

Unearthing the microbial ecology of soil carbon cycling with DNA-SIP

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Submitted to Proceedings of the National Academy of Sciences of the United States of America

Abstract

We explored the dynamics of microbial carbon (C) decomposition in soil by coupling DNA Stable Isotope Probing (SIP) and high throughput sequencing. Our experiment evaluated the degradative succession hypothesis, described dynamics of C metabolism during organic matter degradation, and characterized bacteria that metabolize labile and structural C in soils. We added a complex amendment representing plant derived organic matter to soil substituting ^{13}C -xylose or ^{13}C -cellulose for unlabeled equivalents in two experimental treatments. Xylose and cellulose are abundant components in plant biomass and represent labile and structural C pools, respectively. We assessed ^{13}C assimilation into DNA for SSU rRNA gene OTUs finding evidence of ^{13}C -incorporation from ^{13}C -xylose and ^{13}C -cellulose in 49 and 63 OTUs, respectively. Microorganisms primarily assimilated xylose-C into DNA on days 1, 3, and 7 and cellulose-C on days 14 and 30. The types of microorganisms that assimilated xylose-C changed with time initially dominated by *Firmicutes* at day 1 followed by *Bacteroidetes* at day 3 and then *Actinobacteria* at day 7. Temporal dynamics of ^{13}C -labeling suggests C traveled through different trophic levels within the bacteria. Microbes that metabolized cellulose-C belonged to cosmopolitan soil lineages that remain uncharacterized physiologically including *Spartobacteria*, *Chloroflexi* and *Planctomycetes*. Our study links microorganisms to specific soil C processes revealing ecological properties of specific microbial lineages and functionally defined groups of microbes within complex communities.

stable isotope probing | structure-function relationships | soil microbial ecology | 16S rRNA gene

Abbreviations: C, Carbon; OTU, Operational Taxonomic Unit; SOM, Soil Organic Matter; BD, Buoyancy Density; SIP, Stable Isotope Probing

Significance

Soil microorganisms drive C flux through the terrestrial biosphere and accounting for microbial

physiological diversity improves global C models. But, characterizing the ecophysiology of microbes involved with C decomposition in soil has proven difficult due to their overwhelming diversity. We characterized C use of microbial taxa in soil and show different C forms have distinct decomposition dynamics governed by different microbial lineages. For example, we found microbes belonging to poorly characterized but cosmopolitan taxa in soils assimilated cellulose-C into DNA. These microbes may drive cellulose decomposition on a global scale. We identify microbial lineages engaging in labile and structural C decomposition and explore their ecological properties.

Introduction

Soils worldwide contain 2,300 Pg of carbon (C) which accounts for nearly 80% of the C present in the terrestrial biosphere [1, 2]. C respiration by soil microorganisms produces annually tenfold more CO_2 than fossil fuel emissions [3]. Despite the contribution of microorganisms to global C flux, many global C models ignore microbial physiological diversity and its impacts on microbial activity in soils. [4–6]. Further, predictions of climate change feedbacks on soil C flux improve when biogeochemical models explicitly represent microbial physiology [7]. However, we still know little about the ecophysiology of soil microorganisms, and such knowledge should assist the development and refinement of global C models [8–10].

Cellulose comprises most plant C (30-50%) followed by hemicellulose (20-40%), and lignin (15-

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25%) [11]. Hemicellulose, being the most soluble, degrades in the early stages of decomposition. Xylans are often an abundant component of hemicellulose, and xylans themselves include differing amounts of xylose, glucose, arabinose, galactose, mannose, and rhamnose [12]. Xylose is often the most abundant sugar in hemicellulose, comprising as much as 60–90% of xylan in some plants (e.g. hardwoods) [13], wheat [14], and switchgrass [15]. Microbes that respire sugars proliferate during the initial stages of decomposition [16, 17], and metabolize as much as 75% of sugar C during the first 5 days of decomposition [18]. In contrast, cellulose decomposition proceeds more slowly with rates increasing for approximately 15 days while degradation continues for 30–90 days [18, 19]. It is hypothesized that different microbial guilds mediate the decomposition of different plant biomass components [19–22]. The degradative succession hypothesis posits that fast growing organisms proliferate in response to the labile fraction of plant biomass such as sugars [23, 24] followed by slow growing organisms targeting structural C such as cellulose [23]. Evidence to support the degradative succession hypothesis comes from observing soil respiration dynamics and characterizing microbes cultured at different stages of decomposition. The degree to which the succession hypothesis presents an accurate model of litter decomposition has been called into question [21, 25, 26] and it’s clear that we need new approaches to dissect microbial contributions to C transformations in soils.

Though microorganisms mediate 80–90% of the soil C-cycle [27, 28], and microbial community composition can account for significant variation in C mineralization [29], terrestrial C-cycle models rarely consider the community composition of soils [30, 31]. We measure rates of soil C transformations without knowledge of the organisms that mediate these reactions [28] leaving undefined the importance of community membership towards maintaining ecosystem function [28, 32, 33]. Variation in microbial community composition can be linked effectively to rates of soil processes when diagnostic genes for specific functions are available (e.g. denitrification [34], nitrification [35–37], methanotrophy [38], and nitrogen fixation [39]). However, the complexity of soil C transformations and the lack of diagnostic genes for describing these transformations has limited progress in characterizing the contributions of individual microbes to the soil C-cycle. Remarkably, we still lack basic information on the physiology and ecology of the majority of organisms that live in soils. For example, contributions to soil processes remain uncharacterized for entire and cosmopolitan bacterial phyla in soil such as *Acidobacteria*, *Chloroflexi*, *Planctomycetes*, and *Verrucomicrobia*. These phyla combined can

comprise 32% of soil microbial communities (based on surveys of the SSU rRNA genes in soil) [40, 41].

Characterizing the functions of microbial taxa has relied historically on culturing microorganisms and subsequently characterizing physiology in the laboratory and on environmental surveys of genes diagnostic for specific processes. However, most microorganisms are difficult to grow in culture [40] and many processes lack suitable diagnostic genes. Nucleic acid stable-isotope probing (SIP) links genetic identity and activity without the need to grow microorganisms in culture and has expanded our knowledge of microbial contributions to biogeochemical processes [42]. However, nucleic acid SIP has notable complications including the need to add large amounts of labeled substrate [43], label dilution resulting in partial labelling of nucleic acids [43–45], the potential for cross-feeding and secondary label incorporation [45–50], and variation in genome G+C content [51–54]. As a result, most applications of SIP have targeted specialized microorganisms such as methanotrophs [43], methanogens [55], syntrophs [56], or microbes that target pollutants [57]. SIP has proved less useful for exploring the soil C-cycle because it has lacked the resolution necessary to manage effectively the signal complexity that results from adding components of plant biomass to microbial communities in soil. High throughput DNA sequencing technology, however, improves the resolving power of SIP [58].

Coupling SIP with high throughput DNA sequencing now enables exploration of microbial C-cycling in soils. SSU rRNA amplicons can be sequenced from numerous density gradient fractions across multiple samples thereby increasing the resolution of a typical nucleic acid SIP experiment [59]. It is now possible to use far less isotopically labeled substrate resulting in more environmentally realistic experimental conditions [58]. We have employed such a high resolution DNA stable isotope probing approach to explore the assimilation of ¹³C labeled xylose and/or cellulose into bacterial DNA in an agricultural soil.

Specifically, we added to soil a complex amendment that simulated organic matter derived from fresh plant biomass. All treatments received the same amendment but the identity of the isotopically labeled substrate was varied between treatments. We set up a control treatment where all components were unlabeled, a treatment with ¹³C-xylose, and a treatment with ¹³C-cellulose. Soil was sampled at days 1, 3, 7, 14, and 30 and we identified which microorganisms had assimilated ¹³C into DNA at each point in time. The experiment was designed to provide a test of the degradative succession hypothesis in the context of soil bacteria, to identify soil bacteria that metabolize

xylose and cellulose, and to characterize tempo-
ral dynamics of xylose and cellulose metabolism in
soil.

Results

After adding an organic matter amendment to soil,
we tracked the flow of C from xylose or cellulose
into microbial DNA over time using DNA-SIP
(Figure S1). The amendment consisted of various
plant biomass compounds including cellulose,
lignin, sugars found in hemicellulose, amino acids,
and inorganic salts (see Supplemental Methods).
The amendment was added at 2.3 mg C g⁻¹ soil
dry weight (d.w.), and this comprised 16% of the
total C in the soil. The cellulose-C (0.88 mg C g⁻¹
soil d.w.) and xylose-C (0.42 mg C g⁻¹ soil d.w.)
in the amendment comprised 6% and 3% of the
total C in the soil, respectively. The soil microbial
community respired 65% of the xylose within one
day and 29% of the added xylose remained in the
soil at day 30 (Figure S2). In contrast, cellulose-C
declined at a constant rate of approximately 18 µg
C d⁻¹ g⁻¹ soil d.w. and 40% of added cellulose-C
remained in the soil at day 30 (Figure S2).

13C-labeling of OTUs changed with time and substrate. We assessed assimilation of ¹³C into microbial DNA by comparing the SSU rRNA gene sequence composition of SIP density gradient fractions from ¹³C treatments to control (see Methods and SI). All treatments used the same amendment which included xylose and cellulose, but ¹³C-xylose or ¹³C-cellulose was substituted for its unlabeled equivalent in two amendments. A treatment without isotopically labeled components served as the “control”. In the gradient density fractions of the control treatment, fraction density represented the majority of the variance in SSU rRNA gene composition (Figure 1). DNA buoyant density correlates positively with G+C content [51] and therefore DNA G+C content influences variation in the SSU rRNA gene composition of density gradient fractions. For the ¹³C-cellulose treatment, SSU rRNA gene composition in gradient fractions deviated from control at high density (> 1.72 g mL⁻¹) on days 14 and 30 (Figure 1). For the ¹³C-xylose treatment, SSU rRNA gene composition in density gradient fractions also deviated from control in high density fractions, but in contrast to the ¹³C-cellulose treatment it deviated from control on days 1, 3, and 7 (Figure 1). SSU rRNA gene composition from ¹³C-cellulose treatment and ¹³C-xylose treatment density fractions differed at high density indicating different microorganisms assimilated C from xylose than cellulose (Figure 1). Further, in the ¹³C-cellulose treatment, the SSU rRNA gene sequence composition of high density

fractions at days 14 and 30 was similar indicating similar microorganisms had ¹³C labeled DNA in ¹³C-cellulose treatments at days 14 and 30. In contrast, in the ¹³C-xylose treatment, the SSU rRNA gene composition high density fractions varied between days 1, 3, and 7 indicating that different microbes had ¹³C labeled DNA on these days. In the ¹³C-xylose treatment, the SSU gene composition of high density fractions was similar to control on days 14 and 30 (Figure 1) indicating that ¹³C was no longer detectable in bacterial DNA on these days for this treatment.

Temporal dynamics DNA ¹³C incorporation of OTUs. We monitored the soil microcosm microbial community over the course of the experiment by surveying SSU rRNA genes in non-fractionated DNA from the experimental soil. The SSU rRNA gene composition of the non-fractionated DNA changed with time (Figure S3, P-value = 0.023, R² = 0.63, Adonis test [60]). In contrast, the community showed no statistical evidence for changing with treatment (P-value was 0.23) (Figure S3). The latter result demonstrates the substitution of ¹³C-labeled substrates for unlabeled equivalents could not be shown to alter community composition. Twenty-nine OTUs exhibited sufficient statistical evidence (adjusted P-value < 0.10) to conclude they changed in relative abundance over the course of the experiment (Figure S4). When SSU rRNA gene abundances were combined at the taxonomic rank of “class”, the classes that changed in abundance (P-value < 0.10) were the *Bacilli* (decreased), *Flavobacteria* (decreased), *Gamma proteobacteria* (decreased), and *Herpetosiphonales* (increased) (Figure S5). Of the 29 OTUs that changed in relative abundance over time, 14 putatively incorporated ¹³C into DNA (Figure S4). OTUs that likely assimilated ¹³C from ¹³C-cellulose into DNA tended to increase in relative abundance with time whereas OTUs that assimilated ¹³C from ¹³C-xylose tended to decrease (Figure S6). OTUs that responded to both substrates did not exhibit a consistent relative abundance response over time as a group (Figure S4 and S6).

OTUs that assimilated ¹³C into DNA. If an OTU exhibited strong evidence for assimilating ¹³C into DNA, we refer to that OTU as a “responder” (see Methods for our operational definition of “responder”). The SSU rRNA gene sequences produced in this study could be distributed into 5,940 OTUs and we assessed the evidence of ¹³C incorporation into DNA from ¹³C-cellulose and ¹³C-xylose for each OTU. Forty-one OTUs responded to ¹³C-xylose, 55 OTUs responded to ¹³C-cellulose, and 8 OTUs responded to both xylose and cellulose

(Figure 2, Figure 3, Figure S7, Table S1, and Table S2). The number of xylose responders peaked at days 1 and 3 and declined with time. In contrast, the number of cellulose responders increased with time peaking at days 14 and 30 (Figure S8).

The phylogenetic composition of xylose responders changed with time and 86% of xylose responders shared > 97% SSU rRNA gene sequence identity with bacteria cultured in isolation (Figure 2 and 4). On day 1, *Bacilli* OTUs represented 84% of xylose responders and the majority of these OTUs were closely related to cultured representatives of the genus *Paenibacillus* (Table S1, Figure 3). For example, “OTU.57” (Table S1), annotated as *Paenibacillus*, had a strong signal of ¹³C-labeling at day 1 coinciding with its maximum relative abundance in non-fractionated DNA. The relative abundance of “OTU.57” declined until day 14 and did not appear to be ¹³C labeled after day 1 (Figure S9). On day 3, *Bacteroidetes* OTUs comprised 63% of xylose responders (Figure 4) and these OTUs were closely related to cultured representatives of the *Flavobacteriales* and *Sphingobacteriales* (Table S1, Figure 3). For example, “OTU.14”, annotated as a flavobacterium, had a strong signal for ¹³C labeling in the ¹³C-xylose treatment at days 1 and 3 coinciding with its maximum relative abundance in non-fractionated DNA. The relative abundance of “OTU.14” then declined until day 14 and did not show evidence of ¹³C labeling beyond day 3 (Figure S9). Finally, on day 7, *Actinobacteria* OTUs represented 53% of the xylose responders and these OTUs were closely related to cultured representatives of *Micrococcales* (Table S1, Figure 3). For example, “OTU.4”, annotated as *Agromyces*, had signal of ¹³C labeling in the ¹³C-xylose treatment on days 1, 3 and 7 with the strongest evidence of ¹³C labeling at day 7 and did not appear ¹³C labeled at days 14 and 30. “OTU.4” relative abundance in non-fractionated DNA increased until day 3 and then declined until day 30 (Figure S9). *Proteobacteria* were also common among xylose responders at day 7 where they comprised 40% of xylose responder OTUs. Notably, *Proteobacteria* represented the majority (6 of 8) of OTUs that responded to both cellulose and xylose (Figure S7).

The phylogenetic composition of cellulose responders did not change with time to the same extent as the xylose responders. Also, in contrast to xylose responders, cellulose responders often were not closely related (< 97% SSU rRNA gene sequence identity) to cultured isolates. Both the relative abundance and the number of cellulose responders increased over time peaking at days 14 and 30 (Figures 2, S8, and S6). Cellulose responders belonged to the *Proteobacteria* (46%), *Verrucomicrobia* (16%), *Planctomycetes* (16%), *Chloro-*

roflexi (8%), *Bacteroidetes* (8%), *Actinobacteria* (3%), and *Melainabacteria* (1 OTU) (Table S2).

The majority (86%) of cellulose responders in the *Proteobacteria* were closely related (> 97% identity) to bacteria cultured in isolation, including representatives of the genera: *Cellvibrio*, *Devosia*, *Rhizobium*, and *Sorangium*, which are all known for their ability to degrade cellulose (Table S2). Proteobacterial cellulose responders belonged to *Alpha-* (13 OTUs), *Beta-* (4 OTUs), *Gamma-* (5 OTUs), and *Deltaproteobacteria* (6 OTUs).

The majority (85%) of cellulose responders outside of the *Proteobacteria* shared < 97% SSU rRNA gene sequence identity to bacteria cultured in isolation. For example, 70% of the *Verrucomicrobia* cellulose responders fell within unidentified *Spartobacteria* clades (Figure 3), and these shared < 85% SSU rRNA gene sequence identity to any characterized isolate. The *Spartobacteria* OTU “OTU.2192” exemplified many cellulose responders (Table S2, Figure S9). “OTU.2192” increased in non-fractionated DNA relative abundance with time and evidence for ¹³C labeling of “OTU.2192” in the ¹³C-cellulose treatment increased over time with the strongest evidence at days 14 and 30 (Figure S9). Most *Chloflexi* cellulose responders belonged to an unidentified clade within the *Herpetosiphonales* (Figure 3) and they shared < 89% SSU rRNA gene sequence identity to any characterized isolate. Characteristic of *Chloroflexi* cellulose responders, “OTU.64” increased in relative abundance over 30 days and evidence for ¹³C labeling of “OTU.64” in the ¹³C-cellulose treatment peaked days 14 and 30 (Figure S9). Cellulose responders found within the *Bacteroidetes* fell within the *Cytophagales* contrasting with *Bacteroidetes* xylose responders that fell instead within the *Flavobacteriales* or *Sphingobacteriales* (Figure 3). *Bacteroidetes* cellulose responders included one OTU that shared 100% SSU rRNA gene sequence identity to species of *Sporocytophaga*, a genus that includes known cellulose degraders.

Characteristics of cellulose and xylose responders.

Cellulose responders, relative to xylose responders, tended to have lower relative abundance in non-fractionated DNA, demonstrated signal consistent with higher atom % ¹³C in labeled DNA, and had lower estimated *rrn* copy number (Figure 5). In the non-fractionated DNA, cellulose responders had lower relative abundance ($7e^{-4}$ (s.d. $2e^{-3}$)) than xylose responders ($2e^{-3}$ (s.d. $4e^{-3}$)) (Figure 4, P-value = 0.00028, Wilcoxon Rank Sum test). Six of the ten most common OTUs observed in the non-fractionated DNA responded to xylose, and, eight of the ten most abundant responders

to xylose or cellulose in the non-fractionated DNA
425 were xylose responders.

DNA buoyant density (BD) increases in proportion to the atom % ^{13}C of the DNA. Hence, the extent of ^{13}C incorporation into DNA can be evaluated by the difference in BD between ^{13}C -labeled
430 and unlabeled DNA. We calculated for each OTU its mean BD weighted by relative abundance to determine its “center of mass” within a given density gradient. We then quantified for each OTU the difference in center of mass between control
435 gradients and gradients from ^{13}C -xylose or ^{13}C -cellulose treatments (see SI for the detailed calculation). We refer to the change in center of mass position for an OTU in response to ^{13}C labeling as $\Delta\hat{B}D$. $\Delta\hat{B}D$ can be used to compare
440 relative differences in ^{13}C labeling between OTUs.

$\Delta\hat{B}D$ values, however, are not comparable to the BD changes observed for DNA from pure cultures which generate molecules uniform in isotopic labeling, in part because $\Delta\hat{B}D$ is based on relative
445 abundance in density gradient fractions (and not DNA concentration) and in part because all members of an OTU may not respond uniformly to the isotopic label. Cellulose responder $\Delta\hat{B}D$ (0.0163 g mL $^{-1}$ (s.d. 0.0094)) was greater than that of
450 xylose responders (0.0097 g mL $^{-1}$ (s.d. 0.0094)) (Figure 5, P-value = 1.8610e $^{-6}$, Wilcoxon Rank Sum test).

We predicted the *rrn* gene copy number for responders as described [61]. The number of *rrn*
455 gene copies a microorganism has is correlated to its ability to proliferate after rapid nutrient influx [62]. Cellulose responders possessed fewer estimated *rrn* copy numbers (2.7 (1.2 s.d.)) than xylose responders (6.2 (3.4 s.d.)) (Figures 5 and
460 S10; P = 1.878e $^{-9}$). Furthermore, the estimated *rrn* gene copy number for xylose responders was inversely related to the day of first response (P = 2.02e $^{-15}$, Figure S10, Figure 5).

We assessed phylogenetic clustering of ^{13}C -
465 responsive OTUs with the Nearest Taxon Index (NTI) and the Net Relatedness Index (NRI) [63]. We also quantified the average clade depth of cellulose and xylose responders with the consenTRAIT metric [64]. Briefly, the NRI and NTI evaluate
470 phylogenetic clustering against a null model for the distribution of a trait in a phylogeny. The NRI and NTI values are z-scores or standard deviations from the mean and thus the greater the magnitude of the NRI/NTI, the stronger the evidence for clustering (positive values) or overdispersion (negative values). NRI assesses overall clustering whereas the NTI assesses terminal clustering [65]. The consenTRAIT metric is a measure of the average clade depth for a trait in a phylogenetic
475 tree. NRI values indicate that cellulose responders clustered overall and at the tips of the phylogeny
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(NRI: 4.49, NTI: 1.43) while xylose responders clustered terminally (NRI: -1.33, NTI: 2.69). The consenTRAIT clade depth for xylose and cellulose
485 responders was 0.012 and 0.028 SSU rRNA gene sequence dissimilarity, respectively. As reference, the average clade depth is approximately 0.017 SSU rRNA gene sequence dissimilarity for arabinose (another five C sugar found in hemicellulose)
490 utilization as inferred from genomic analyses, and was 0.013 and 0.034 SSU rRNA gene sequence dissimilarity for glucosidase and cellulase genomic potential, respectively [64, 66]. These results indicate xylose responders form terminal clusters dispersed throughout the phylogeny while cellulose responders form deep clades of terminally clustered OTUs.

Discussion

We identified microorganisms participating in soil
500 C cycling using a nucleic acid SIP approach. Specifically, we observed assimilation of ^{13}C from either ^{13}C -xylose or ^{13}C -cellulose into DNA for 104 OTUs in an agricultural soil. We found ^{13}C from ^{13}C -xylose appeared to move into and then out of groups of related OTUs over time. By coupling nucleic acid SIP to high throughput sequencing we could diagnose OTU activity even when OTUs were at low relative abundance in non-fractionated DNA (e.g. on three occasions we did not detect
510 responders in the non-fractionated DNA). Our results support the degradative succession hypothesis, elucidate ecophysiological properties of soil microorganisms, reveal activity of widespread uncultured soil bacteria, and begin to piece together the
515 microbial food web in soils.

The degradative succession hypothesis predicts an ecological transition in activity during the decomposition of plant matter from microbes that decompose labile plant biomass C to those that
520 decompose structural more recalcitrant C. Our results concur with the degradative succession hypothesis. Microorganisms consumed xylose-C before cellulose-C and assimilated xylose-C into DNA faster than to cellulose-C. Xylose is major constituent of hemicellulose and is a labile component of fresh plant biomass. The phylogenetic composition of xylose responders changed between days 1, 3 and 7 and few OTUs appeared ^{13}C -labeled in the ^{13}C -xylose treatment after day 7. In
530 the ^{13}C -cellulose treatment few OTUs were ^{13}C -labeled in the beginning of the experiment but ^{13}C labelled OTUs increased at day 14 and maintained ^{13}C -labelling through day 30. Finally, few (8 of 104) OTUs appeared to metabolize both
535 xylose and cellulose meaning over 30 days cellulose responders replaced xylose responders in activity. In addition to agreeing with the degradative suc-

cession hypothesis, our results suggest complex interactions between microbes occur during labile C decomposition.

Correlations between community composition and environmental characteristics often indirectly reveal microorganisms that belong to ecologically consistent groups [67]. In this experiment, we directly identified ecological groups as a function of *in situ* metabolism and inferred group ecological properties through phylogenetic affiliation, temporal dynamics of ^{13}C -assimilation, and the extent of ^{13}C -labeling per OTU. Xylose responders grew faster than cellulose responders and appeared to assimilate C from multiple sources. Xylose responders assimilated xylose-C into DNA within 24 hours and had low ΔBD relative to cellulose responders suggesting xylose was not the sole C source used for growth. Xylose represented 20% of the amendment and 3.5% of total soil C. Xylose responders often included the most abundant OTUs within the non-fractionated DNA and had high estimated *rrn* copy number relative to cellulose responders. However, to some degree, high *rrn* gene copy number may inflate observed xylose responder relative abundance. Notably, the majority of xylose responder SSU rRNA genes (86%) matched SSU rRNA genes from cultured isolates at high sequence identity (> 97%).

Cellulose responders, on the other hand, incorporated ^{13}C into DNA after xylose responders and appeared to specialize in using cellulose as a C source. Cellulose responders grew over a span of weeks and had high ΔBD indicating cellulose remained the dominant C source for cellulose responders even though multiple sources of C were present (cellulose represented 6% of total C present in soil at the start of the experiment). Cellulose responders were also lower in relative abundance on average within the non-fractionated DNA and had lower estimated *rrn* copy number than xylose responders. The majority of cellulose responders were not close relatives of cultured isolates although a number of cellulose responders shared high SSU rRNA gene sequence identity with cultured *Proteobacteria* (e.g. *Cellvibrio*). We identified cellulose responders among phyla such as *Verrucomicrobia*, *Chloroflexi*, and *Planctomycetes* – phyla whose functions within soil communities remain unknown.

Verrucomicrobia made up 16% of the cellulose responders. *Verrucomicrobia* are cosmopolitan soil microbes [68] that can make up to 23% of SSU rRNA gene sequences in soils [68] and 9.8% of soil SSU rRNA [69]. Genomic analyses and laboratory experiments show that various isolates within the *Verrucomicrobia* are capable of methanotrophy, diazotrophy, and cellulose degradation [70, 71]. Moreover, *Verrucomicrobia* have

been hypothesized to degrade polysaccharides in many environments [72–74]. However, only one of the 15 most abundant verrucomicrobial photypes in globally distributed soil samples shared > 93% SSU rRNA gene sequence identity with a cultured isolate [68] and hence the role of soil *Verrucomicrobia* in global C-cycling remains unknown. The majority of verrucomicrobial cellulose responders belonged to two clades that fall within the *Spartobacteria* (Figure 3). *Spartobacteria* outnumbered all other *Verrucomicrobia* photypes in SSU rRNA gene surveys of 181 globally distributed soil samples [68]. Given their ubiquity and abundance in soil as well as their demonstrated incorporation of ^{13}C from ^{13}C -cellulose, *Verrucomicrobia* lineages, particularly *Spartobacteria*, may be important contributors to cellulose decomposition on a global scale.

Other notable cellulose responders include OTUs in the *Planctomycetes* and *Chloroflexi* both of which have previously been shown to assimilate ^{13}C from ^{13}C -cellulose added to soil [75]. *Planctomycetes* are common in soil [40], comprising 4 - 7% of bacterial cells in many soils [76, 77] and 7% \pm 5% of SSU rRNA [78]. Although soil *Planctomycetes* are widespread, their activities in soil remain poorly characterized. *Planctomycetes* represented 16% of cellulose responders and shared < 92% SSU rRNA gene sequence identity to their most closely related cultured isolates. *Chloroflexi* are known for metabolically dynamic lifestyles ranging from anoxygenic phototrophy to organohalide respiration [79] and are among the six most abundant bacterial phyla in soil [40]. Recent studies have focused on *Chloroflexi* roles in C cycling [79–81] and several *Chloroflexi* isolates use cellulose [79–81]. Four of the five *Chloroflexi* cellulose responders belong to a single clade within the *Herpetosiphonales* (Figure 3).

Finally, a single cellulose responder belonged to the *Melanabacteria* phylum (95% shared SSU rRNA gene sequence identity with *Vampirovibrio chlorellavorus*). The phylogenetic position of *Melanabacteria* is debated but *Melanabacteria* have been proposed to be a non-phototrophic sister phylum to *Cyanobacteria*. An analysis of a *Melanabacteria* genome [82] suggests the genomic capacity to degrade polysaccharides though *Vampirovibrio chlorellavorus* is an obligate predator of green alga [83]. The *Melanabacteria* cellulose responder did not respond to xylose so if it is predatory, it may prey specifically on structural C degraders (i.e. cellulose responders).

Responders did not necessarily assimilate ^{13}C into DNA directly from ^{13}C -xylose or ^{13}C -cellulose. In many ways, knowledge of secondary C degradation and/or microbial biomass turnover may be more interesting with respect to the soil

C-cycle than knowledge of primary degradation. The response to xylose suggests xylose-C moved through different trophic levels within the soil food web. The *Bacilli* degraded xylose first (65% of the xylose-C had been respired by day 1) representing 84% of day 1 xylose responders. *Bacilli* also comprised about 6% of SSU rRNA genes present in non-fractionated DNA on day 1. However, few *Bacilli* remained ¹³C-labeled by day 3 and their abundance declined reaching about 2% of soil SSU rRNA genes by day 30. Members of the *Bacillus* [84] and *Paenibacillus* in particular [59] have been previously implicated as labile C decomposers. The decline in relative abundance of *Bacilli* could be attributed to mortality and/or sporulation coupled to mother cell lysis. Concomitant with the decline in relative abundance and loss of ¹³C-label of *Bacilli*, *Bacteroidetes* OTUs appeared ¹³C-labeled at day 3. Finally, *Actinobacteria* appeared ¹³C-labeled at day 7 as *Bacteroidetes* xylose responders declined in relative abundance and became unlabeled. Hence, it seems reasonable to propose that *Bacteroidetes* and *Actinobacteria* xylose responders became ¹³C-labeled via the consumption ¹³C-labeled microbial biomass.

The inferred physiology of *Actinobacteria* and *Bacteroidetes* xylose responders provides further evidence that the activity dynamics represent C transfer between microbes by saprotrophy and/or predation. Most of the *Actinobacteria* xylose responders that appeared ¹³C-labeled at day 7 were members of the *Micrococcales* (Figure 3) and the most abundant ¹³C-labeled *Micrococcales* OTU at day 7 (OTU.4, Table S1) is annotated as belonging in the *Agromyces*. *Agromyces* are facultative predators that feed on the gram-positive *Luteobacter* in culture [85]. Additionally, certain types of *Bacteroidetes* can assimilate ¹³C from ¹³C-labeled *Escherichia coli* added to soil [86]. However, it is also possible that *Bacilli*, *Bacteroidetes*, and *Actinobacteria* are adapted to use xylose at different concentrations and that the observed activity dynamics resulted from changes in xylose concentration over time. If trophic transfer caused the activity dynamics, at least three different ecological groups exchanged C in 7 days. Models of the soil C cycle often exclude trophic interactions between soil bacteria (e.g. [87]), yet when soil C models do account for predators and/or saprophytes, trophic interactions are predicted to have significant effects on the fate of soil C [88].

705 Implications for soil C cycling models. Functional niche characterization for soil microorganisms is necessary to predict whether and how biogeochemical processes vary with microbial community composition. Functional niches are defined by soil microbiologists and have been successfully incor-

porated into biogeochemical process models (E.g. [88, 89]). In some C models ecological strategies such as growth rate and substrate specificity are parameters for functional niche behavior [88]. The phylogenetic breadth of a functionally defined group is often inferred from the distribution of diagnostic genes across genomes [66] or from the physiology of isolates cultured on laboratory media [64]. For instance, the wide distribution of the glycolysis operon in microbial genomes is interpreted as evidence that many soil microorganisms participate in glucose turnover [10]. However, the functional niche may depend less on the distribution of diagnostic genes across genomes and more on life history traits that allow organisms to compete for a given substrate as it occurs in the soil. For instance, fast growth and rapid resuscitation allow microorganisms to compete for labile C which may often be transient in soil. Hence, life history traits may constrain the diversity of microbes that metabolize a given C source in the soil under a given set of conditions.

Biogeochemical processes mediated by a broad array of taxa are assumed to be less influenced by 735 community change than narrow processes that involve a single, specific chemical transformation by a narrow suite of microbial participants [10, 90]. In addition, the diversity of a functionally defined group engaged in a specific C transformation is expected to correlate with C lability [10]. However, the diversity of active labile C and recalcitrant C decomposers in soil has not been directly quantified. We found comparable numbers of OTUs responded to ¹³C-cellulose and ¹³C-xylose (63 and 49, respectively). We also found that cellulose responders are phylogenetically clustered, and this suggests that the ability to degrade cellulose is phylogenetically conserved. The clade depth of cellulose responders, 0.028 SSU rRNA gene sequence dissimilarity, is on the same order as that observed for glycoside hydrolases which are diagnostic enzymes for cellulose degradation [66]. Xylose responders clustered in terminal branches indicating groups of closely related taxa used xylose 755 but xylose responders also clustered phylogenetically with respect to time of first response (Figure 3, Figure 4). For example, xylose responders on day 1 are dominated by members of *Paenibacillus*. Thus, microorganisms that degraded labile C and structural C were both limited in diversity. Although the genes for xylose metabolism are likely widespread in the soil community, it's possible limited groups of organisms had the ecological characteristics required to degrade xylose under the experimental conditions. Therefore it's possible few phylogenetically coherent taxa actually participate in the metabolism of labile C-sources under a given set of conditions, and hence changes in community

composition may alter the dynamics of structural ⁸²⁰ and labile C-transformations in soil.

Broadly, we observed labile C use by fast growing generalists and structural C use by slow growing specialists. These results agree with the MIMICS model which simulates leaf litter decomposition by ⁷⁷⁵ modeling the microbial decomposers as two functionally defined groups, copiotrophs or oligotrophs [89]. Including these functional types improved the predictions of C storage in response to environmental change relative to models that did not consider ⁷⁸⁰ any microbial physiological diversity. We identified microbial lineages engaged in labile and structural C decomposition or simply, copiotrophs and oligotrophs. We also observed potentially greater turnover – and at the very least rate differences ⁷⁸⁵ in turnover – for copiotroph biomass relative to oligotroph biomass which may be important to consider when modeling microbial turnover input to SOM. It's also clear that there may be more than two vital functional types mediating ⁷⁹⁰ C-cycling in soil. That is, C in soil may travel through many microbial trophic levels where each C transfer represents an opportunity for C stabilization in association with soil minerals or C loss by respiration.

⁷⁹⁵ **Conclusion.** Microorganisms sequester atmospheric C and respire SOM influencing climate change on a global scale but we do not know which microorganisms carry out specific soil C transformations. In this experiment microbes from physiologically un-⁸⁰⁰ characterized but cosmopolitan soil lineages participated in cellulose decomposition. Cellulose responders included members of the *Verrucomicrobia* (*Spartobacteria*), *Chloroflexi*, *Bacteroidetes* and *Planctomycetes*. *Spartobacteria* in particular ⁸⁰⁵ are globally cosmopolitan soil microorganisms and are often the most abundant *Verrucomicrobia* order in soil [68]. Fast-growing aerobic spore formers from *Firmicutes* assimilated labile C in the form of xylose. Xylose responders within the *Bacteroidetes* ⁸¹⁰ and *Actinobacteria* are likely assimilated xylose-C by saprotrophy or predation. Our results suggest that cosmopolitan *Spartobacteria* may degrade cel-⁸¹⁵ lulose on a global scale, labile plant biomass C may travel through a trophic cascade within the bac-⁸²⁰ teria that includes predators and/or saprotrophs, and life history traits may act as a filter constraining the diversity of active microorganisms relative to those with the genomic potential for a given metabolism.

Methods

Additional information on sample collection and analytical methods is provided in Supplemental Materials and Methods.

Twelve soil cores (5 cm diameter x 10 cm depth) ⁸²⁵ were collected from six sampling locations within an organically managed agricultural field in Penn Yan, New York. Soils were sieved (2 mm), homogenized, distributed into flasks (10 g in each 250 ml flask, n = 36) and equilibrated for 2 weeks. Soils ⁸³⁰ were amended with a mixture containing 5.3 mg C g⁻¹ soil dry weight (d.w.) and brought to 50% water holding capacity. The mixture contained 38% cellulose, 23% lignin, 20% xylose, 3% arabinose, 1% galactose, 1% glucose, and 0.5% mannose by ⁸³⁵ mass, with the remaining 13.5% mass composed of an amino acid (in-house made replica of Teknova C0705) and macronutrient mixture (Murashige and Skoog, Sigma Aldrich M5524). This mixture approximates the molecular composition of switch-⁸⁴⁰ grass biomass with hemicellulose replaced by its constituent monomers [91]. We set up three parallel treatments varying the isotopically labeled component in each treatment. The treatments were ⁸⁴⁵ (1) a control treatment with all unlabeled components, (2) a treatment with ¹³C-cellulose instead of unlabeled cellulose (synthesized as described in Supplemental Methods), and (3) a treatment with ¹³C-xylose (98 atom% ¹³C, Sigma Aldrich) instead of unlabeled xylose. Other details relating ⁸⁵⁰ to substrate addition can be found in Supplemental Methods. Microcosms were sampled destructively at days 1 (control and xylose only), 3, 7, 14, and 30 and soils were stored at -80°C until nucleic acid extraction. In the manuscript figures, the abbrevi-⁸⁵⁵ ation 13CXPS refers to the 13C-xylose treatment (¹³C Xylose Plant Simulant), 13CCPS refers to the ¹³C-cellulose treatment, and 12CCPS refers to the control treatment.

We used DESeq2 (R package), an RNA-Seq differential expression statistical framework [92], to identify OTUs that were enriched in high density gradient fractions from ¹³C-treatments relative to corresponding density fractions from control treatments (for review of RNA-Seq differential expression statistics applied to microbiome OTU count data see (30)). We define “high density gradient fractions” as gradient fractions whose density falls between 1.7125 and 1.755 g ml⁻¹. Briefly, DESeq2 includes several features that enable robust ⁸⁶⁰ estimates of standard error in addition to reliable ranking of logarithmic fold change (LFC) in abundance (i.e. gamma-Poisson regression coefficients) in abundance even with low count groups where LFC can often be noisy. Further, statistical evalua-⁸⁶⁵ tion of LFC can be performed with user-selected thresholds as opposed to the often default null hypothesis that differential abundance for an OTU is

exactly zero enabling the most biologically interesting OTUs to be identified for subsequent analyses. We calculated LFC and corresponding standard errors for enrichment in ^{13}C treatments relative to control (high density fractions only) for each OTU. Subsequently, a one-sided Wald test was used to statistically assess LFC values (using corresponding standard errors). The user-defined null hypothesis for the Wald test was that LFC was less than one standard deviation above the mean of all LFC values. P-values were corrected for multiple comparisons by using the Benjamini and Hochberg method [93]. We independently filtered OTUs on the basis of sparsity prior to correcting P-values for multiple comparisons. The sparsity value that yielded the most adjusted P-values less than 0.10 was selected for independent filtering by sparsity. Briefly, OTUs were eliminated if they failed to appear in at least 45% of high density gradient fractions for a given ^{13}C /control treatment pair, these sparse OTUs are unlikely to have sufficient data to allow for the determination of statistical significance. We selected a false discovery rate of 10% to denote statistical significance.

See Supplemental Information for DNA extraction, PCR, DNA sequence quality control, OTU ecological characteristic calculations, and SIP density gradient fractionation methods.

References

- Amundson R (2001) The carbon budget in soils. *Annu Rev Earth Planet Sci* 29(1): 535–562.
- Batjes N-H (1996) Total carbon and nitrogen in the soils of the world. *Eur J Soil Sci* 47(2): 151–163.
- Chapin F (2002) Principles of terrestrial ecosystem ecology. (Springer, New York)
- Allison S-D, Wallenstein M-D, Bradford M-A (2010) Soil-carbon response to warming dependent on microbial physiology. *Nat Geosci* 3(5): 336–340.
- Six J, Frey S-D, Thiet R-K, Batten K-M (2006) Bacterial and fungal contributions to carbon sequestration in agroecosystems. *Soil Sci Soc Am J* 70(2): 555.
- Treseder K-K, Balser T-C, Bradford M-A, Brodie E-L, Dubinsky E-A, Evner V-T, et al. (2011) Integrating microbial ecology into ecosystem models: challenges and priorities. *Biogeochemistry* 109(1–3): 7–18.
- Wieder W-R, Bonan G-B, Allison S-D (2013) Global soil carbon projections are improved by modelling microbial processes. *Nat Clim Chang* 3(10): 909–912.
- Bradford M-A, Fierer N, Reynolds J-F (2008) Soil carbon stocks in experimental mesocosms
- are dependent on the rate of labile carbon, nitrogen and phosphorus inputs to soils. *Funct Ecol* 22(6): 964–974.
- Neff J-C, Asner G-P (2001) Dissolved organic carbon in terrestrial ecosystems: synthesis and a model. *Ecosystems* 4(1): 29–48.
- McGuire K-L, Treseder K-K (2010) Microbial communities and their relevance for ecosystem models: Decomposition as a case study. *Soil Biol Biochem* 42(4): 529–535.
- Lynd L-R, Weimer P-J, van Zyl W-H, Pretorius I-S (2002) Microbial cellulose utilization: fundamentals and biotechnology. *Microbiology and molecular biology reviews* 66(3): 506–table of contents.
- Saha B-C (2003) Hemicellulose bioconversion. *J Ind Microbiol Biotechnol* 30(5): 279–291.
- Spiridon I, Popa V-I (2008) Chapter 13 - Hemicelluloses: Major Sources, Properties and Applications. *Monomers, Polymers and Composites from Renewable Resources*, , eds. Belgacem M-N, Gandini A (Elsevier, New York), pp 289–304.
- Sun X-F, Xu F, Zhao H, Sun R-C, Fowler P, Baird M-S (2005) Physicochemical characterisation of residual hemicelluloses isolated with cyanamide-activated hydrogen peroxide from organosolv pre-treated wheat straw. *Bioresour Technol* 96(12): 1342–1349.
- Bunnell K, Rich A, Luckett C, Wang Y-J, Martin E, Carrier D-J (2013) Plant maturity effects on the physicochemical properties and dilute acid hydrolysis of switchgrass (*Panicum virgatum*, l.) hemicelluloses. *ACS Sustain Chem Eng* 1(6): 649–654.
- Garrett S-D (1951) Ecological groups of soil fungi: a survey of substrate relationships. *New Phytol* 50(2): 149–166.
- Alexander M (1964) Biochemical ecology of soil microorganisms. *Annual Rev Microbiol* 18(1): 217–250.
- Engelking B, Flessa H, Joergensen R-G (2007) Microbial use of maize cellulose and sugarcane sucrose monitored by changes in the $^{13}\text{C}/^{12}\text{C}$ ratio. *Soil Biol Biochem* 39(8): 1888–1896.
- Hu S, van Bruggen A-HC (1997) Microbial dynamics associated with multiphasic decomposition of ^{14}C -labeled cellulose in soil. *Microb Ecol* 33(2): 134–143.
- Rui J, Peng J, Lu Y (2009) Succession of bacterial populations during plant residue decomposition in rice field soil. *Appl Environ Microbiol* 75(14): 4879–4886.
- Kjøller A-H, Struwe S (2002) Fungal Communities, Succession, Enzymes, and Decomposition. *Enzymes in the Environment*, Books in Soils, Plants, and the Environment (Marcel Dekker, New York), pp 306–324.

22. Bastian F, Bouziri L, Nicolardot B, Ranjard L (2009) Impact of wheat straw decomposition on successional patterns of soil microbial community structure. *Soil Biol Biochem* 41(2): 262–275.
- 995 23. Garrett S-D (1963) Soil Fungi and soil fertility. (Pergamon Press, New York)
- 1000 24. Bremer E, Kuikman P (1994) Microbial utilization of $^{14}\text{C}[\text{U}]$ glucose in soil is affected by the amount and timing of glucose additions. *Soil Biol Biochem* 26(4): 511–517.
- 1005 25. Frankland J-C (1998) Fungal succession – unravelling the unpredictable. *Mycol Res* 102(1): 1–15.
- 1010 26. Osono T (2005) Colonization and succession of fungi during decomposition of Swida controversa leaf litter. *Mycologia* 97(3): 589–597.
- 1015 27. Coleman D-C, Crossley D-A (1996) fundamentals of soil ecology. (Academic Press, Waltham, Massachusetts)
- 1020 28. Nannipieri P, Ascher J, Ceccherini M-T, Landi L, Pietramellara G, Renella G (2003) Microbial diversity and soil functions. *Eur J Soil Sci* 54(4): 655–670.
- 1025 29. Strickland M-S, Lauber C, Fierer N, Bradford M-A (2009) Testing the functional significance of microbial community composition. *Ecology* 90(2): 441–451.
- 1030 30. Zak D-R, Blackwood C-B, Waldrop M-P (2006) A molecular dawn for biogeochemistry. *Trends Ecol Evol* 21(6): 288–295.
- 1035 31. Reed H-E, Martiny J-BH (2007) Testing the functional significance of microbial composition in natural communities. *FEMS Microbiol Ecol* 62(2): 161–170.
- 1040 32. Schimel J-P, Schaeffer S-M (2012) Microbial control over carbon cycling in soil. *Front Microbiol* 3: 348. doi: 10.3389/fmicb.2012.00348
- 1045 33. Allison S-D, Martiny J-BH (2008) Resistance resilience, and redundancy in microbial communities. *Proc Natl Acad Sci USA* 105(Supplement 1): 11512–11519.
- 1050 34. Cavigelli M-A, Robertson G-P (2000) The functional significance of denitrifier community composition in a terrestrial ecosystem. *Ecology* 81(5): 1402–1414.
- 1055 35. Carney K-M, Matson P-A, Bohannan B-JM (2004) Diversity and composition of tropical soil nitrifiers across a plant diversity gradient and among land-use types. *Ecol Lett* 7(8): 684–694.
- 1060 36. Hawkes C-V, Wren I-F, Herman D-J, Firestone M-K (2005) Plant invasion alters nitrogen cycling by modifying the soil nitrifying community. *Ecol Lett* 8(9): 976–985.
- 1065 37. Webster G, Embley T-M, Freitag T-E, Smith Z, Prosser J-I (2005) Links between ammonia oxidizer species composition, functional diver-
- sity and nitrification kinetics in grassland soils. *Environ Microbiol* 7(5): 676–684.
38. Gulledge J, Doyle A-P, Schimel J-P (1997) Different NH_4^+ -inhibition patterns of soil CH_4 consumption: A result of distinct CH_4 -oxidizer populations across sites? *Soil Biol Biochem* 29(1): 13–21.
39. Hsu S-F, Buckley D-H (2009) Evidence for the functional significance of diazotroph community structure in soil. *ISME J* 3(1): 124–136.
- 1070 40. Janssen P-H (2006) Identifying the dominant soil bacterial taxa in libraries of 16S rRNA and 16S rRNA genes. *Appl Environ Microbiol* 72(3): 1719–1728.
41. Buckley D-H, Schmidt T-M (2002) Exploring the diversity of soil - a microbial rainforest. *Biodiversity of Microbial Life: Foundation of Earth's Biosphere*, ed. Reysenbach A-L (Wiley, New York, New York, USA), pp 183–208.
42. Chen Y, Murrell J-C (2010) When metagenomics meets stable-isotope probing: progress and perspectives. *Trends Microbiol* 18(4): 157–163.
43. Radajewski S, Ineson P, Parekh N-R, Murrell J-C (2000) Stable-isotope probing as a tool in microbial ecology. *Nature* 403(6770): 646–649.
44. Manefield M, Whiteley A-S, Griffiths R-I, Bailey M-J (2002) RNA Stable isotope probing a novel means of linking microbial community function to phylogeny. *Appl Environ Microbiol* 68(11): 5367–5373.
45. McDonald I-R, Radajewski S, Murrell J-C (2005) Stable isotope probing of nucleic acids in methanotrophs and methylotrophs: A review. *Org Geochem* 36(5): 779–787.
46. Morris S-A, Radajewski S, Willison T-W, Murrell J-C (2002) Identification of the functionally active methanotroph population in a peat soil microcosm by stable-isotope probing. *Appl Environ Microbiol* 68(3): 1446–1453.
47. Hutchens E, Radajewski S, Dumont M-G, McDonald I-R, Murrell J-C (2004) Analysis of methanotrophic bacteria in Movile Cave by stable isotope probing. *Environ Microbiol* 6(2): 111–120.
- 1080 48. Lueders T, Manefield M, Friedrich M (2004) Enhanced sensitivity of DNA- and rRNA-based stable isotope probing by fractionation and quantitative analysis of isopycnic centrifugation gradients.. *Environ Microbiol* 6: 73–8.
- 1085 49. DeRito C-M, Pumphrey G-M, Madsen E-L (2005) Use of field-based stable isotope probing to identify adapted populations and track carbon flow through a phenol-degrading soil microbial community. *Appl Environ Microbiol* 71(12): 7858–7865.
50. Ziegler S-E, White P-M, Wolf D-C, Thoma G-J (2005) Tracking the fate and recycling of ^{13}C -

- labeled glucose in soil. *Soil Sci* 170(10): 767–778.
- 1110 51. Buckley D-H, Huangyutitham V, Hsu S-F, Nelson T-A (2007) Stable isotope probing with ^{15}N achieved by disentangling the effects₁₁₇₀ of genome G+C content and isotope enrichment on DNA density. *Appl Environ Microbiol* 73(10): 3189–3195.
- 1115 52. Birnie G-D (1978) Centrifugal separations in Molecular and cell biology. (Butterworth & Co₁₁₇₅ Publishers Ltd, Boston)
- 1120 53. Holben W-E, Harris D (1995) DNA-based monitoring of total bacterial community structure in environmental samples. *Molecular Ecology* 4(5): 627–632.
- 1125 54. Nüsslein K, Tiedje J-M (1999) Soil bacterial community shift correlated with change from forest to pasture vegetation in a tropical soil. *Appl Environ Microbiol* 65(8): 3622–3626.
- 1130 55. Lu Y, Conrad R (2005) In situ stable isotope₁₁₈₅ probing of methanogenic archaea in the rice rhizosphere. *Science* 309(5737): 1088–1090.
- 1135 56. Lueders T, Pommerenke B, Friedrich M-W (2004) Stable-isotope probing of microorganisms thriving at thermodynamic limits: syn-₁₁₉₀trophic propionate oxidation in flooded soil. *Appl Environ Microbiol* 70(10): 5778–5786.
- 1140 57. DeRito C-M, Pumphrey G-M, Madsen E-L (2005) Use of field-based stable isotope probing to identify adapted populations and track₁₁₉₅ carbon flow through a phenol-degrading soil microbial community. *Appl Environ Microbiol* 71(12): 7858–7865.
- 1145 58. Aoyagi T, Hanada S, Itoh H, Sato Y, Ogata A, Friedrich M-W, et al. (2015) Ultra-high-₁₂₀₀ sensitivity stable-isotope probing of rRNA by high-throughput sequencing of isopycnic centrifugation gradients. *Environ Microbiol Rep* 7(2): 282–287.
- 1150 59. Verastegui Y, Cheng J, Engel K, Kolczynski₁₂₀₅ D, Mortimer S, Lavigne J, et al. (2014) Multistubstrate isotope labeling and metagenomic analysis of active soil bacterial communities. *mBio* 5(4): e01157–14.
- 1155 60. Anderson M-J (2001) A new method for non-₁₂₁₀ parametric multivariate analysis of variance. *Austral Ecol* 26(1): 32–46.
- 1160 61. Kembel S-W, Wu M, Eisen J-A, Green J-L (2012) Incorporating 16S gene copy number information improves estimates of microbial₁₂₁₅ diversity and abundance. *PLoS Comput Biol* 8(10): e1002743.
- 1165 62. Klappenbach J-A, Dunbar J-M, Schmidt T-M (2000) rRNA Operon copy number reflects ecological strategies of bacteria. *Appl Environ Mi-₁₂₂₀crobiol* 66(4): 1328–1333.
63. Webb C-O (2000) Exploring the phylogenetic structure of ecological communities: an exam-
- ple for rain forest trees.. *Am Nat* 156(2): 145–155.
64. Martiny A-C, Treseder K, Pusch G (2013) Phylogenetic conservatism of functional traits in microorganisms. *ISME J* 7(4): 830–838.
65. Evans S-E, Wallenstein M-D (2014) Climate change alters ecological strategies of soil bacteria. *Ecol Lett* 17(2): 155–164.
66. Berlemont R, Martiny A-C (2013) Phylogenetic distribution of potential cellulases in bacteria. *Appl Environ Microbiol* 79(5): 1545–1554.
67. Fierer N, Bradford M-A, Jackson R-B (2007) Toward an ecological classification of soil bacteria. *Ecology* 88(6): 1354–1364.
68. Bergmann G-T, Bates S-T, Eilers K-G, Lauber C-L, Caporaso J-G, Walters W-A, et al. (2011) The under-recognized dominance of Verrucomicrobia in soil bacterial communities. *Soil Biol Biochem* 43(7): 1450–1455.
69. Buckley D-H, Schmidt T-M (2001) Environmental factors influencing the distribution of rRNA from Verrucomicrobia in soil. *FEMS Microbiol Ecol* 35(1): 105–112.
70. Wertz J-T, Kim E, Breznak J-A, Schmidt T-M, Rodrigues J-LM (2011) Genomic and physiological characterization of the Verrucomicrobia isolate *diplosphaera colitermitum* gen. nov. sp. nov., reveals microaerophily and nitrogen fixation genes. *Appl Environ Microbiol* 78(5): 1544–1555.
71. Otsuka S, Ueda H, Suenaga T, Uchino Y, Hamada M, Yokota A, et al. (2012) Roseimicrobium gellanilyticum gen. nov. sp. nov., a new member of the class Verrucomicrobiae. *Int J Syst Evol Microbiol* 63(Pt 6): 1982–1986.
72. Fierer N, Ladau J, Clemente J-C, Leff J-W, Owens S-M, Pollard K-S, et al. (2013) Reconstructing the microbial diversity and function of pre-agricultural tallgrass prairie soils in the united states. *Science* 342(6158): 621–624.
73. Chin K-J, Hahn D, Hengstmann U, Liesack W, Janssen P-H (1999) Characterization and identification of numerically abundant culturable bacteria from the anoxic bulk soil of rice paddy microcosms. *Appl Environ Microbiol* 65(11): 5042–5049.
74. Herlemann D-PR, Lundin D, Labrenz M, Jürgens K, Zheng Z, Aspeborg H, et al. (2013) Metagenomic de novo assembly of an aquatic representative of the verrucomicrobial class spartobacteria. *mBio* 4(3): e0056912.
75. Schellenberger S, Kolb S, Drake H-L (2010) Metabolic responses of novel cellulolytic and saccharolytic agricultural soil Bacteria to oxygen. *Environ Microbiol* 12(4): 845–861.
76. Zarda B, Hahn D, Chatzinotas A, Schnhuber W, Neef A, Amann R-I, et al. (1997) Anal-

- ysis of bacterial community structure in bulk soil by in situ hybridization. *Arch Microbiol* 168(3): 185–192.
77. Chatzinotas A, Sandaa R-A, Schnhuber W, Amann R, Daae F-L, Torsvik V, et al. (1998) Analysis of broad-scale differences in microbial community composition of two pristine forest soils. *Syst Appl Microbiol* 21(4): 579–587.
78. Buckley D-H, Schmidt T-M (2003) Diversity and dynamics of microbial communities in soils from agro-ecosystems. *Environ Microbiol* 5(6): 441–452.
79. Hug L-A, Castelle C-J, Wrighton K-C, Thomas B-C, Sharon I, Frischkorn K-R, et al. (2013) Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. *Microbiome* 1(1): 22.
80. Goldfarb K-C, Karaoz U, Hanson C-A, Santee C-A, Bradford M-A, Treseder K-K, et al. (2011) Differential growth responses of soil bacterial taxa to carbon substrates of varying chemical recalcitrance. *Front Microbiol* 2: 94. doi: 10.3389/fmicb.2011.00094
81. Cole J-K, Gieler B-A, Heisler D-L, Palisoc M-M, Williams A-J, Dohnalkova A-C, et al. (2013) *Kallotenu papyrolyticum* gen. nov. sp. nov., a cellulolytic and filamentous thermophile that represents a novel lineage (Kallotenuales ord. nov., Kallotenuaceae fam. nov.) within the class Chloroflexia. *Int J Syst Evol Microbiol* 63(Pt 12): 4675–4682.
82. Rienzi S-CD, Sharon I, Wrighton K-C, Koren O, Hug L-A, Thomas B-C, et al. (2013) The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. *eLIFE* 2: e01102.
83. Gromov B-V, Mamkaeva K-A (1972) [Electron microscopic study of parasitism by Bdellovibrio chlorellavorus bacteria on cells of the green alga Chlorella vulgaris]. *Tsitologiya* 14(2): 256–260.
84. Cleveland C-C, Nemergut D-R, Schmidt S-K, Townsend A-R (2007) Increases in soil respiration following labile carbon additions linked to rapid shifts in soil microbial community composition. *Biogeochemistry* 82(3): 229–240.
85. Casida L-E (1983) Interaction of *Agromyces ramosus* with other bacteria in soil.. *Appl Environ Microbiol* 46(4): 881–888.
86. Lueders T, Kindler R, Miltner A, Friedrich M-W, Kaestner M (2006) Identification of bacterial micropredators distinctively active in a soil microbial food web. *Appl Environ Microbiol* 72(8): 5342–5348.
87. Moore J-C, Walter D-E, Hunt H-W (1988) Arthropod regulation of micro- and mesobiota in below-ground detrital food webs. *Annu Rev Entomol* 33(1): 419–435.
88. Kaiser C, Franklin O, Dieckmann U, Richter A (2014) Microbial community dynamics alleviate stoichiometric constraints during litter decay. *Ecol Lett* 17(6): 680–690.
89. Wieder W-R, Grandy A-S, Kallenbach C-M, Bonan G-B (2014) Integrating microbial physiology and physio-chemical principles in soils with the MiCrobial-MIneral Carbon Stabilization (MIMICS) model. *Biogeosciences* 11(14): 3899–3917.
90. Schimel J (1995) Ecosystem consequences of microbial diversity and community structure. *Arctic and alpine biodiversity: patterns, causes and ecosystem consequences*, , eds. Chapin III F-S, Körner C, Ecological Studies (Springer, Berlin Heidelberg), pp 239–254.
91. Schneckenberger K, Demin D, Stahr K, Kuzyakov Y (2008) Microbial utilization and mineralization of ¹⁴C glucose added in six orders of concentration to soil. *Soil Biol Biochem* 40(8): 1981–1988.
92. Love M-I, Huber W, Anders S (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15(12): 550.
93. Benjamini Y, Hochberg Y (1995) Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society. Series B (Methodological)* 57(1): 289–300.

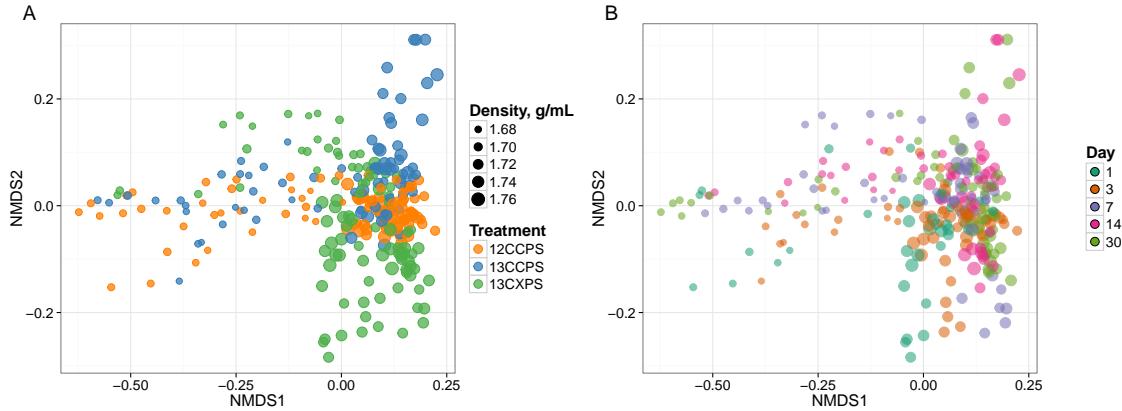


Fig. 1. NMDS analysis from weighted unifrac distances of 454 sequence data from SIP fractions of each treatment over time. Twenty fractions from a CsCl gradient fractionation for each treatment at each time point were sequenced (Fig. S1). Each point on the NMDS represents the bacterial composition based on 16S sequencing for a single fraction where the size of the point is representative of the density of that fraction and the colors represent the treatments (A) or days (B).

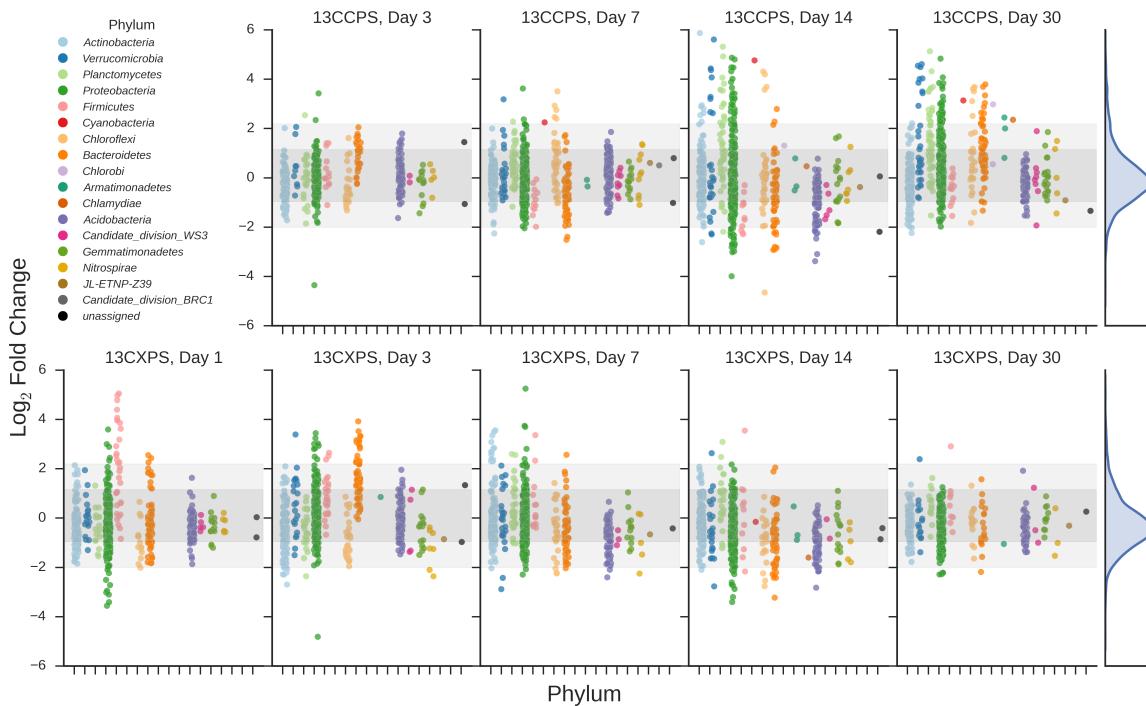


Fig. 2. Log₂ fold change of ¹³C-responders in cellulose treatment (top) and xylose treatment (bottom). Log₂ fold change is based on the relative abundance in the experimental treatment compared to the control within the density range 1.7125–1.755 g ml⁻¹. Taxa are colored by phylum. The last column shows the distribution of all fold change values in each row. The darker gray band represents one standard deviation and the lighter band represents two standard deviations about the mean of all fold change values for both treatments.

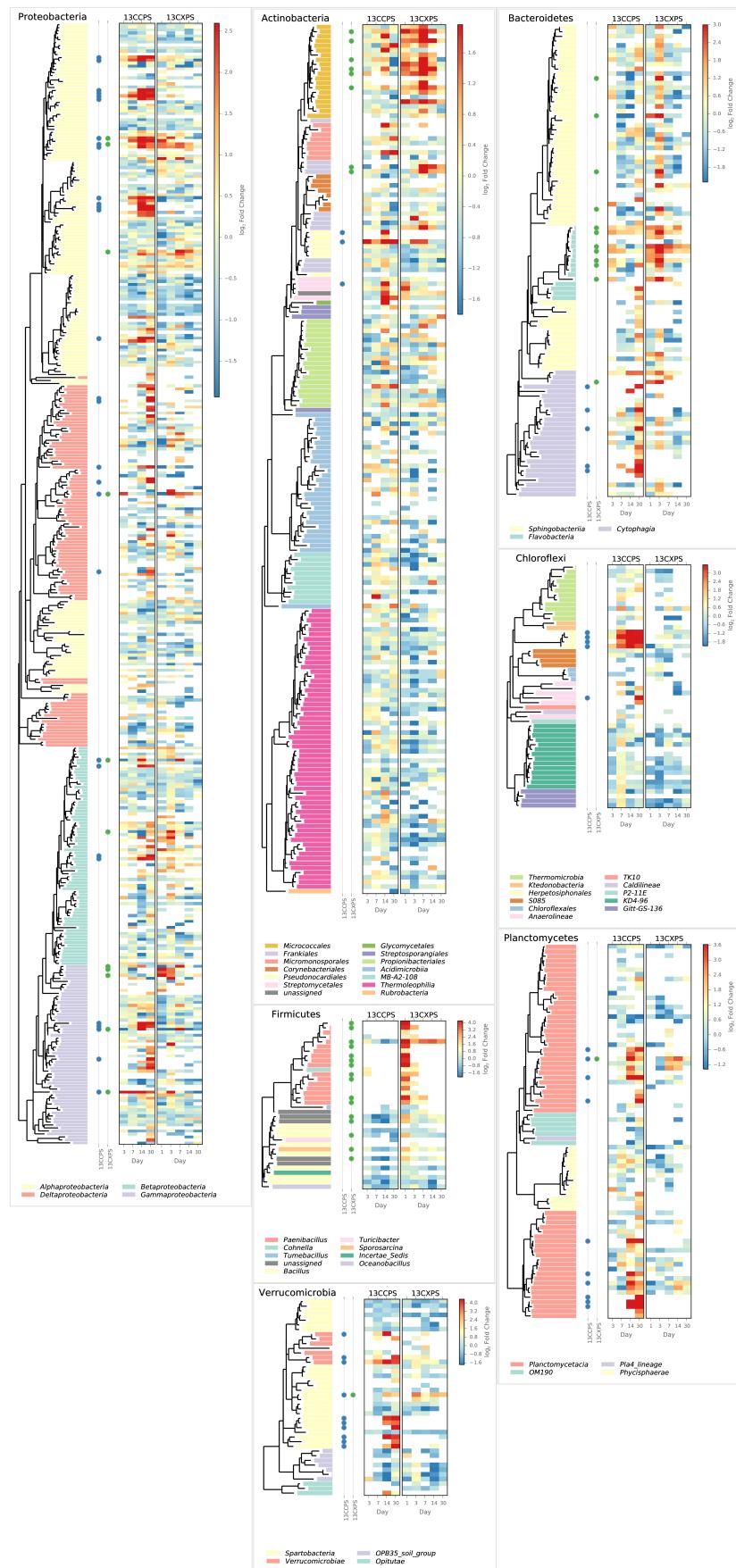


Fig. 3. Phylum specific trees. Heatmap indicates fold change between heavy fractions of control gradients versus labeled gradients. Dots indicate the position of “responders” to ^{13}C -xylose (green) or ^{13}C -cellulose (blue).

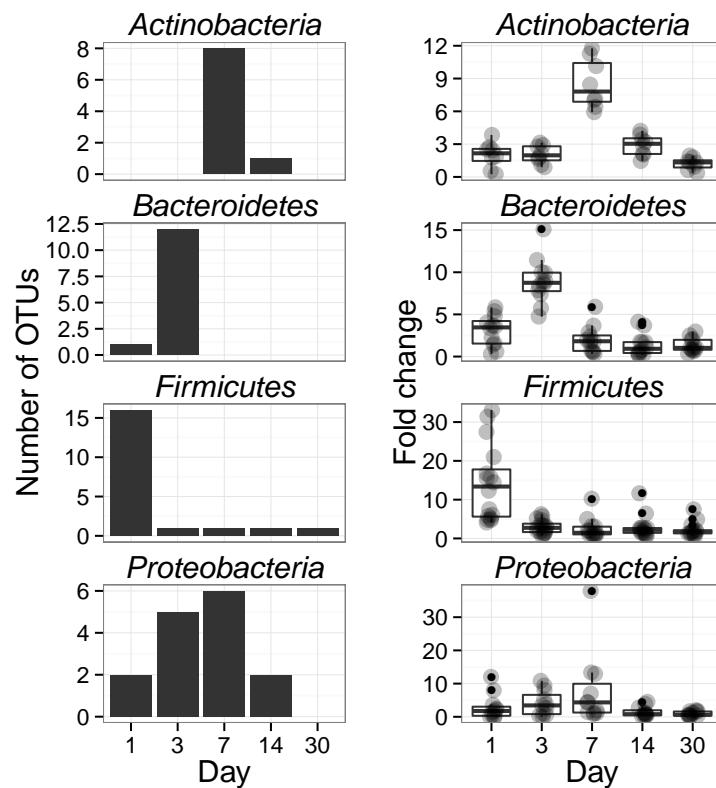


Fig. 4. Left column shows counts of ^{13}C -xylose responders in the *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria* at days 1, 3, 7 and 30. Right panel shows OTU fold enrichment in heavy gradient fractions for ^{13}C -xylose amendment DNA relative to corresponding control fractions.

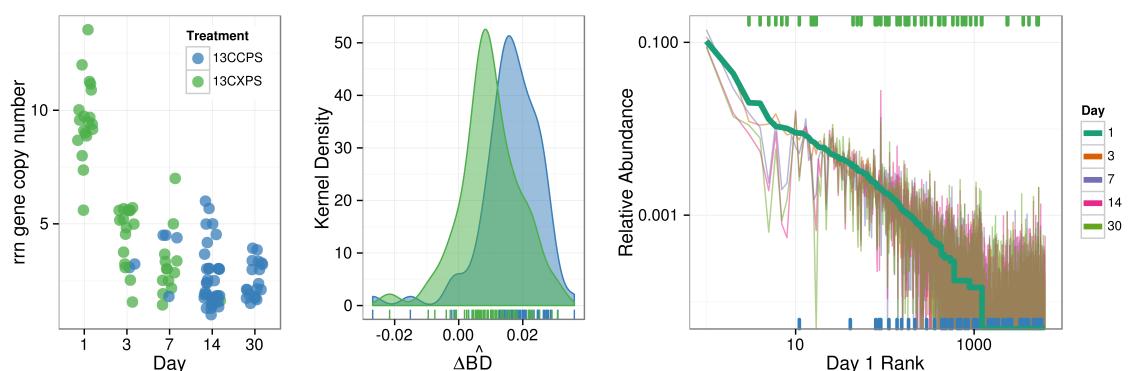


Fig. 5. ^{13}C -responder characteristics based on density shift (A) and rank (B). Kernel density estimation of ^{13}C -responder's density shift in cellulose treatment (blue) and xylose treatment (green) demonstrates degree of labeling for responders for each respective substrate. ^{13}C -responders in rank abundance are labeled by substrate (cellulose, blue; xylose, green). Ticks at top indicate location of ^{13}C -xylose responders in bulk community. Ticks at bottom indicate location of ^{13}C -cellulose responders in bulk community. OTU rank was assessed from day 1 bulk samples.

Supplemental Figures and Tables

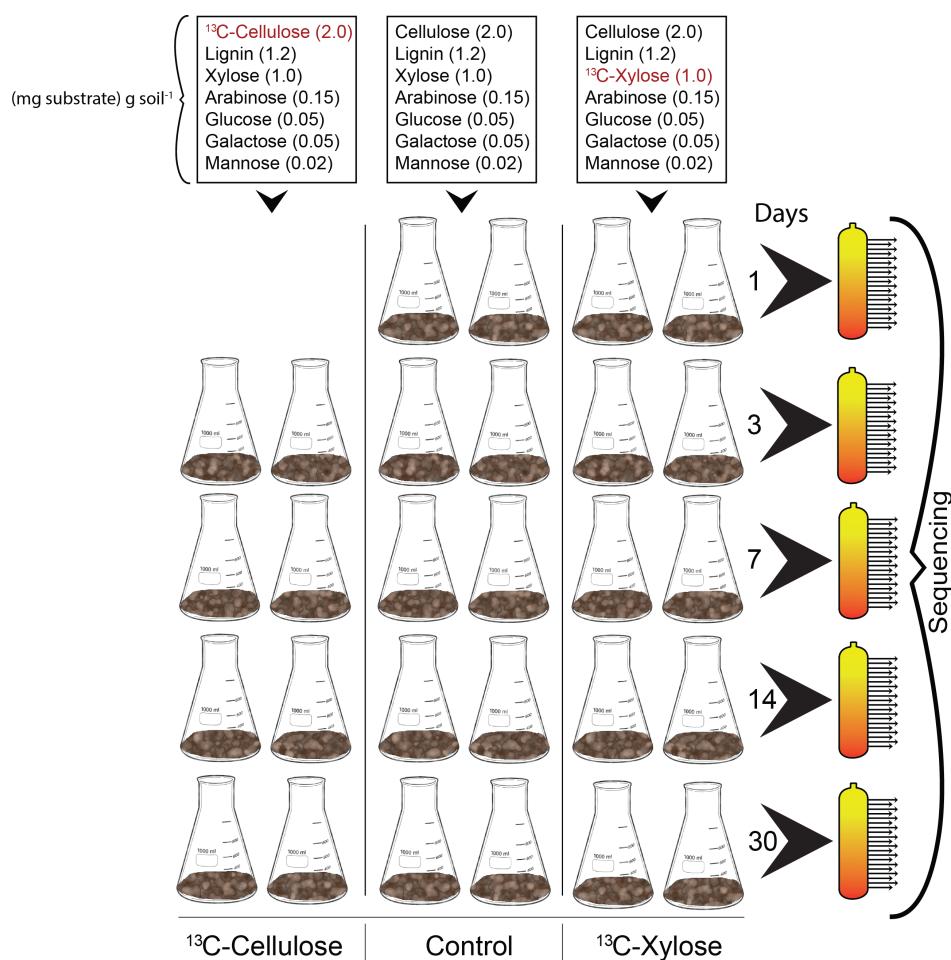


Fig. S1. The experimental design. A carbon mixture, in addition to inorganic salts and amino acids (not shown here), was added to each soil microcosm where the only difference between treatments is the ¹³C-labeled isotope (in red). At days 1, 3, 7, 14, and 30 replicate microcosms were destructively harvested for downstream molecular applications. Bulk DNA from each treatment and time point ($n = 14$) was CsCl density separated by centrifuged and fractionated (orange tubes wherein each arrow represents a fraction from the density gradient). Fractions were 16S gene sequenced using next generation sequencing technology.

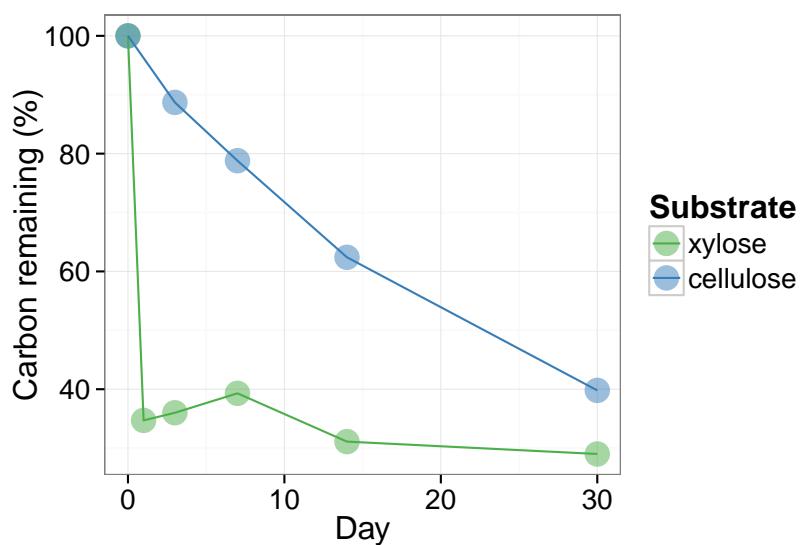
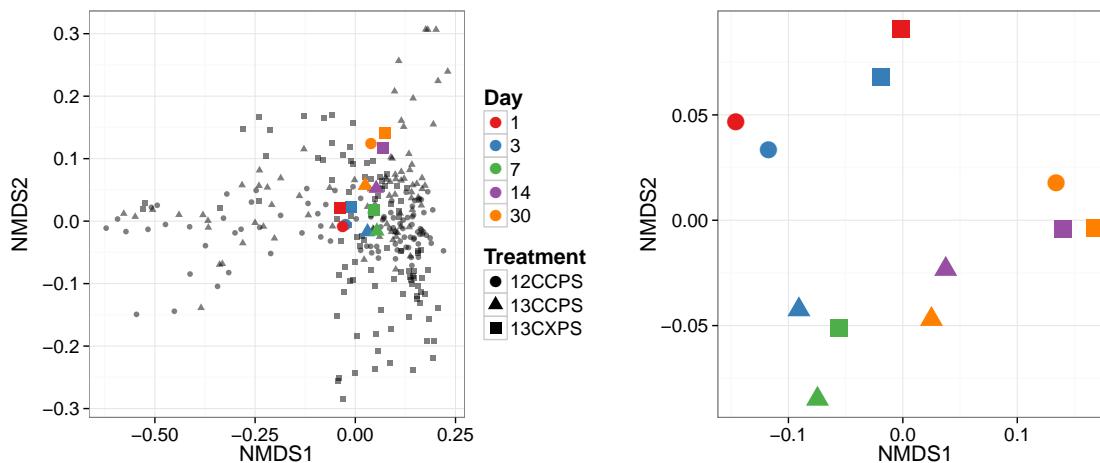
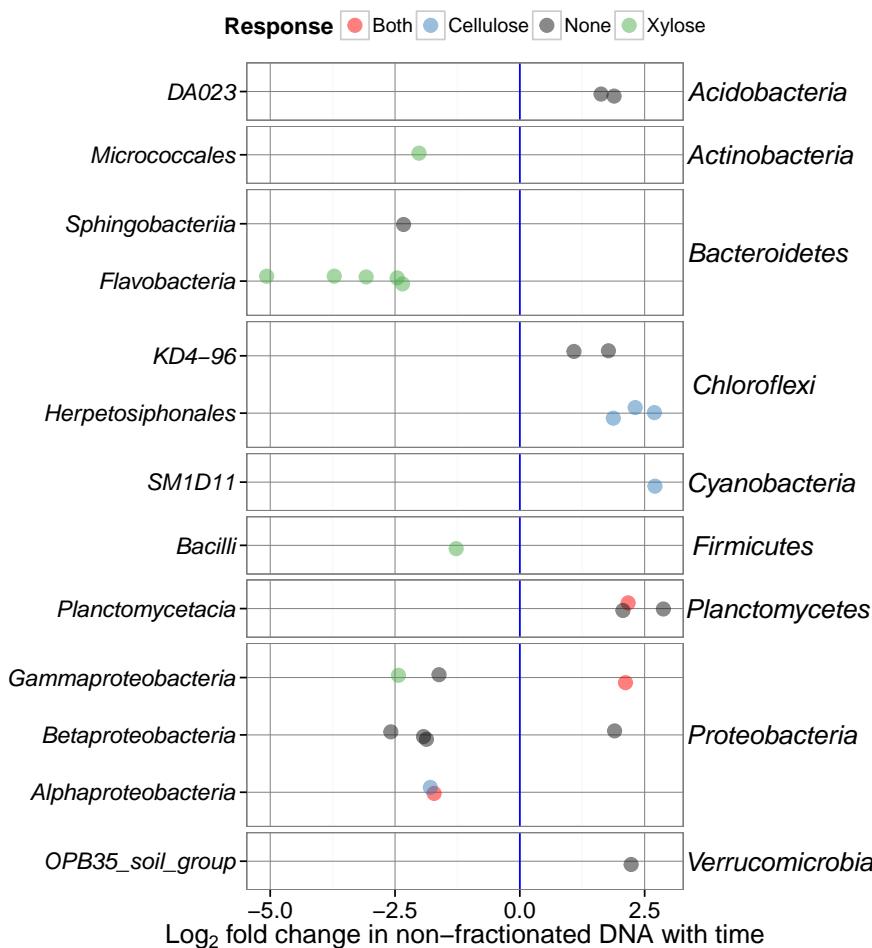


Fig. S2. Percentage of added ¹³C remaining in soil over time.

**Fig. S3.** Ordination of bulk gradient fraction phylogenetic profiles.**Fig. S4.** Fold change time⁻¹ for OTUs that changed significantly in abundance over time. One panel per phylum (phyla indicated on the right). Taxonomic class indicated on the left.

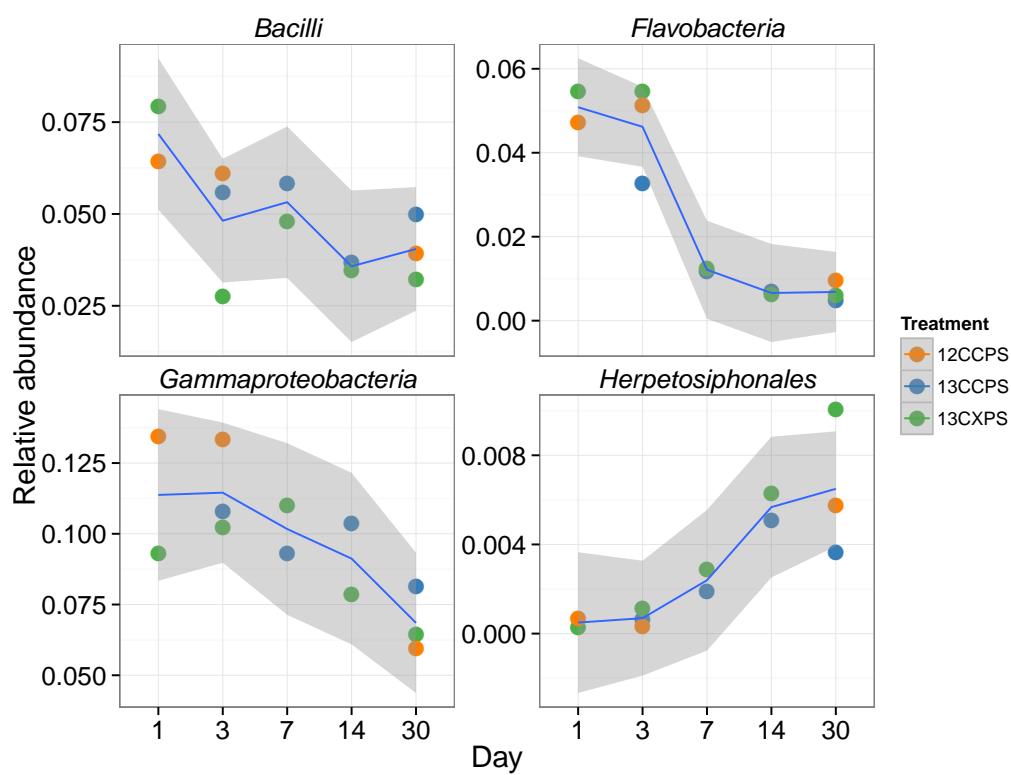
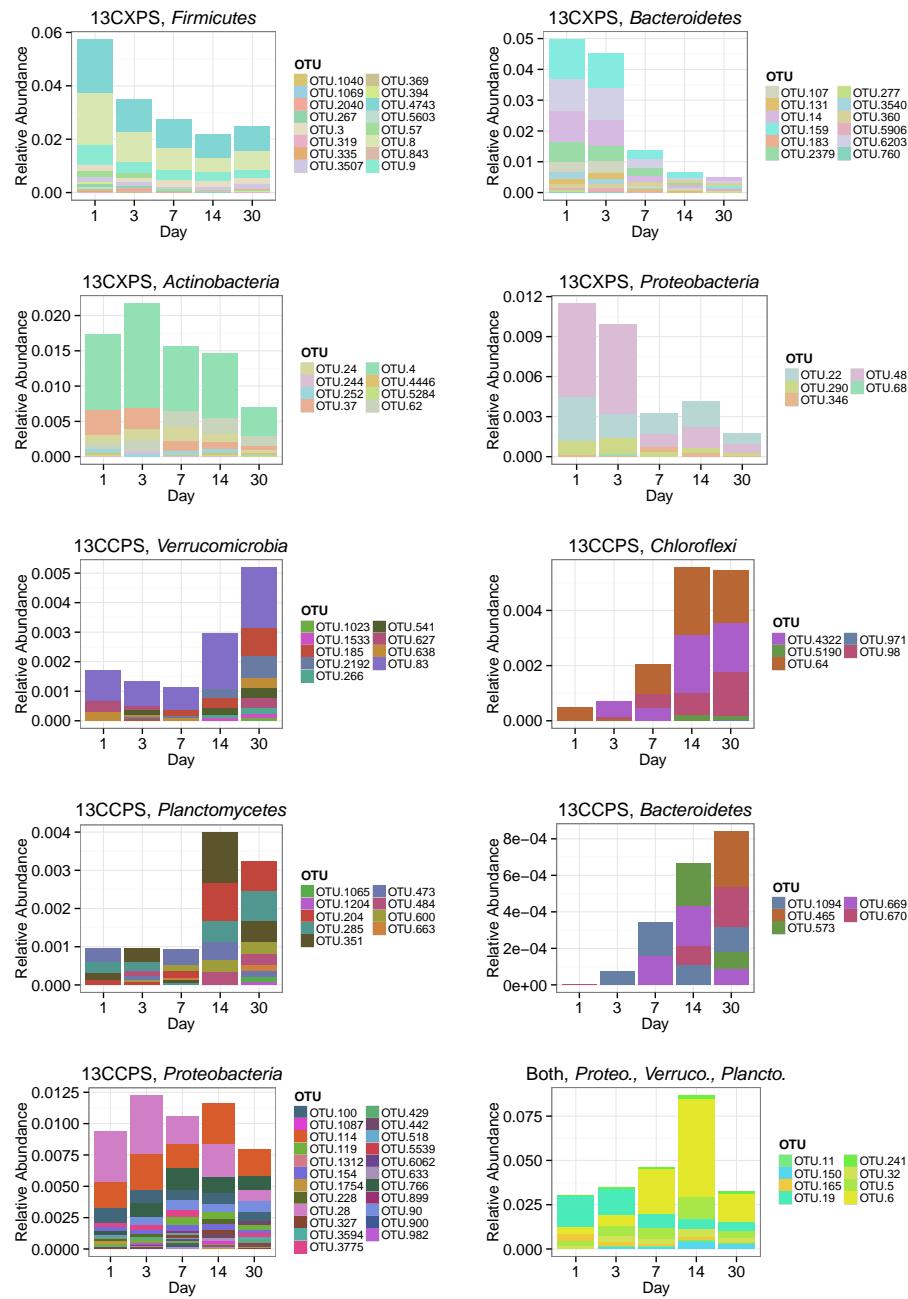


Fig. S5. Relative abundance versus day for classes that changed significantly in relative abundance with time.

**Fig. S6.** Sum of bulk abundances with selected phylum for responder OTUs.

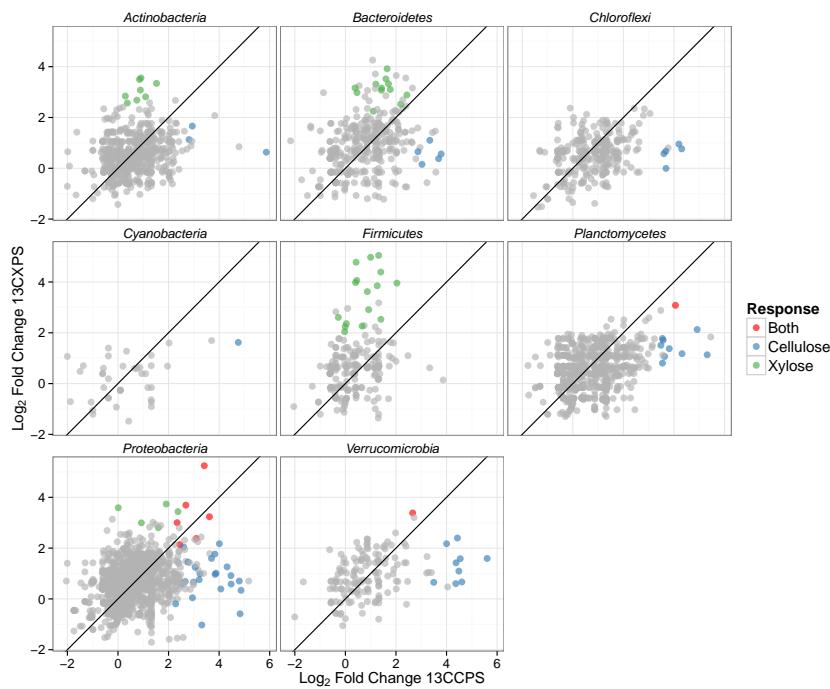


Fig. S7. Maximum \log_2 fold change in response to labeled substrate incorporation for each substrate and all OTUs that pass sparsity filtering in both substrate analyses. Points colored by response. Line has slope of 1 with intercept at the origin. OTUs falling in the top-right quadrant responded to both substrates while those in the top-left and bottom-right responded to ^{13}C -xylose and ^{13}C -cellulose, respectively.

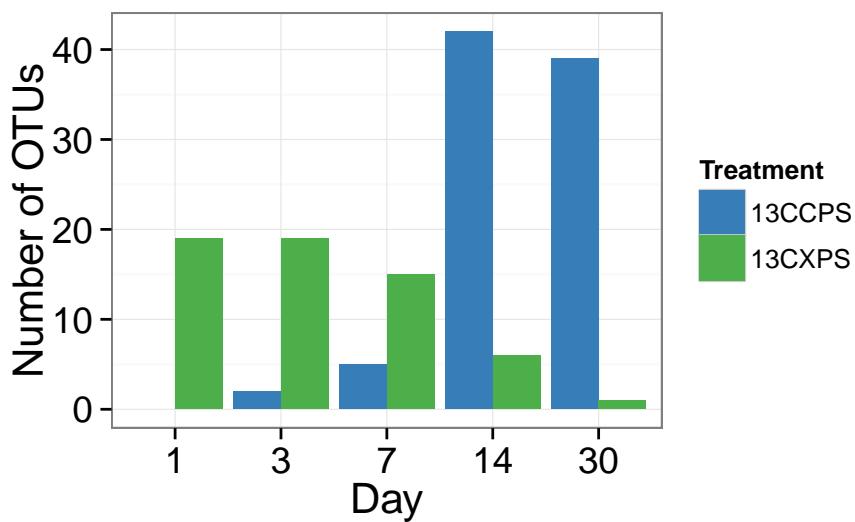


Fig. S8. Counts of responders to each isotopically labeled substrate (cellulose and xylose) over time.

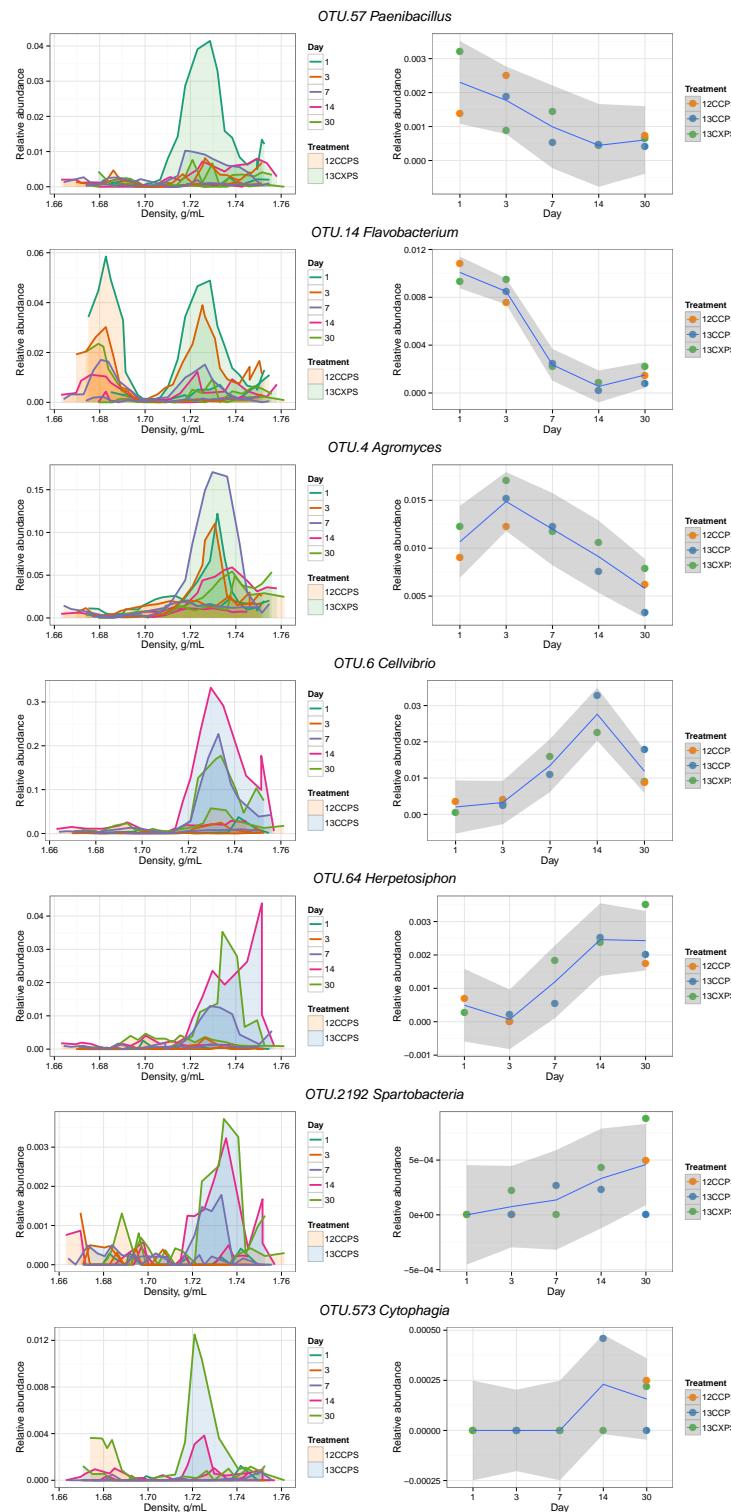


Fig. S9. The left column shows DNA-SIP density fraction relative abundances for all gradients for each of the OTUs. Gradient profiles are shaded by treatment where orange represents “control” profiles, blue “¹³C-cellulose”, and green “¹³C-xylose.” The right column shows the abundance of each OTU in non-fractionated DNA (i.e. the DNA that was subsequently fractionated on the density gradient). Enrichment in the heavy end of the gradient in ¹³C treatments indicates an OTU has ¹³C-labeled DNA that is greater in buoyant density than it would be unlabeled.

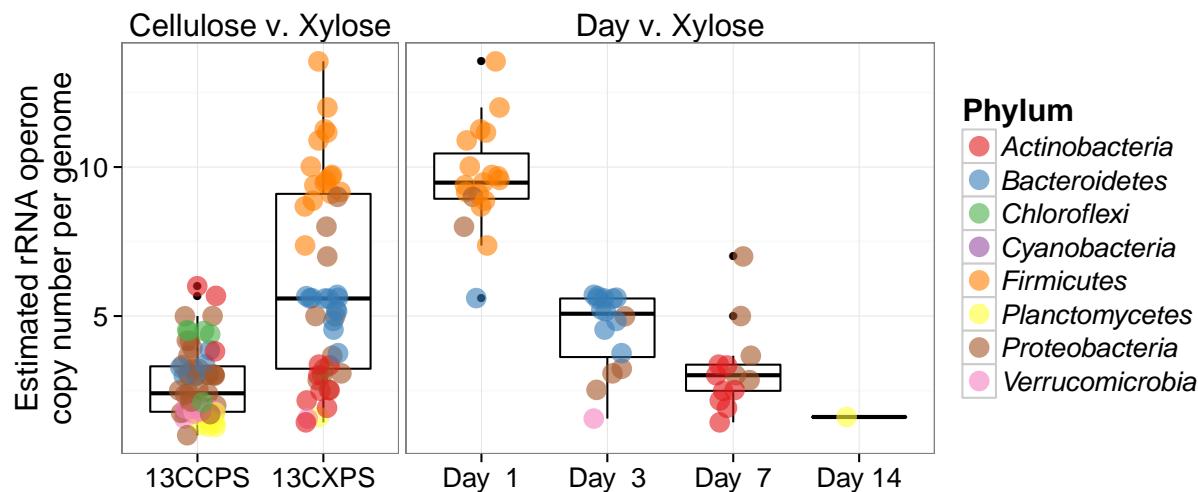


Fig. S10. Estimated rRNA operon copy number per genome for ^{13}C responding OTUs. Panel titles indicate which labeled substrate(s) are depicted.

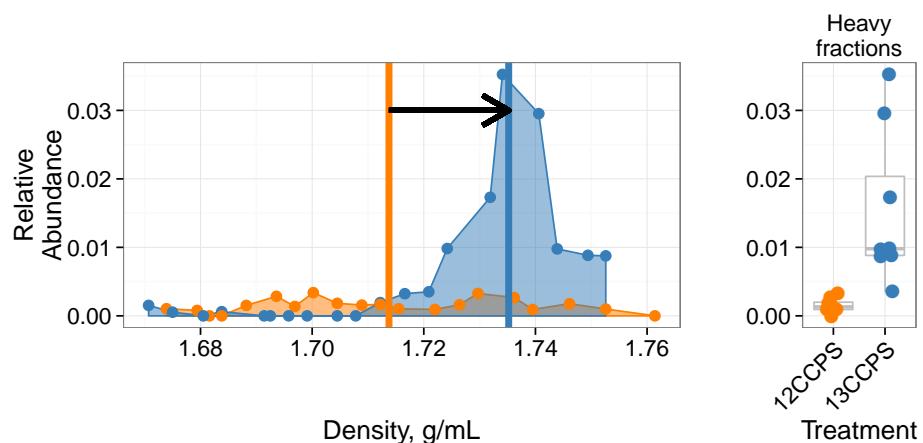


Fig. S11. Density profile for a single ^{13}C -cellulose “responder” OTU in the labeled gradient, blue, and the control gradient, orange. Vertical lines show center of mass for each density profile and arrow denotes the magnitude and direction of the BD shift upon labeling. Panel at right shows relative abundance values in the heavy fractions for each gradient.

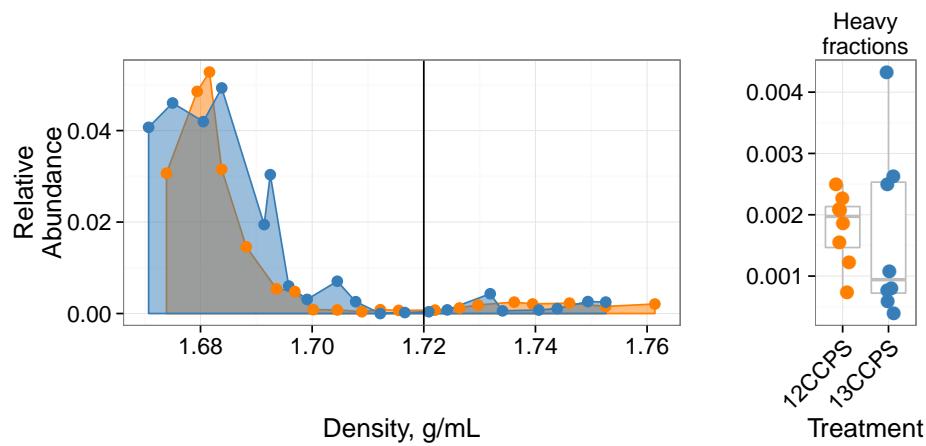


Fig. S12. Density profile for a single ^{13}C -cellulose "non-responder" OTU in the labeled gradient, blue, and the control gradient, orange. Vertical line shows where "heavy" fractions begin as defined in our analysis. Panel at right shows relative abundance values in the heavy fractions for each gradient.

Table S1: ¹³C-xylose responders BLAST against Living Tree Project

OTU ID	Fold change ^a	Day ^b	All days ^c	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.1040	4.78	1	1	<i>Paenibacillus daejeonensis</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.1069	3.85	1	1	<i>Paenibacillus terrigena</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.107	2.25	3	3	<i>Flavobacterium sp. 15C3</i> , <i>Flavobacterium banpakuense</i>	99.54	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.11	5.25	7	7	<i>Stenotrophomonas pavani</i> i, <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.131	3.07	3	3	<i>Flavobacterium fluvii</i> , <i>Flavobacterium bacterium HMD1033</i> , <i>Flavobacterium sp. HMD1001</i>	100.0	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.14	3.92	3	1, 3	<i>Flavobacterium oncorhynchi</i> , <i>Flavobacterium glycines</i> , <i>Flavobacterium succinicans</i>	99.09	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.150	3.08	14	14	No hits of at least 90% identity	86.76	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.159	3.16	3	3	<i>Flavobacterium hibernum</i>	98.17	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.165	2.38	3	3	<i>Rhizobium skieniewicense</i> , <i>Rhizobium vignae</i> , <i>Rhizobium larrymoorei</i> , <i>Rhizobium alkalisolii</i> , <i>Rhizobium galegae</i> , <i>Rhizobium huautlense</i>	100.0	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.183	3.31	3	3	No hits of at least 90% identity	89.5	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.19	2.14	7	7	<i>Rhizobium alamii</i> , <i>Rhizobium mesosinicium</i> , <i>Rhizobium mongolense</i> , <i>Arthrobacter viscosus</i> , <i>Rhizobium sullae</i> , <i>Rhizobium yanglingense</i> , <i>Rhizobium loessense</i>	99.54	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.2040	2.91	1	1	<i>Paenibacillus pectinilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.22	2.8	7	7, 14	<i>Paracoccus sp. NB88</i>	99.09	<i>Proteobacteria Alphaproteobacteria Rhodobacterales</i>
OTU.2379	3.1	3	3	<i>Flavobacterium pectinovorum</i> , <i>Flavobacterium sp. CS100</i>	97.72	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.24	2.81	7	7	<i>Cellulomonas aerilata</i> , <i>Cellulomonas humilata</i> , <i>Cellulomonas terrae</i> , <i>Cellulomonas soli</i> , <i>Cellulomonas xylanilytica</i>	100.0	<i>Actinobacteria Micrococcales Cellulomonadaceae</i>
OTU.241	3.38	3	3, 14	No hits of at least 90% identity	87.73	<i>Verrucomicrobia Spartobacteria Chthoniobacteriales</i>
OTU.244	3.08	7	7	<i>Cellulosimicrobium funkei</i> , <i>Cellulosimicrobium terreum</i>	100.0	<i>Actinobacteria Micrococcales Promicromonosporaceae</i>
OTU.252	3.34	7	7	<i>Promicromonospora thailandica</i>	100.0	<i>Actinobacteria Micrococcales Promicromonosporaceae</i>
OTU.267	4.97	1	1	<i>Paenibacillus pabuli</i> , <i>Paenibacillus tundrae</i> , <i>Paenibacillus taichungensis</i> , <i>Paenibacillus xylohexedens</i> , <i>Paenibacillus xylanilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.277	3.52	3	3	<i>Solibius ginsengiterrae</i>	95.43	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>

Table S1 – continued from previous page

OTU ID	Fold change	Day	All days	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.290	3.59	1	1	<i>Pantoea spp.</i> , <i>Kluyvera spp.</i> , <i>Klebsiella spp.</i> , <i>Erwinia spp.</i> , <i>Enterobacter spp.</i> , <i>Buttiauxella spp.</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Enterobacteriales</i>
OTU.3	2.61	1	1	[<i>Brevibacterium</i>] <i>frigoritolerans</i> , <i>Bacillus sp. LMG 20238</i> , <i>Bacillus coahuilensis m4-4</i> , <i>Bacillus simplex</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.319	3.98	1	1	<i>Paenibacillus xinjiangensis</i>	97.25	<i>Firmicutes Bacilli Bacillales</i>
OTU.32	3.0	3	3, 7, 14	<i>Sandaracinus amyloyticus</i>	94.98	<i>Proteobacteria Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.335	2.53	1	1	<i>Paenibacillus thailandensis</i>	98.17	<i>Firmicutes Bacilli Bacillales</i>
OTU.346	3.44	3	3	<i>Pseudoduganella violaceinigra</i>	99.54	<i>Proteobacteria Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.3507	2.36	1	1	<i>Bacillus spp.</i>	98.63	<i>Firmicutes Bacilli Bacillales</i>
OTU.3540	2.52	3	3	<i>Flavobacterium terrigena</i>	99.54	<i>Bacteroidetes Flavobacteria</i> <i>Flavobacteriales</i>
OTU.360	2.98	3	3	<i>Flavisolibacter ginsengisoli</i>	95.0	<i>Bacteroidetes Sphingobacteriia</i> <i>Sphingobacteriales</i>
OTU.369	5.05	1	1	<i>Paenibacillus sp. D75</i> , <i>Paenibacillus glycansilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.37	2.68	7	7	<i>Phycicola gilvus</i> , <i>Microterricola viridarii</i> , <i>Frigoribacterium faeni</i> , <i>Frondihabitans sp. RS-15</i> , <i>Frondihabitans australicus</i>	100.0	<i>Actinobacteria Micrococcales</i> <i>Microbacteriaceae</i>
OTU.394	4.06	1	1	<i>Paenibacillus pocheonensis</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.4	2.84	7	7, 14	<i>Agromyces ramosus</i>	100.0	<i>Actinobacteria Micrococcales</i> <i>Microbacteriaceae</i>
OTU.4446	3.49	7	7	<i>Catenuloplanes niger</i> , <i>Catenuloplanes castaneus</i> , <i>Catenuloplanes atrovinosus</i> , <i>Catenuloplanes crispus</i> , <i>Catenuloplanes nepalensis</i> , <i>Catenuloplanes japonicus</i>	97.72	<i>Actinobacteria Frankiales</i> <i>Nakamurellaceae</i>
OTU.4743	2.24	1	1	<i>Lysinibacillus fusiformis</i> , <i>Lysinibacillus sphaericus</i>	99.09	<i>Firmicutes Bacilli Bacillales</i>
OTU.48	2.99	1	1, 3	<i>Aeromonas spp.</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria aaa34a10</i>
OTU.5	3.69	7	7	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	<i>Proteobacteria Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5284	3.56	7	7	<i>Isoptericola nanjingensis</i> , <i>Isoptericola hypogaeus</i> , <i>Isoptericola variabilis</i>	98.63	<i>Actinobacteria Micrococcales</i> <i>Promicromonosporaceae</i>
OTU.5603	3.96	1	1	<i>Paenibacillus uliginis</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.57	4.39	1	1, 3, 7, 14, 30	<i>Paenibacillus castaneae</i>	98.62	<i>Firmicutes Bacilli Bacillales</i>
OTU.5906	3.16	3	3	<i>Terrimonas sp. M-8</i>	96.8	<i>Bacteroidetes Sphingobacteriia</i> <i>Sphingobacteriales</i>
OTU.6	3.24	3	3	<i>Cellvibrio fulvus</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i>

Table S1 – continued from previous page

OTU ID	Fold change	Day	All days	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.62	2.57	7	7	<i>Nakamurella flava</i>	100.0	<i>Actinobacteria Frankiales Nakamurellaceae</i>
OTU.6203	3.32	3	3	<i>Flavobacterium granuli</i> , <i>Flavobacterium glaciei</i>	100.0	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.68	3.74	7	7	<i>Shigella flexneri</i> , <i>Escherichia fergusonii</i> , <i>Escherichia coli</i> , <i>Shigella sonnei</i>	100.0	<i>Proteobacteria Gammaproteobacteria Enterobacteriales</i>
OTU.760	2.89	3	3	<i>Dyadobacter hamtensis</i>	98.63	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.8	2.26	1	1	<i>Bacillus niaci</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.843	3.62	1	1	<i>Paenibacillus agarizedens</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.9	2.04	1	1	<i>Bacillus megaterium</i> , <i>Bacillus flexus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>

^a Maximum observed \log_2 of fold change.^b Day of maximum fold change.^c All response days.

Table S2: ¹³C-cellulose responders BLAST against Living Tree Project

OTU ID	Fold change ^a	Day ^b	All days ^c	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.100	2.66	14	14	<i>Pseudoxanthomonas sacheonensis</i> , <i>Pseudoxanthomonas dokdonensis</i>	100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.1023	4.61	30	30	No hits of at least 90% identity	80.54	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.1065	5.31	14	14, 30	No hits of at least 90% identity	84.55	Planctomycetes Planctomycetacia Planctomycetales
OTU.1087	4.32	14	14, 30	<i>Devosia soli</i> , <i>Devosia crocina</i> , <i>Devosia riboflavina</i>	99.09	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.1094	3.69	30	30	<i>Sporocytophaga myxococcoides</i>	99.55	Bacteroidetes Cytophagia Cytophagales
OTU.11	3.41	14	14	<i>Stenotrophomonas pavani</i> , <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.114	2.78	14	14	<i>Herbaspirillum sp. SUEMI03</i> , <i>Herbaspirillum sp. SUEMI10</i> , <i>Oxalicibacterium solurbis</i> , <i>Herminiumonas fonticola</i> , <i>Oxalicibacterium horti</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.119	3.31	14	14, 30	<i>Brevundimonas alba</i>	100.0	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.120	4.76	14	14, 30	<i>Vampirovibrio chlorellavorus</i>	94.52	Cyanobacteria SM1D11 uncultured-bacterium
OTU.1204	4.32	30	30	<i>Planctomyces limnophilus</i>	91.78	Planctomycetes Planctomycetacia Planctomycetales
OTU.1312	4.07	30	30	<i>Paucimonas lemoignei</i>	99.54	Proteobacteria Betaproteobacteria Burkholderiales
OTU.132	2.81	14	14	<i>Streptomyces spp.</i>	100.0	Actinobacteria Streptomycetales Streptomycetaceae
OTU.150	4.06	14	14	No hits of at least 90% identity	86.76	Planctomycetes Planctomycetacia Planctomycetales
OTU.1533	3.43	30	30	No hits of at least 90% identity	82.27	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.154	3.24	14	14	<i>Pseudoxanthomonas mexicana</i> , <i>Pseudoxanthomonas japonensis</i>	100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.165	3.1	14	14	<i>Rhizobium skieniewicense</i> , <i>Rhizobium vignae</i> , <i>Rhizobium larrymoorei</i> , <i>Rhizobium alkalisolii</i> , <i>Rhizobium galegae</i> , <i>Rhizobium huautlense</i>	100.0	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.1754	4.48	14	14	<i>Asticcacaulis biprosthecum</i> , <i>Asticcacaulis benevestitus</i>	96.8	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.185	4.37	14	14, 30	No hits of at least 90% identity	85.14	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.19	2.44	14	14	<i>Rhizobium alamii</i> , <i>Rhizobium mesosinicum</i> , <i>Rhizobium mongolense</i> , <i>Arthrobacter viscosus</i> , <i>Rhizobium sullae</i> , <i>Rhizobium yanglingense</i> , <i>Rhizobium loessense</i>	99.54	Proteobacteria Alphaproteobacteria Rhizobiales

Table S2 – continued from previous page

OTU ID	Fold change	Day	All days	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.2192	3.49	30	14, 30	No hits of at least 90% identity	83.56	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.228	2.54	30	30	<i>Sorangium cellulosum</i>	98.17	Proteobacteria Deltaproteobacteria Myxococcales
OTU.241	2.66	14	14	No hits of at least 90% identity	87.73	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.257	2.94	14	14	<i>Lentzea waywayandensis</i> , <i>Lentzea flaviverrucosa</i>	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.266	4.54	30	14, 30	No hits of at least 90% identity	83.64	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.28	2.59	14	14	<i>Rhizobium giardinii</i> , <i>Rhizobium tubonense</i> , <i>Rhizobium tibeticum</i> , <i>Rhizobium mesoamericanum CCGE 501</i> , <i>Rhizobium herbae</i> , <i>Rhizobium endophyticum</i>	99.54	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.285	3.55	30	14, 30	<i>Blastopirellula marina</i>	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.32	2.34	3	3	<i>Sandaracinus amyloyticus</i>	94.98	Proteobacteria Deltaproteobacteria Myxococcales
OTU.327	2.99	14	14	<i>Asticcacaulis biprostheciun</i> , <i>Asticcacaulis benevestitus</i>	98.63	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.351	3.54	14	14, 30	<i>Pirellula staleyi DSM 6068</i>	91.86	Planctomycetes Planctomycetacia Planctomycetales
OTU.3594	3.83	30	30	<i>Chondromyces robustus</i>	90.41	Proteobacteria Deltaproteobacteria Myxococcales
OTU.3775	3.88	14	14	<i>Devasia glacialis</i> , <i>Devasia chinhatensis</i> , <i>Devasia geoensis</i> , <i>Devasia yakushimensis</i>	98.63	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.429	3.7	30	14, 30	<i>Devasia limi</i> , <i>Devasia psychrophila</i>	97.72	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.4322	4.19	14	7, 14, 30	No hits of at least 90% identity	89.14	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.442	3.05	30	30	<i>Chondromyces robustus</i>	92.24	Proteobacteria Deltaproteobacteria Myxococcales
OTU.465	3.79	30	30	<i>Ohtaekwangia kribbensis</i>	92.73	Bacteroidetes Cytophagia Cytophagales
OTU.473	3.58	14	14	<i>Pirellula staleyi DSM 6068</i>	90.91	Planctomycetes Planctomycetacia Planctomycetales
OTU.484	4.92	14	14, 30	No hits of at least 90% identity	89.09	Planctomycetes Planctomycetacia Planctomycetales
OTU.5	2.69	14	14	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.518	4.8	14	14	<i>Hydrogenophaga intermedia</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.5190	3.6	30	14, 30	No hits of at least 90% identity	88.13	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.541	4.49	30	30	No hits of at least 90% identity	84.23	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.5539	4.01	14	14	<i>Devasia subaequoris</i>	98.17	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.573	3.03	30	30	<i>Adhaeribacter aerophilus</i>	92.76	Bacteroidetes Cytophagia Cytophagales

Table S2 – continued from previous page

OTU ID	Fold change	Day	All days	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.6	3.62	7	3, 7, 14	<i>Cellvibrio fulvus</i>	100.0	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.600	3.48	30	30	No hits of at least 90% identity	80.37	Planctomycetes Planctomycetacia Planctomycetales
OTU.6062	4.83	30	30	<i>Dokdonella sp. DC-3</i> , <i>Luteibacter rhizovicinus</i>	97.26	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.627	4.43	14	14	<i>Verrucomicrobiaceae bacterium DC2a-G7</i>	100.0	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales
OTU.633	3.84	30	30	No hits of at least 90% identity	89.5	Proteobacteria Deltaproteobacteria Myxococcales
OTU.638	4.0	30	30	<i>Luteolibacter sp. CCTCC AB 2010415</i> , <i>Luteolibacter algae</i>	93.61	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales
OTU.64	4.31	14	7, 14, 30	No hits of at least 90% identity	89.5	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.663	3.63	30	30	<i>Pirellula staleyi DSM 6068</i>	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.669	3.34	30	30	<i>Ohtaekwangia koreensis</i>	92.69	Bacteroidetes Cytophagia Cytophagales
OTU.670	2.87	30	30	<i>Adhaeribacter aerophilus</i>	91.78	Bacteroidetes Cytophagia Cytophagales
OTU.766	3.21	14	14, 30	<i>Devosia insulae</i>	99.54	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.83	5.61	14	7, 14, 30	<i>Luteolibacter sp. CCTCC AB 2010415</i>	97.72	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales
OTU.862	5.87	14	14	<i>Allotkutznheria albata</i>	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.899	2.28	30	30	<i>Enhygromyxa salina</i>	97.72	Proteobacteria Deltaproteobacteria Myxococcales
OTU.90	2.94	14	14, 30	<i>Sphingopyxis panaciterrae</i> , <i>Sphingopyxis chilensis</i> , <i>Sphingopyxis sp. BZ30</i> , <i>Sphingomonas sp.</i>	100.0	Proteobacteria Alphaproteobacteria Sphingomonadales
OTU.900	4.87	14	14	<i>Brevundimonas vesicularis</i> , <i>Brevundimonas nasdae</i>	100.0	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.971	3.68	30	30	No hits of at least 90% identity	78.57	Chloroflexi Anaerolineae Anaerolineales
OTU.98	3.68	14	7, 14, 30	No hits of at least 90% identity	88.18	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.982	4.47	14	14	<i>Devosia neptuniae</i>	100.0	Proteobacteria Alphaproteobacteria Rhizobiales

^a Maximum observed \log_2 of fold change.^b Day of maximum fold change.^c All response days.