Temperature-driven Shifts in Soil Microbial Community Composition Are Not Soil Dependent

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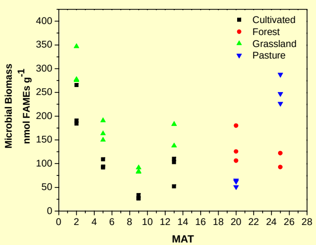
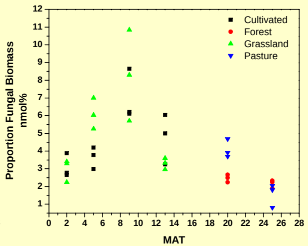
Our research indicates that the temperature sensitivity of soil organic matter (OM) decomposition **increases** with decreasing soil OM lability. Thus, as temperature increases the rate of decomposition also increases due to **metabolism of more recalcitrant organic matter** rather than by increasing the decomposition rate of labile material. An important corollary hypothesis is that the abundance of microbes able to decompose more recalcitrant organic matter increases with increasing temperature.

To test this hypothesis we began by examining microbial community composition using fatty acid methyl ester (FAME) profiling of mollisols collected across a series of sites with widely varying mean annual temperatures (MAT).

Trends in Microbial Biomass Across Temperature Gradient

MAT, °C	Precip, mm	Site	Silt+Clay, %
2	400	Indian Head, SK	83
5	400	Mandan, ND	71
9	420	Akron, CO	70
13	475	Bushland, TX	70
20	2520	Costa Rica	allophanic
25	1550	Brazil	65-70





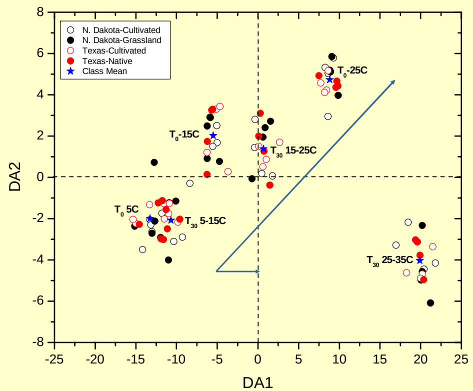
- Microbial biomass (MB) from cultivated (wheat) and forest/grassland sites follows a parabolic trend with increasing MAT. Annual precipitation was **not** a factor in this trend.
- Fungal biomass dominated MB at intermediate MAT, declining at colder and warmer MAT. A similar relationship to Ct was found by Amelung et al. (Soil Sci. Soc. Am. J. 63-86, 1999) for fungal biomass by the aminosugar method.
- Bacterial dominance at colder and warmer MAT may be related to preferential stabilization within aggregates, rates of soil organic matter turnover, and differing temperature sensitivities of microbial species.

We then selected two soils (North Dakota and Texas, with cultivated and native grassland vegetation) and incubated soils at 5, 15 or 25 ºC for 150 days and then raised the temperature 10 ºC, assessing microbial community composition before (T_0) and 30 days (T_{30}) after the temperature bump.

Microbial Biomass Response to Temperature Bump

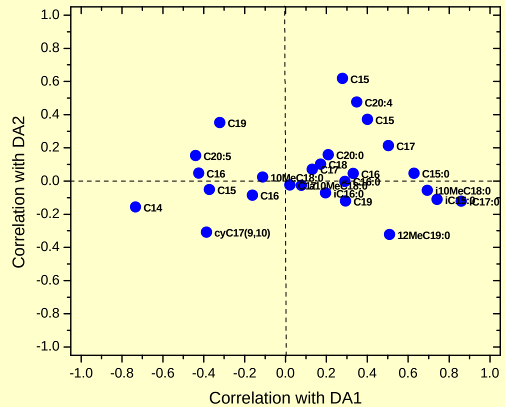
- Regardless of soil, shifts in MB in response to temperature were similar among all four soils, with Texas having a lower overall microbial biomass than North Dakota.
- MB decreased as incubation temperature increased.
- In N. Dakota, there was no change in MB due to the bump. However, in Texas there was a decrease in MB in the 15-25 bump, only, for both the cultivated and grassland soils.

Discriminant Analysis of Microbial FAME Profiles



- We found consistent changes in the lipid profiles of the soil microbial community in response to temperature despite differing community structure among the soils.
  - Diagonal shift in community profile with increasing temperature of incubation
  - Smaller shift along axis DA1 for temperature bump of 10 ºC, but with large negative shift along DA2 after 30 days incubation at 35 ºC.
- Although this in part may signal a membrane response within individual cells, it most likely represents a community shift due to the large number of fatty acids included in the discriminant model.

Correlation of FAMEs with the Discriminant Axes



- Although fungal biomass showed a hyperbolic response to the temperature gradient in the field, the fungal biomarkers, C18:2(9,11) and C18:1(9), did not factor into the discriminant analysis.
- With the exception of two eukaryotic markers, C20:4 and C20:5, the separation among temperature treatments was largely driven by changes in the bacterial community.
- Branched-chain fatty acids, particularly iso-branched and 10-methyl branched fatty acids, increased in relative abundance with temperature and may indicate dominance of gram positive organisms.
- Actinobacteria responded positively to the 25 to 35 ºC temperature bump, and due to their diverse catabolic abilities, may suggest degradation of more recalcitrant organic matter such as lignin.

Conclusions

- Results from this research will provide insight into soil organic matter stability under pressures from global warming across a large MAT gradient.
- Furthermore, it will direct future research on microbial adaptations to global temperature change.

Acknowledgements

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