Supplemental Figure 1

Dissolved organic carbon assessed at the end of the experiment: carbon only effect. Displayed on boxplots are the median, the two hinges of the box represent the interquartile range, and the whiskers extend 1.5 \* interquartile range, outlying points are plotted individually. Different letters denote statistically significant treatment effects based on pairwise comparisons adjusted using Tukey’s test., alpha = 0.1. Different letters denote statistically significant treatment effects based on pairwise comparisons adjusted using Tukey’s test., alpha = 0.1.



Supplemental Figure 2: Simpson Diversity for the carbon source x soil moisture effect (A), and the carbon source effect (BDisplayed on boxplots are the median, the two hinges of the box represent the interquartile range, and the whiskers extend 1.5 \* interquartile range, outlying points are plotted individually. Different letters denote statistically significant treatment effects based on pairwise comparisons adjusted using Tukey’s test., alpha = 0.1.



Supplemental Figure 3 The phyla retained in the best-subsets multiple regression, and that had significant C amendment interaction with moisture for microbial activity. Dendrograms on heat maps reflect similarity of relative abundance patterns of phyla between carbon treatments (complete-linkage clustering) - they do not reflect phylogenetic relationships.



Supplemental Figure 4: The most abundant families found in each of phyla retained in the best-subsets multiple regression, and that had significant C amendment effects for microbial activity (A), and total extractable N (B). Dendrograms on heat maps reflect similarity of relative abundance patterns of phyla between carbon treatments (complete-linkage clustering) - they do not reflect phylogenetic relationships.



Supplemental Table 1: The top 8 families with greater than 0.1% abundance from the phyla that were retained in the best-subsets multiple regression models; \* *P* < 0.1, \*\* *P* < 0.05, N.S. (Not significant) *P* > 0.1.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phyla | Family | Relative Abundance | Carbon | Carbon X Moisture |
| Actinobacteria | Gaiellaceae | 0.0083 | \* | \*\* |
| 67-14 | 0.0071 | \*\* | N.S. |
| Mycobacteriaceae | 0.0063 | \*\* | \*\* |
| Nocardioidaceae | 0.0058 | \*\* | N.S. |
| Solirubrobacteraceae | 0.0046 | N.S. | N.S. |
| Micrococcaceae | 0.0043 | \*\* | N.S. |
| Micromonosporaceae | 0.0039 | N.S. | N.S. |
| Pseudonocardiaceae | 0.0025 | N.S. | N.S. |
| Bacteroidetes | Chitinophagaceae | 0.0433 | \*\* | \*\* |
| Microscillaceae | 0.0193 | \*\* | \*\* |
| env.OPS\_17 | 0.0081 | N.S. | N.S. |
| Flavobacteriaceae | 0.0075 | N.S. | \*\* |
| Saprospiraceae | 0.0063 | \*\* | N.S. |
| AKYH767 | 0.0059 | N.S. | N.S. |
| KD3-93 | 0.0013 | \*\* | \*\* |
| BSV26 | 0.0012 | \* | N.S. |
| Chloroflexi | A4b | 0.0022 | \* | \*\* |
| Roseiflexaceae | 0.0014 | \*\* | N.S. |
| Proteobacteria | Xanthobacteraceae | 0.0672 | \* | N.S. |
| Nitrosomonadaceae | 0.0439 | N.S. | N.S. |
| Methylophilaceae | 0.0317 | \*\* | \*\* |
| Burkholderiaceae | 0.0289 | \*\* | \*\* |
| SC-I-84 | 0.0145 | N.S. | N.S. |
| Unknown\_Family | 0.0145 | \* | N.S. |
| Steroidobacteraceae | 0.0132 | N.S. | N.S. |
| Sphingomonadaceae | 0.0114 | \*\* | \*\* |
| Verrucomicrobia | Chthoniobacteraceae | 0.0371 | \*\* | \* |
| Pedosphaeraceae | 0.0293 | N.S. | N.S. |
| Xiphinematobacteraceae | 0.0047 | \*\* | N.S. |
| Opitutaceae | 0.0034 | N.S. | \* |
| Verrucomicrobiaceae | 0.0013 | \*\* | N.S. |
| Rubritaleaceae | 0.0011 | N.S. | N.S. |