Microbial Extracellular Enzyme Activity and Community Assembly Post Fire Disturbance

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Introduction

- Microbes regulate major biogeochemical cycles (Nemergut *et al*. in press).
- The factors that directly impact microbial community assemblies and extracellular enzyme activity (EEA).
- Two microbial assembly processes are: neutral, or stochastic, and niche-based, or deterministic.
- The relationship between microbial community assemblage and EEA in response to burn events was analyzed by comparing unburned plot samples and burned plot samples in order to further our knowledge of microbial community assemblies and biogeochemical processes
- This study draws on samples from the Fourmile Canyon Fire, which occurred in September 2010 in the Rocky Mountain Front Range adjacent to Boulder, Colorado in steep, rugged terrain (Graham *et al*. 2012).

Figure 1: Burned plot; July 18, 2013.

Figure 2: Unburned plot, July 18, 2013.

Methods

- Each treatment, October 2010 burned plots and January 2011 unburned and burned plots, had 8 samples.
- DNA extractions were conducted for 16S rRNA genes and microbial metagenomics were inferred by 16S rRNA phylogenics using PICRUSt.
- Fluorimetric assays measured potential NAG and BG enzyme activity.
- Soil moisture, pH, and total carbon and nitrogen for all samples; ammonium, dissolved organic nitrogen (DON), and dissolved organic carbon (DOC) were only measured for 16 week samples.
- Correlations, ANOVAs, and linear stepwise regressions were conducted using the R statistical platform (R Development Core Team 2011).

Figure 4A (top left) Soil sample collection from unburned site July 2013.

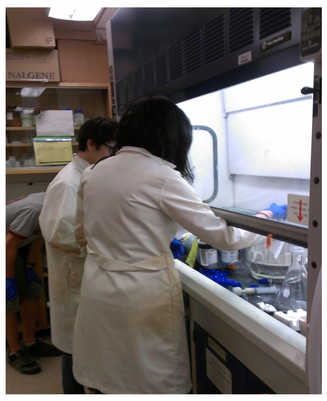

Figure 5B (bottom left). Fumigating samples with chloroform in order to measure DOC and DON.

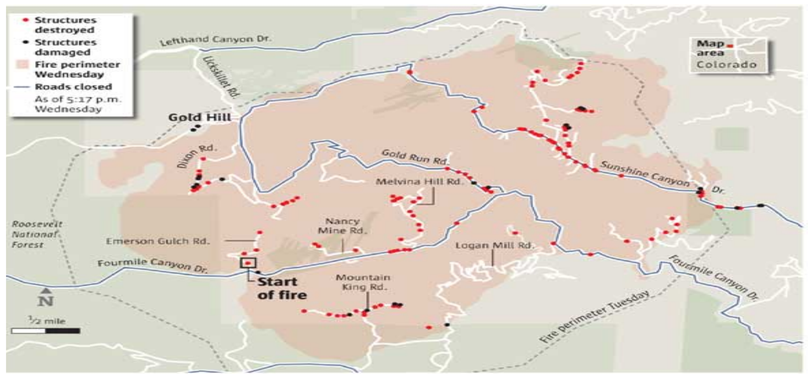

Figure 3. Map showing the extent of the Fourmile Canyon fire in relation to Gold Hill that occurred in September 2010. Soils were sampled near the southeastern edge of the Fourmile Fire (40.039N, 105.3891W) on the eastern slope of the Colorado Front Range (Ferrenberg *et al*. 2013). (http://www.denverpost.com/news/ci_16021847)

Results

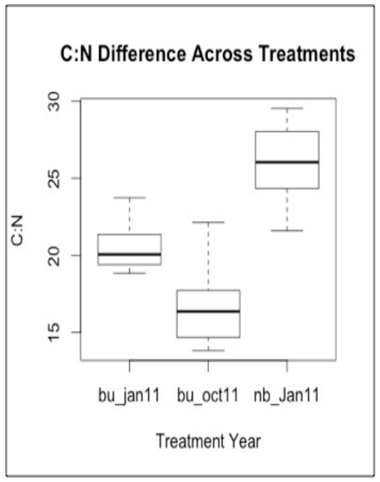

Figure 6. Boxplot of C:N ratio difference (overall p-value=6.66e-7) across the three treatments (October 2010 burned, January 2011 burned, & January 2011 unburned).

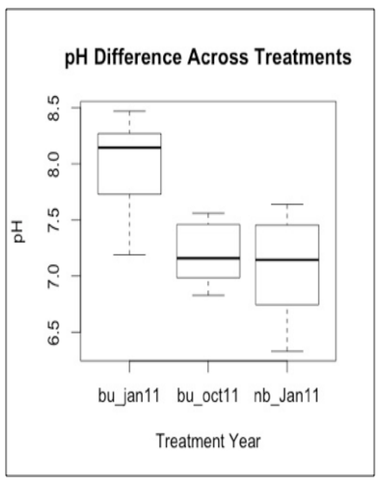

Figure 7 (left). Boxplot of pH difference (overall p-value=0.0003) across the three treatments (October 2010 burned, January 2011 burned, & January 2011 unburned).

Process		Edaphic Model	Microbial Model	Overall Model
BG	Predictors	n/s	n/s	n/s
	Statistical Results	n/s	n/s	n/s
NAG	Predictors	n/s	PCO1_w_actino, PCO3_oct_b10	n/s
	Statistical Results	n/s	Model P= 0.006 Adjusted R^2 = 0.882	n/s

Table 1. Models created by regressions from October 2010 burned plots. Only edaphic models were found significant (alpha=0.05) for these data.

Process		Edaphic Model	Microbial Model	Overall Model
BG	Predictors	n/s	n/s	n/s
	Statistical Results	n/s	n/s	n/s
NAG	Predictors	pH, C_N_biomass	n/s	n/s
	Statistical Results	Model P=0.047 Adjusted R^2 = 0.587	n/s	n/s

Table 2. Models created by regressions from January 2011 unburned plots. No significant (alpha=0.05) microbial models were found.

Process		Edaphic Model	Microbial Model	Overall Model
BG	Predictors	mg.N_g_dry_soil_DON, mg.C_g_drysoil_DOC, percent_Nitrogen, C_N	PCO3_beta, PCO1_acido	PCO3_beta, Mg.C_g_drysoil_DOC
	Statistical Results	Model P=0.035 Adjusted R^2 =0.861	Model P=0.046 Adjusted R^2 =0.592	Model P=0.027 Adjusted R^2 = 0.669
NAG	Predictors	mg.C_g_drysoil_DOC, percent_Nitrogen	n/s	n/s
	Statistical Results	Model P=0.029 Adjusted R^2 =0.778	n/s	n/s

Table 3. Models created by regressions from January 2011 unburned plot data. Overall model was created since both microbial and edaphic models were significant.

Discussion

- For October 2010 burned, microbial models significantly predicted NAG activity, suggesting stochastic assembly. Because actinobacteria and NAG enzymes assist in carbon cycling, this phyla may be particiulary important to understanding post fire carbon cycling.
- A shift occurred from 4-week samples to 16-week samples as edaphic models significantly predicted NAG activity in January 2011 burned samples, suggesting edaphic predictors are more important than microbial predictors in carbon cycling here.
- January 2011 unburned samples were significantly predicted by edaphic and microbial models. This could be interpreted as the edaphic factors driving the microbial enzyme activity.

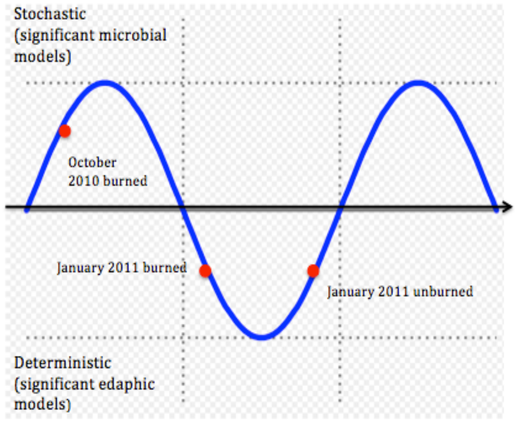

Figure 8. Conceptual model of shift in assembly processes through time for samples. Adapted from Ferrenberg *et al.* (2013).

Conclusion

- Post fire, microbial community assembly began stochastically and progressed into assembling deterministically.
- Ferrenberg *et al.* (2013) hypothesized that over longer time scales, the environment will become less harsh and neutral processes will become the more important factor in structuring community assembly.
- The data presented here show that microbial community diversity is more important to predicting EEA shortly after disturbance, correlating with a shift in stochastic to deterministic microbial community assembly processes.
- The relationship between microbial community assembly processes and EEA is vital in understanding the implications for the future biogeochemical cycling following an environment disturbed by fire .

References

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