Integration of microbial communities into large-scale ecosystem models

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Diverse microbial communities drive biogeochemical processes

- Genetic and metabolic diversity:
  - $10^9$ bacteria/fungi per gram soil
  - $10^7$ bacteria per ml seawater

- Challenge: Integrate microbes into models
Example: Soil warming model

sensu Schimel and Weintraub, 2003
Explaining ephemeral CO$_2$ response to warming (e.g. Melillo et al. 2002)

- Substrate depletion: CO$_2$ respiration returns to control levels because SOC pools are depleted.

- Thermal adaptation (or acclimation): Microbial physiological parameters change in a way that reduces CO$_2$ respiration.

- Focus on Carbon Use Efficiency
  \[ = \frac{\text{C assim}}{\text{C uptake}} \]
Warming with constant CUE

Temperature

CO₂ Flux (mg/g/h)

Control vs. Warm + Const CUE

Microbial Biomass/Enzymes (mg/g)

SOC (mg/g)

Years

Variable CUE eliminates C losses!
Acclimation of CUE restores losses

Graphs showing changes in CUE, CO₂ flux, microbial biomass/ enzymes, and SOC over years.
When might we need to model microbial communities explicitly?

Taxon-specific contribution to process rate changes with disturbance
How do we aggregate taxa in microbial communities?

- Total biomass or implicit biomass (e.g. k-values)
- Based on phylogeny
- Based on functional traits
A lesson from dynamic vegetation models

- DGVMs incorporate plant functional types
- Aggregation based on leaf traits, growth form, and phenology
- E.g. “deciduous broadleaf trees”
Processes may be broad or narrow (Schimel, 1995).

Many versus few microbial groups contribute.
Trait-based aggregation also possible (e.g. Moorhead and Sinsabaugh 2006)
Models of microbial processes across scales

- Single-cell enzyme foraging and uptake: Vetter et al. 1998
- Population/simple community at ~100 micron scale: Allison 2005
- Ecosystem to global scale: CENTURY
Spatial aggregation hypothesis
Research needs

- Explicit modeling of microbial communities
- Data on microbial physiological parameters and distribution across taxa
  - Isolation and manipulation
  - Functional gene distributions
- Measurements of processes across scales

Questions?