R² = 0.97, p<0.0001

(l) y = -4.04ln(x) + 7.88
R² = 0.91, p<0.0001
Summary

• Apparently different endpoints (alternate states) under contrasting warming rates
  – CO₂ & CH₄, microbial identity
  – Biomass stoichiometry, enzyme expression

• Microbial demand likely drives enzyme kinetics
  – Greater C demand vs. nutrients under fast warming rate
  – More N vs. P starvation under fast warming rate

• Findings identify need for improved representation of warming in decomposition models.
  – Parameterization experiments as well as inclusion of stoichiometry
Stoichiometric Model

Pool$_1$: C and N (or P)

Pool$_2$: C only

V$_{max1}$, K$_m1$

V$_{max2}$, K$_m2$

DON (or P)

MBN (or P)

MBN (or P)

MBC

DOC

N(orP)Enz

C Enz

CO$_2$ + CH$_4$ (Modified from Moorhead et al., 2012)
Thank you!

- Authors would like to thank:
  - Dr. Mark Clark
  - Joshua R. Papacek, Dorah K. Foster
  - Dr. Stefan Gerber
- The project was supported by National Science Foundation (NSF) grant DEB 0841596.