

Unearthing the soil carbon food web with DNA-SIP

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Abstract

We describe an approach for identifying microbial contributions to soil C cycling using nucleic acid stable isotope probing (SIP) coupled with next generation sequencing. ^{13}C -xylose or ^{13}C -cellulose were chosen to carry the isotopic label for DNA-SIP. Microcosm DNA was interrogated for ^{13}C incorporation at days 1, 3, 7, 14 and 30. Incorporation of ^{13}C from xylose into microcosm DNA was observed at days 1, 3, and 7, while incorporation of ^{13}C from cellulose peaked at day 14 and was maintained through day 30. From approximately 6,000 OTUs detected, a total of 49 and 63 unique OTUs assimilated ^{13}C from xylose and cellulose into DNA, respectively. Xylose assimilating OTUs were more abundant in the microcosm community than cellulose assimilating OTUs, while cellulose OTUs demonstrated a greater substrate specificity than xylose OTUs.

monolayer | structure | x-ray reflectivity | molecular electronics

Abbreviations: SAM, self-assembled monolayer; OTS, octadecyltrichlorosilane

Introduction

Excluding plant biomass, there are 2,300 Pg of carbon (C) stored in soils worldwide which accounts for ~80% of the global terrestrial C pool [1, 2]. When organic C from plants reaches soil it is degraded by fungi, archaea, and bacteria. The majority of plant biomass C in soil is respired and produces 10 times more CO_2 annually than anthropogenic emissions [3]. Global changes in atmospheric CO_2 , temperature, and ecosystem nitrogen inputs are expected to impact soil C input [4]. Current climate change models concur on atmospheric and oceanic but not terrestrial C predictions [5]. Contrasting terrestrial C model predictions reflect how little is known about soil C cycling. Inconsistencies in terrestrial modeling could be improved by elucidating the relationship between dissolved organic C and soil microbial community composition [6].

An important step in understanding soil C cycling dynamics is identifying the *in situ* activity of specific microbial lineages to establish relation-

ship between community structure and function [7]. An estimated 80–90% of soil C cycling is mediated by microorganisms [8, 9] but understanding microbial processing of soil nutrients is challenging due to soil’s heterogeneous nature and methods limitations. The vast majority of microorganisms resist cultivation in the laboratory. Stable-isotope probing (SIP) links microbial identity and activity without cultivation and has expanded our knowledge of microbial contributions to biogeochemical processes [10]. The most successful applications of SIP have identified organisms which mediate processes performed by a narrow set of functional guilds such as methanogens [11]. SIP has been less applicable to the study of soil C cycling because of limitations in resolving power as a result of simultaneous labeling of many different organisms in the community. Additionally, molecular applications such as tRFLP, DGGE and cloning that are frequently used in conjunction with SIP provide insufficient resolution of taxon identity and/or depth of coverage. We developed an approach called High Resolution-SIP (HR-SIP) that employs a complex mixture of substrates added to soil at a low concentration relative to soil organic matter pools along with high throughput DNA sequencing. This greatly expands the ability of nucleic acid SIP to explore complex patterns of C-cycling in microbial communities with increased resolution.

A temporal activity cascade occurs in natural microbial communities during plant biomass degradation in which labile C is degraded before polymeric C [12, 13]. The aim of this study was to observe temporal dynamics of C assimilation through discrete soil community members. Our ex-

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perimental approach included the addition of a soil organic matter (SOM) simulant (a complex mixture of model carbon sources and inorganic nutrients common to plant biomass) so soil microcosms where a single C component is substituted for its ^{13}C -labeled equivalent. Parallel incubations of soils amended with this complex C mixture allows us to observe how different C substrates move through the soil microbial community. In this study we used ^{13}C -xylose and ^{13}C -cellulose as a proxy for labile and polymeric C, respectively, and coupled nucleic acid stable isotope probing with high throughput DNA sequencing. Amplicon sequencing of 16S rRNA gene fragments from many gradient fractions and multiple gradients make it possible to track C associated activities for hundreds of soil taxa.

Results

We observed C use dynamics in an agricultural soil microbial community by conducting a nucleic acid SIP experiment wherein xylose or cellulose carried the isotopic label. We set up three soil microcosm series. Each microcosm was amended with a C substrate mixture that included cellulose and xylose. The C substrate mixture approximated the chemical composition of fresh plant biomass. The same mixture was added to microcosms in each series, however, for each series except the control, xylose or cellulose was substituted for its ^{13}C counterpart. Microcosm amendments are shorthand identified in figures by the following code: “13CXPS” refers to the amendment with ^{13}C -xylose (that is ^{13}C Xylose Plant Simulant), “13CCPS” refers to the ^{13}C -cellulose amendment and “12CCPS” refers to the amendment that only contained ^{12}C substrates (i.e. control). 5.3 mg of C gram $^{-1}$ soil C substrate mixture was added to each microcosm representing 18% of the soil C. The mixture included 0.42 mg xylose-C and 0.88 mg cellulose-C g soil $^{-1}$. Microcosms were harvested at days 1, 3, 7, 14 and 30 during a 30 day incubation. ^{13}C -xylose assimilation peaked immediately and tapered over the 30 day incubation whereas ^{13}C -cellulose assimilation peaked two weeks after amendment additions (Figure 1).

See Supplemental Note XX for sequencing and density fractionation statistics.

Soil microcosm microbial community changes with time. Bulk soil DNA SSU rRNA gene amplicon sequencing revealed changes in the soil microcosm microbial community structure and membership correlated significantly with incubation time (Figure S8B, p-value 0.23, R 2 0.63, Adonis test [14]). The identity of the ^{13}C -labeled substrate added to the microcosms did not significantly cor-

relate with community structure and membership (p-value 0.35). Additionally, microcosm beta diversity was significantly less than gradient fraction beta diversity (p-value 0.003, “betadisper” function R Vegan package [15, 16]). Twenty-nine OTUs significantly changed in relative abundance with time (“BH” adjusted p-value <0.10, [17]) (Figure S3). OTUs that significantly increased in relative abundance with time included OTUs in the *Verrucomicrobia*, *Proteobacteria*, *Planctomycetes*, *Cyanobacteria*, *Chloroflexi* and *Actinobacteria*. OTUs that significantly decreased in relative abundance with time included OTUs in the *Proteobacteria*, *Firmicutes*, *Bacteroidetes* and *Actinobacteria* (Figure S3). *Proteobacteria* was the only phylum that had OTUs which increased significantly and OTUs that decreased significantly in abundance with time. If sequences were grouped by taxonomic annotations at the class level, only four classes significantly changed in abundance, *Bacilli* (decreased), *Flavobacteria* (decreased), *Gammaproteobacteria* (decreased) and *Herpetosiphonales* (increased) (Figure S6). Of the 29 OTUs that changed significantly in relative abundance with time, 14 are labeled substrate responders (Figure S3).

Responder abundances summed at phylum level generally increased for ^{13}C -cellulose (Figure S9) whereas ^{13}C -xylose responder abundances summed at the phylum level decreased over time for *Firmicutes*, *Bacteroidetes*, *Actinobacteria* and *Proteobacteria* although *Proteobacteria* spiked at day 14 (Figure S9). Bulk abundance trends are roughly consistent with ^{13}C assimilation.

OTUs that assimilated ^{13}C into DNA. Within the first 7 days of incubation approximately 63% of ^{13}C -xylose was respired and only an additional 6% more was respired from day 7 to 30. At day 30, 30% of the ^{13}C from xylose remained. An average 16% of the ^{13}C -cellulose added was respired within the first 7 days, 38% by day 14, and 60% by day 30.

Isotope incorporation by an OTU is revealed by enrichment of the OTU in heavy CsCl gradient fractions containing ^{13}C labeled DNA relative to heavy fractions from control gradients containing no ^{13}C labeled DNA. We refer to OTUs that putatively incorporated ^{13}C into DNA originally from an isotopically labeled substrate as substrate “responders”. At day 1, 84% of ^{13}C -xylose responsive OTUs belonged to *Firmicutes*, 11% to *Proteobacteria* and 5% to *Bacteroidetes*. *Firmicutes* responders decreased from 16 OTUs at day 1 to one OTU at day 3 while *Bacteroidetes* responders increased from one OTU at day 1 to 12 OTUs at day 3. The remaining day 3 responders are members of the *Proteobacteria* (26%) and the *Verrucomicrobia*

(5%). Day 7 responders were 53% *Actinobacteria*, 40% *Proteobacteria*, and 7% *Firmicutes*. The identities of ¹³C-xylose responders changed with time. The numerically dominant ¹³C-xylose responder phylum shifted from *Firmicutes* to *Bacteroidetes* and then to *Actinobacteria* across days 1, 3 and 7 (Figure S1, Figure 2).

Only 2 and 5 OTUs had incorporated ¹³C from ¹³C-cellulose at days 3 and 7, respectively. At days 14 and 30 42 and 39 OTUs incorporated ¹³C from ¹³C-cellulose into biomass. A *Cellvibrio* and *Sandaracinaceae* OTU assimilated ¹³C from ¹³C-cellulose at day 3. Day 7 ¹³C-cellulose responders included the same *Cellvibrio* responder as day 3, a *Verrucomicrobia* OTU and three *Chloroflexi* OTUs. 50% of Day 14 responders belong to *Proteobacteria* (66% Alpha-, 19% Gamma-, and 14% Beta-) followed by 17% *Planctomycetes*, 14% *Verrucomicrobia*, 10% *Chloroflexi*, 7% *Actinobacteria* and 2% cyanobacteria. *Bacteroidetes* OTUs began to incorporate ¹³C from cellulose at day 30 (13% of day 30 responders). Other day 30 responding phyla included *Proteobacteria* (30% of day 30 responders; 42% Alpha-, 42% Delta, 8% Gamma-, and 8% Beta-), *Planctomycetes* (20%), *Verrucomicrobia* (20%), *Chloroflexi* (13%) and cyanobacteria (3%). *Proteobacteria*, *Verrucomicrobia*, and *Chloroflexi* had relatively high numbers of responders with strong response across multiple time points (Figure S1).

Ecological strategies of ¹³C responders. ¹³C-xylose responders are generally more abundant members based on relative abundance in bulk DNA SSU rRNA gene content than ¹³C-cellulose responders (Figure 3, p-value 0.00028). However, both abundant and rare OTUs responded to ¹³C-xylose and ¹³C-cellulose (Figure 3). For instance, a *Deltaproteobacteria* ¹³C-cellulose responder is fairly abundant in the bulk samples (“OTU.5”, Table S1). OTU.5 was on average the 13th most abundant OTU in bulk samples. A ¹³C-xylose responder (“OTU.1040”, Table S2) has a mean relative abundance in bulk samples of 3.57×10^{-5} . Two ¹³C-cellulose responders were not found in any bulk samples (“OTU.862” and “OTU.1312”, Table S1). Of the 10 most abundant responders, 8 are ¹³C-xylose responders and 6 of these 8 are consistently among the 10 most abundant OTUs in bulk samples.

Cellulose responders exhibited a greater shift in buoyant density (BD) than xylose responders in response to isotope incorporation (Figure 3, p-value 1.8610×10^{-6}). ¹³C-cellulose responders shifted on average 0.0163 g mL^{-1} (sd 0.0094) whereas xylose responders shifted on average 0.0097 g mL^{-1} (sd 0.0094). For reference, 100% ¹³C DNA BD is 0.04 g mL^{-1} greater than the BD of its ¹²C counter-

part. DNA BD increases as its ratio of ¹³C to ¹²C increases. An organism that only assimilates C into DNA from a ¹³C isotopically labeled source, will have a greater ¹³C:¹²C ratio in its DNA than an organism utilizing a mixture of isotopically labeled and unlabeled C sources (see supplemental note XX).

¹³C-xylose responder estimated *rrn* gene copy number was inversely related time of first response (p-value 2.02×10^{-15} , Figure S2). OTUs that first respond at later time points have fewer estimated *rrn* copy number than OTUs that first respond earlier (Figure S2).

Discussion

Pure culture based studies have historically driven soil microbial ecology research but cultured isolates have not captured *in situ* numerically abundant genera [18]. DNA-SIP can characterize functional roles for thousands of phylotypes in a single experiment without cultivation. We found 104 OTUs in an agricultural soil that can incorporate from xylose and/or cellulose into biomass and also used DNA-SIP to characterize substrate specificity and C-cycling dynamics for soluble and polymeric C degraders. Included in characterized ¹³C-xylose and ¹³C-cellulose responsive OTUs were members of cosmopolitan yet functionally uncharacterized soil phylogenetic groups such as *Verrucomicrobia*, *Planctomycetes* and *Chloroflexi*.

Microbial response to isotopic labels. We propose that C added to soil microcosms in this experiment took the following path through the microbial food web (Figure S13): First, labile C such as xylose was assimilated by fast-growing opportunistic *Firmicutes* spore formers. The remaining labile C and new biomass C was assimilated in succession by slower growing *Bacteroidetes*, *Actinobacteria* and *Proteobacteria* phylotypes that were either tuned to lower C substrate concentrations, were predatory bacteria (e.g. *Agromyces*), and/or were specialized for consuming viral lysate. C from polymeric substrates entered the bacterial community after 14 days. Canonical cellulose degrading bacteria such as *Cellvibrio* degraded cellulose but uncharacterized lineages in the *Chloroflexi*, *Planctomycetes* and *Verrucomicrobia*, specifically the *Spartobacter*, were also significant contributors to cellulose decomposition.

Ecological strategies of soil microorganisms participating in the decomposition of organic matter. We assessed the ecology of ¹³C-responsive OTUs by estimating the *rrn* gene copy number and the BD shift upon labeling for each OTU. *rrn* gene copy number correlates positively with growth rate [19] and BD shift is indicative of substrate

specificity (see results). We also observed how ^{13}C -substrate responsive OTUs changed in relative abundance with time in the microcosms and the abundance rank of ^{13}C -substrate responsive OTUs in the bulk DNA. Ecological metrics show ^{13}C -cellulose responsive OTUs grow slower (Figure 3, Figure S2), have greater substrate specificity (Figure 3), and are generally lower abundance than ^{13}C -xylose responsive OTUs (Figure 3). The higher abundance of xylose responders may also be in part due to their high *rrn* gene copy number resulting in inflated relative abundance per genome. There are only faint ecological differences within the ^{13}C -cellulose responsive OTUs but the combination of *rrn* gene copy number, BD shift, abundance rank and relative abundance change over time is consistent with phylum membership (Figure RADVIZ). ^{13}C -xylose responsive OTU *rrn* gene copy number correlated inversely with the time at which the OTU was first found to incorporate ^{13}C into DNA (Figure 3, Figure S2) suggesting that fast-growing microbes assimilated ^{13}C from xylose before slow growers.

Ecological metrics suggest cellulose degraders are substrate specialists that grow slow and are in low bulk abundance. Labile C responder ecological strategies were more varied perhaps because some ^{13}C labeled microorganisms did not primarily assimilate xylose but became labeled via predatory interactions and/or are saprophytes. ^{13}C -xylose responsive OTUs are generalists, grow faster and are more abundant when compared to ^{13}C -cellulose responders. ^{13}C -xylose responders vary in growth rate and while generally higher abundance than ^{13}C -cellulose responders can also be low abundance microorganisms. It's not clear whether the observed activity succession from *Firmicutes* to *Bacteroidetes* and finally *Actinobacteria* in response to ^{13}C -xylose addition marks a trophic cascade or functional groups tuned to different resource concentrations or both. Notably, each temporally defined response group clustered phylogenetically suggesting a uniform ecological strategy (Figure S7). It's also clear that some of the non-*Firmicutes* ^{13}C -xylose responders are closely related to known predators (*Agromyces*) and many marine predatory bacteria are members of the *Bacteroidetes* ([20]). Further, *Bacteroidetes* have been implicated as soil predatory bacteria previously [21]. If the temporal dynamics of ^{13}C -xylose incorporation are due to trophic interactions, our results suggest that there are many predatory soil bacteria that consume fast-growing, opportunistic, primary labile C assimilating, gram-positive spore-formers. Hence, trophic interactions among soil bacteria may be of importance in soil C turnover models.

How – or if – phylogenetic composition affects SOM dynamics is an open question [22]. Phylogenetic composition could affect SOM dynamics if SOM transformations were not functionally redundant traits and if biology is rate limiting for key C transformations [22]. Alternatively, even with functional redundancy resource allocation at the cell level can influence SOM fate [22]. It is likely that the ability to carry out soil C transformations are redundant within and between soil microbial communities and that in the mineral soil abiotic factors are rate limiting [22]. Therefore phylogenetic composition in mineral soil likely influences soil C fate as opposed to dynamics. We demonstrate a phylogenetically coherent response to soluble C additions – for instance, most of the initial response to xylose can be attributed to aerobic spore formers. Assuming cellular resource allocation is consistent with phylogeny, it follows then that phylogenetic composition can significantly influence SOM fate. Aerobic spore-formers, for example, are found in different proportions across soil biomes [18] and even within regional agricultural soils CITE Berthrong. If present and abundant, aerobic spore-formers may be primary soluble C decomposers and allocate C in specific quantities into intra and extracellular C components. Further, aerobic spore-formers may have a phylogenetically coherent resistance to predation which could further affect soil C fate. Although, not demonstrated in this study, the allocation of C from soluble, labile pools in a soil without or under conditions not suitable for aerobic spore-formers may be significantly different. Polymeric C, on the other hand, did not show the same phylogenetic coherence as soluble C decomposition in this study. This suggests that resource allocation among cellulose degraders would not have a single phylogenetic signal and the fate of polymeric C would not be tied to phylogenetic composition. Though cellulose degraders as a whole likely allocate C differently than labile C degraders.

Conclusion. Microorganisms sequester atmospheric C and respire soil organic matter (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 uncharacterized yet ubiquitous and often abundant soil lineages participated in cellulose decomposition. Cellulose C degraders included members of the *Verrucomicrobia* (*Spartobacteria*), *Chloroflexi*, *Bacteroidetes* and *Planctomycetes*. *Spartobacteria* in particular are abundant microorganisms in many soil biomes and often the most abundant *Verrucomicrobia* order in soil. Our results also suggest that members of the *Bacteroidetes* and *Actinobacteria* act in the cas-

cade of labile, soluble C through soil trophic levels possibly as predators. Both points illustrate the complexity of soil C dynamics and fate. The largely phylogenetically coherent ecological groups observed in this study suggest that soil C fate is tied to phylogenetic composition.

Methods

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

Twelve soil cores (5 cm diameter x 10 cm depth) were collected from six random sampling locations within an organically managed agricultural field in Penn Yan, New York. Soils were pretreated by sieving (2 mm), homogenizing sieved soil, and pre-incubating 10 g of dry soil weight in flasks for 2 weeks. Soils were amended with a 5.3 mg g soil⁻¹ carbon mixture; representative of natural concentrations [23]. Mixture contained 38% cellulose, 23% lignin, 20% xylose, 3% arabinose, 1% galactose, 1% glucose, and 0.5% mannose by mass, with the remaining 13.5% mass composed of an amino acid (in-house made replica of Teknova C0705) and basal salt mixture (Murashige and Skoog, Sigma Aldrich M5524). Three parallel treatments were performed; (1) unlabeled control, (2)¹³C-cellulose, (3)¹³C-xylose (98 atom% ¹³C, Sigma Aldrich). Each treatment had 2 replicates per time point ($n = 4$) except day 30 which had 4 replicates; total microcosms per treatment $n = 12$, except ¹³C-cellulose which was not sampled at day 1, $n = 10$. Other details relating to substrate addition can be found in SI. Microcosms were sampled destructively (stored at -80°C until nucleic acid processing) at days 1 (control and xylose only), 3, 7, 14, and 30.

Nucleic acids were extracted using a modified Griffiths protocol [24]. To prepare nucleic acid extracts for isopycnic centrifugation as previously described [25], DNA was size selected (>4kb) using 1% low melt agarose gel and β -agarase I enzyme extraction per manufacturers protocol (New England Biolab, M0392S). For each time point in the series isopycnic gradients were setup using a modified protocol [26] for a total of five ¹²C-control, five ¹³C-xylose, and four ¹³C-cellulose microcosms. A density gradient (average density 1.69 g mL⁻¹) solution of 1.762 g cesium chloride (CsCl) mL⁻¹ in gradient buffer solution (pH 8.0 15 mM Tris-HCl, 15 mM EDTA, 15 mM KCl) was used to separate ¹³C-enriched and ¹²C-non-enriched DNA. Each gradient was loaded with approximately 5 μ g of DNA and ultracentrifuged for 66 h at 55,000 rpm and room temperature (RT). Fractions of ~100 μ L were collected from below by displacing the DNA-CsCl-gradient buffer solution in the centrifugation

tube with water using a syringe pump at a flow rate of 3.3 μ L s⁻¹ [27] into AcroprepTM 96 filter plate (Pall Life Sciences 5035). The refractive index of each fraction was measured using a Reichart AR200 digital refractometer modified as previously described [25] to measure a volume of 5 μ L. Then buoyant density was calculated from the refractive index as previously described [25] (see also SI). The collected DNA fractions were purified by repetitive washing of Acroprep filter wells with TE. Finally, 50 μ L TE was added to each fraction then resuspended DNA was pipetted off the filter into a new microfuge tube.

For every gradient, 20 fractions were chosen for sequencing between the density range 1.67-1.75 g mL⁻¹. Barcoded 454 primers were designed using 454-specific adapter B, 10 bp barcodes [28], a 2 bp linker (5'-CA-3'), and 806R primer for reverse primer (BA806R); and 454-specific adapter A, a 2 bp linker (5'-TC-3'), and 515F primer for forward primer (BA515F). Each fraction was PCR amplified using 0.25 μ L 5 U μ l⁻¹ AmpliTaq Gold (Life Technologies, Grand Island, NY; N8080243), 2.5 μ L 10X Buffer II (100 mM Tris-HCl, pH 8.3, 500 mM KCl), 2.5 μ L 25 mM MgCl₂, 4 μ L 5 mM dNTP, 1.25 μ L 10 mg mL⁻¹ BSA, 0.5 μ L 10 μ M BA515F, 1 μ L 5 μ M BA806R, 3 μ L H₂O, 10 μ L 1:30 DNA template) in triplicate. Samples were normalized either using Pico green quantification and manual calculation or by SequalPrepTM normalization plates (Invitrogen, Carlsbad, CA; A10510), then pooled in equimolar concentrations. Pooled DNA was gel extracted from a 1% agarose gel using Wizard SV gel and PCR clean-up system (Promega, Madison, WI; A9281) per manufacturer's protocol. Amplicons were sequenced on Roche 454 FLX system using titanium chemistry at Selah Genomics (formerly EnGenCore, Columbia, SC)

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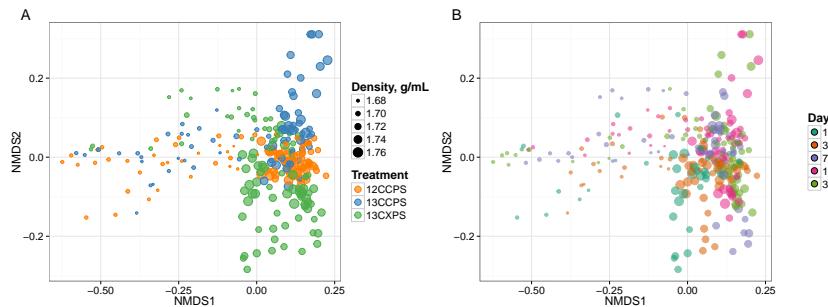


Fig. 1. NMDS analysis from weighted unifrac distances of 454 sequence data from SIP fractions of each treatment over time. Twenty fractions from a CsCl gradient fractionation for each treatment at each time point were sequenced (Fig. S1). Each point on the NMDS represents the bacterial composition based 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).

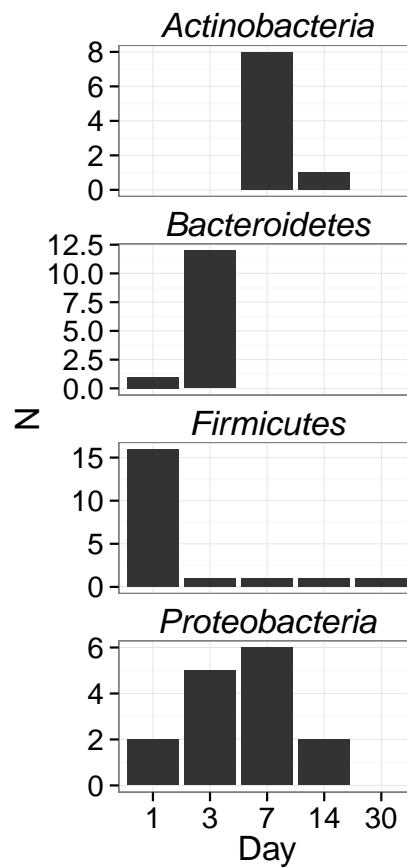


Fig. 2. Counts of ^{13}C -xylose responders in the *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria* at days 1, 3, 7 and 30.

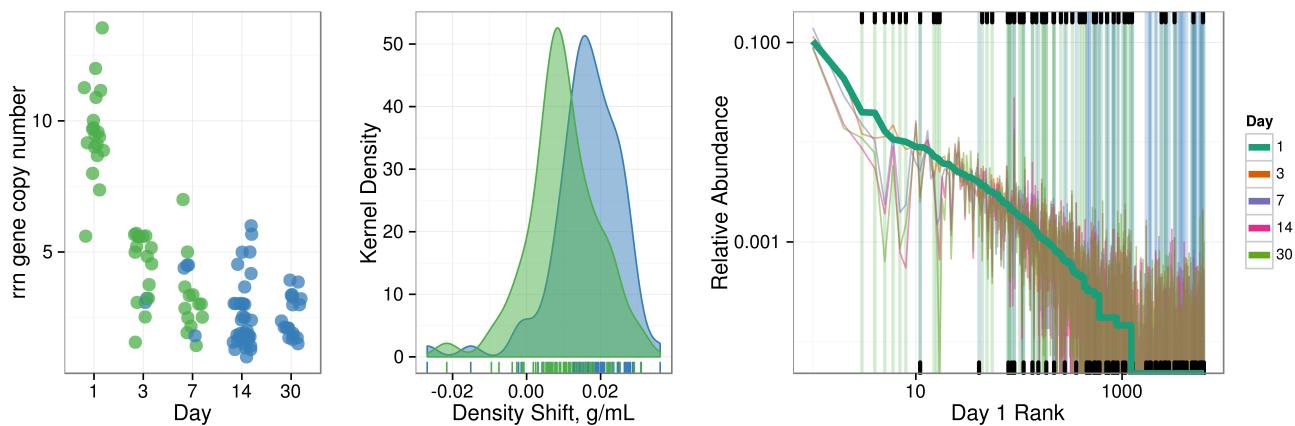


Fig. 3. ^{13}C -responder characteristics based on density shift (A) and rank (B). Kernel density estimation of ^{13}C -responder's density shift in cellulose treatment (blue) and xylose treatment (green) demonstrates degree of labeling for responders for each respective substrate. ^{13}C -responders in rank abundance are labeled by substrate (cellulose, blue; xylose, green). Ticks at top indicate location of ^{13}C -cytose 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

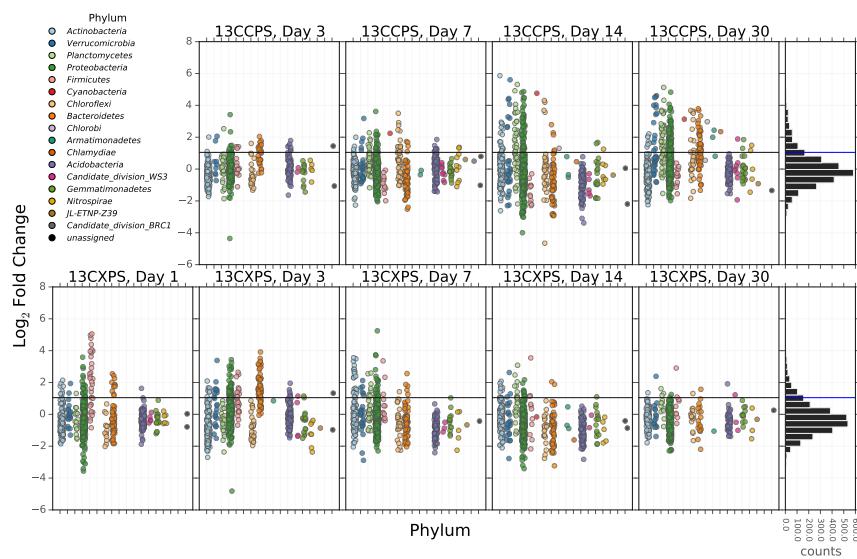


Fig. S1. Log₂ fold change of ¹³C-responders in cellulose treatment (top) and xylose treatment (bottom). Log₂ fold change is based on the relative abundance in the experimental treatment compared to the control within the density range 1.7125–1.755 g ml⁻¹. Taxa are colored by phylum. ‘Counts’ is a histogram of log₂ fold change values.

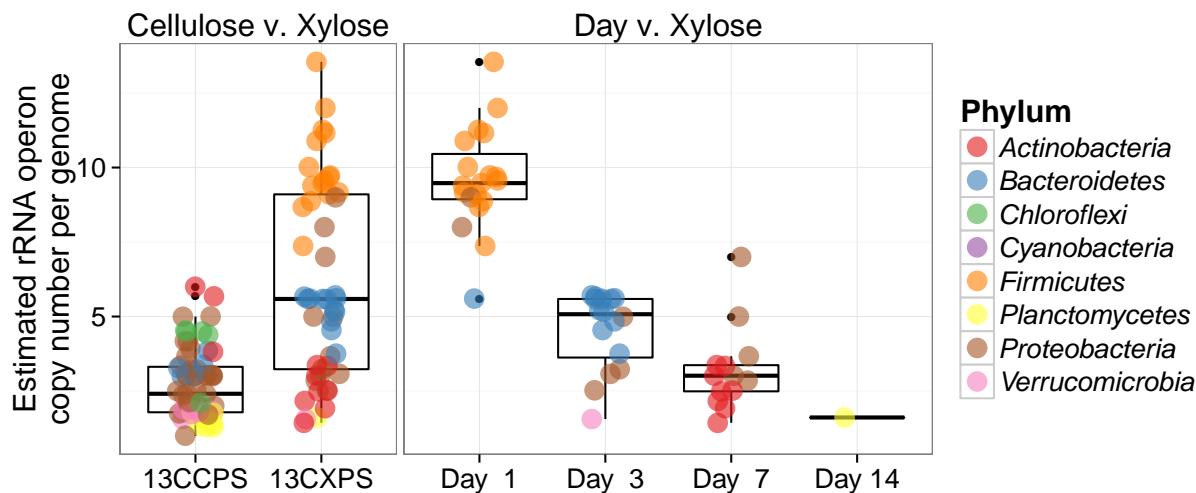


Fig. S2. Estimated rRNA operon copy number per genome for ¹³C responding OTUs. Panel titles indicate which labeled substrate(s) are depicted.

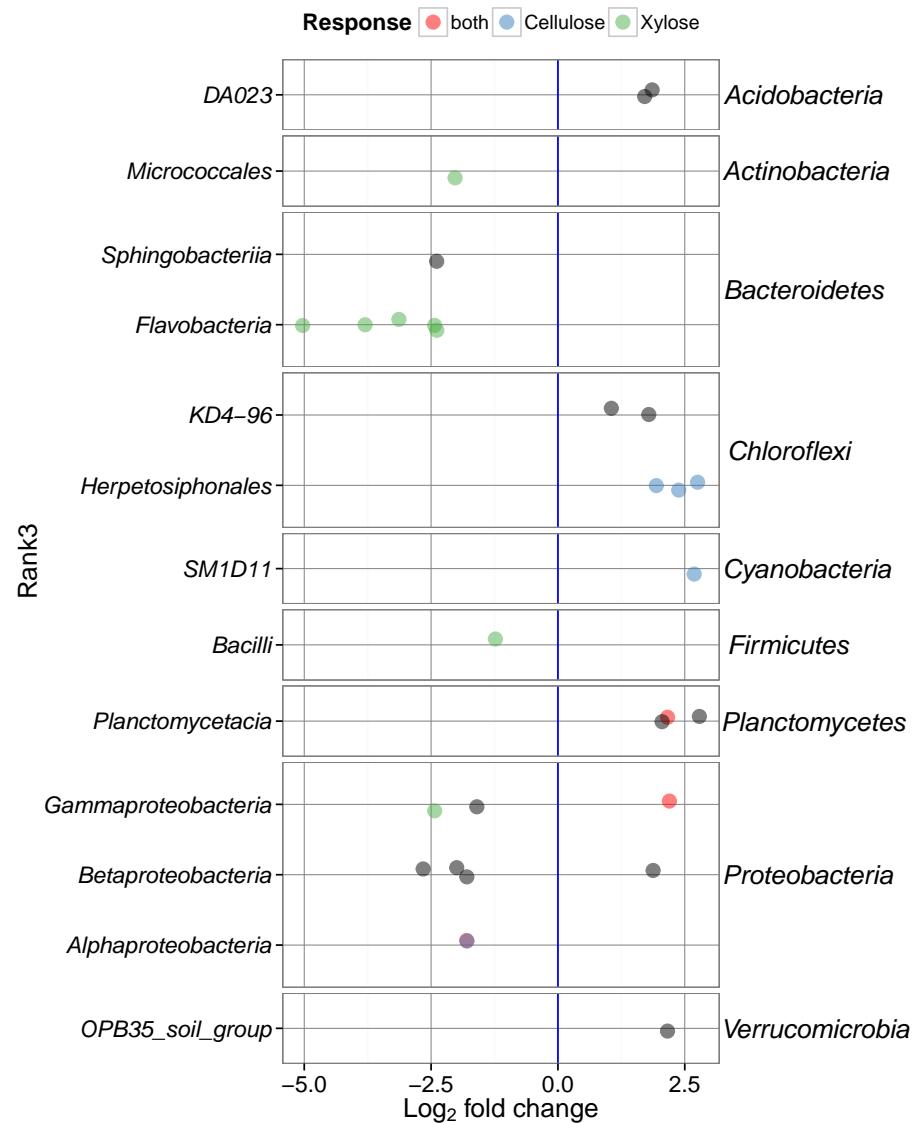


Fig. S3. Fold change time⁻¹ for OTUs that changed significantly in abundance over time. One panel per phylum (phyla indicated on the right). Taxonomic class indicated on the left.

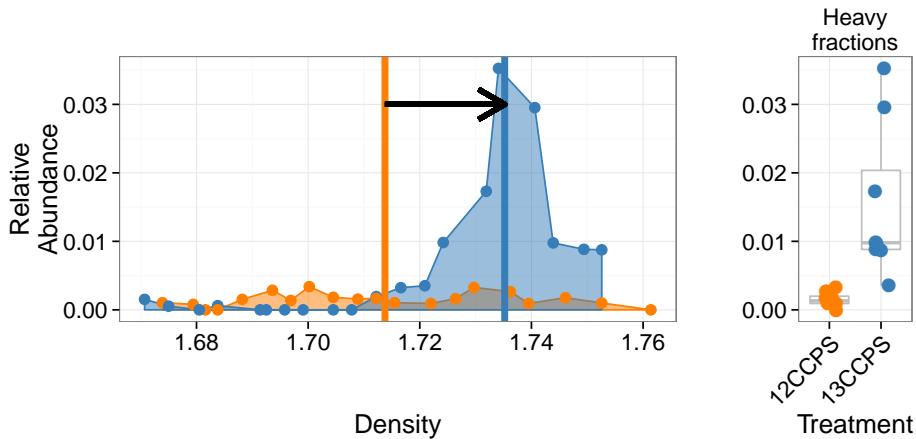


Fig. S4. Density profile for a single ^{13}C -cellulose “responder” OTU in the labeled gradient, blue, and the control gradient, orange. Vertical lines show center of mass for each density profile and arrow denotes the magnitude and direction of the BD shift upon labeling. Panel at right shows relative abundance values in the heavy fractions for each gradient.

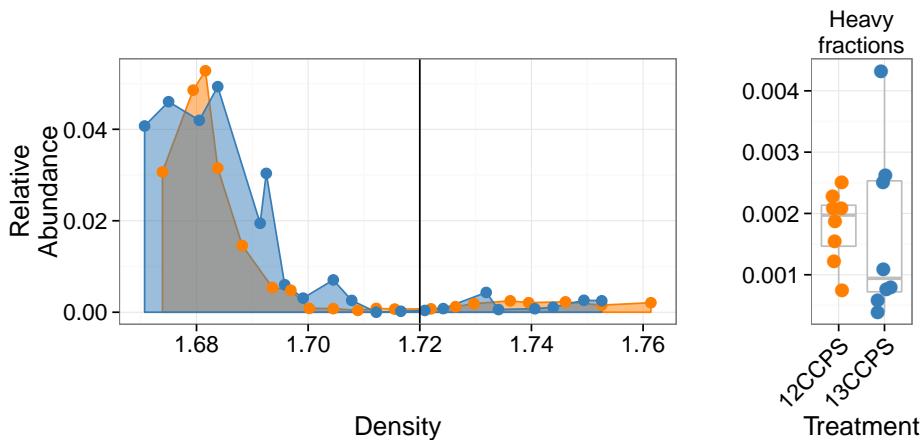


Fig. S5. Density profile for a single ^{13}C -cellulose “non-responder” OTU in the labeled gradient, blue, and the control gradient, orange. Vertical line shows where “heavy” fractions begin as defined in our analysis. Panel at right shows relative abundance values in the heavy fractions for each gradient.

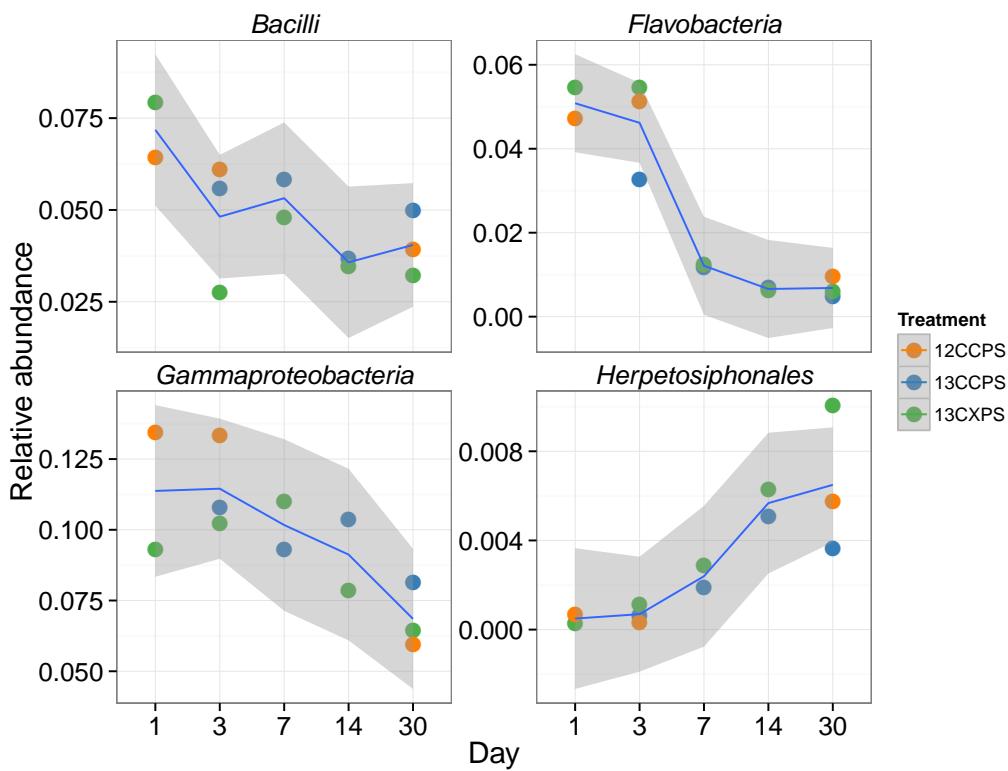


Fig. S6. Relative abundance versus day for classes that changed significantly in relative abundance with time.

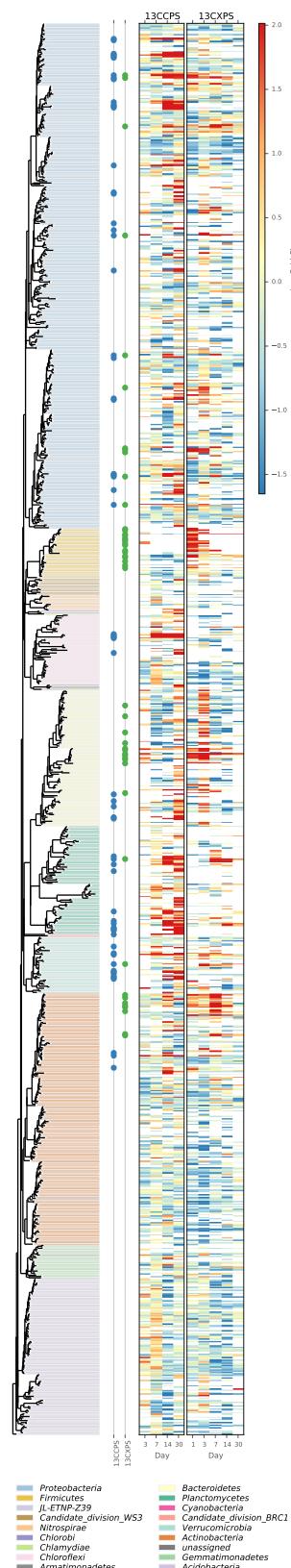


Fig. S7. Phylogenetic tree of sequences passing a user defined sparsity threshold (0.6) for at least one day of the time series. Branches are colored by phylum. ^{13}C -responders for cellulose (blue) and xylose (green) are indicated by a point beside the respective branch. Heatmap demonstrates \log_2 fold change of each taxa through the full time series for both treatments (cellulose, left; xylose, right).

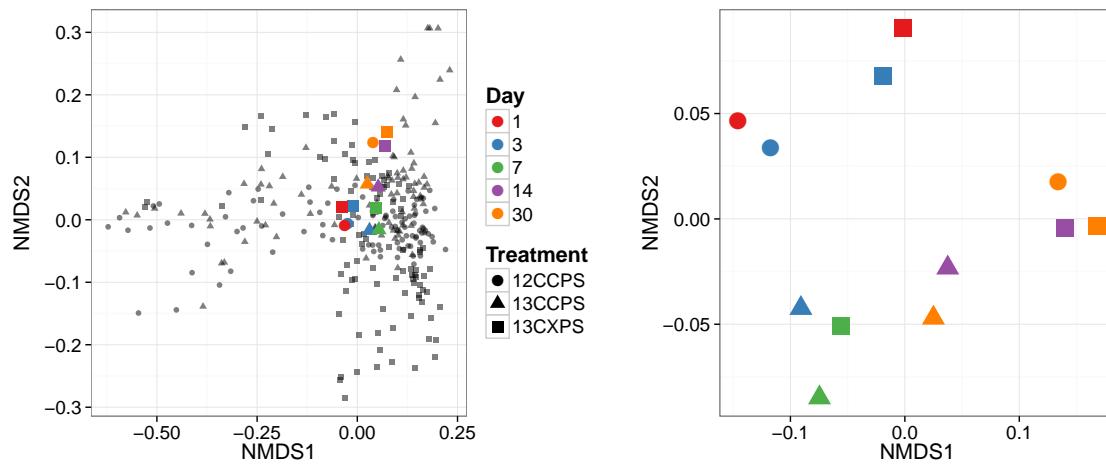
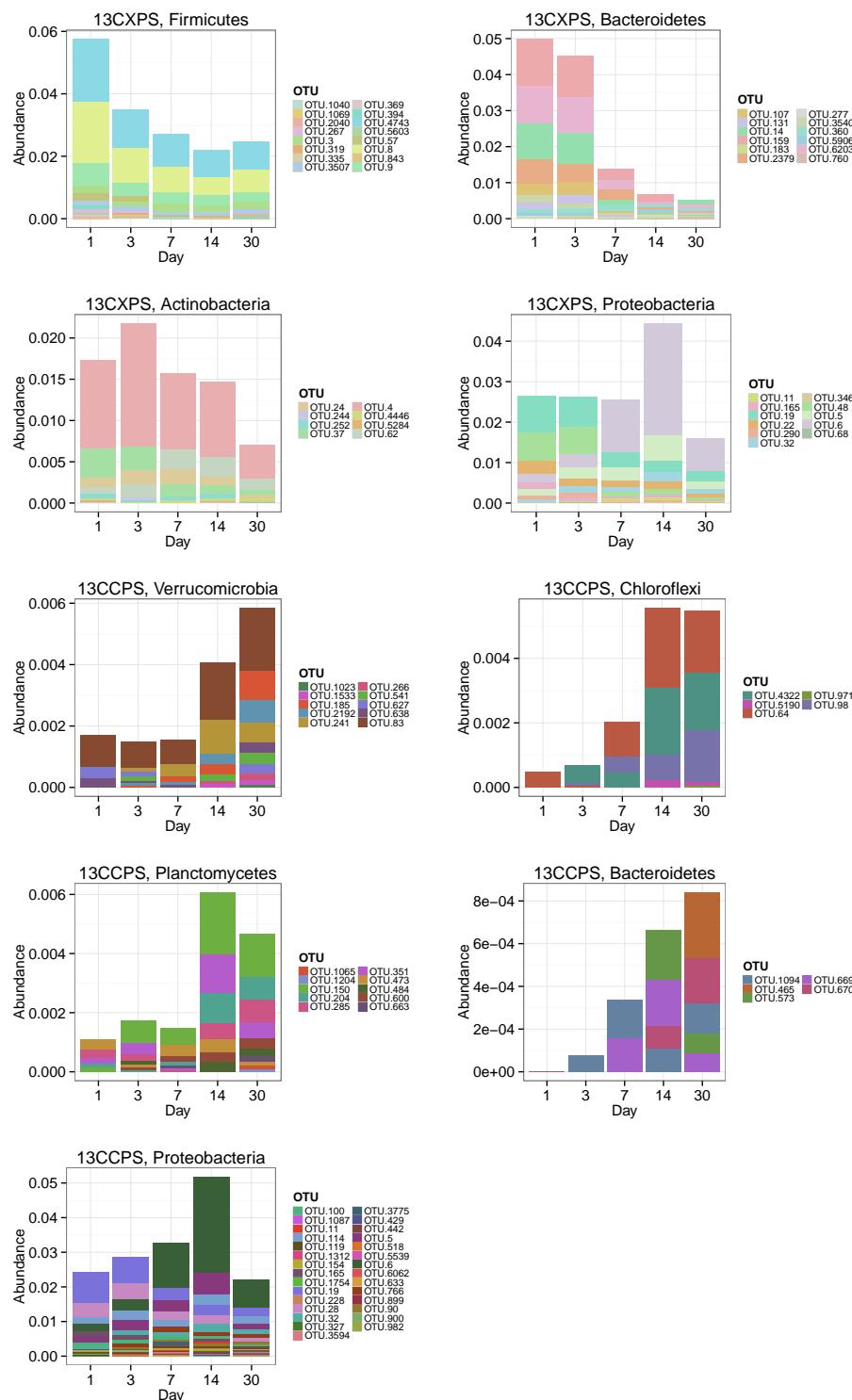


Fig. S8. Ordination of bulk gradient fraction phylogenetic profiles.

**Fig. S9.** Sum of bulk abundances with selected phylum for responder OTUs.

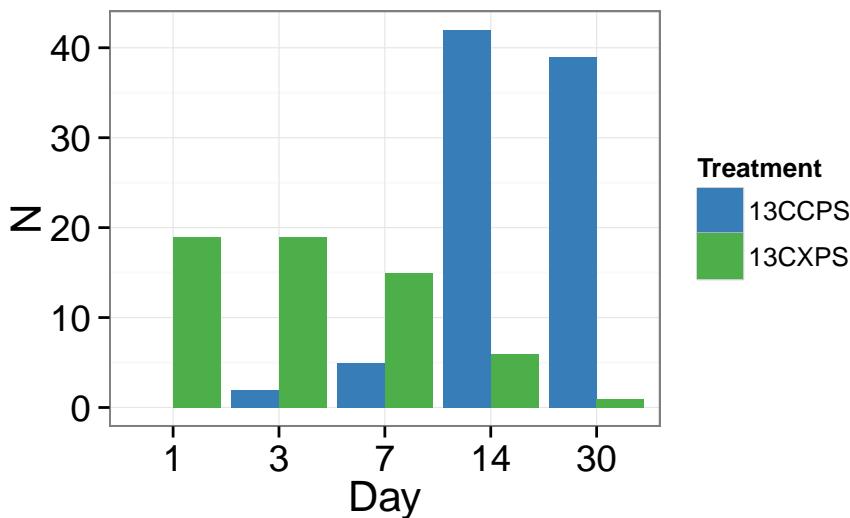


Fig. S10. Counts of responders to each isotopically labeled substrate (cellulose and xylose) over time.

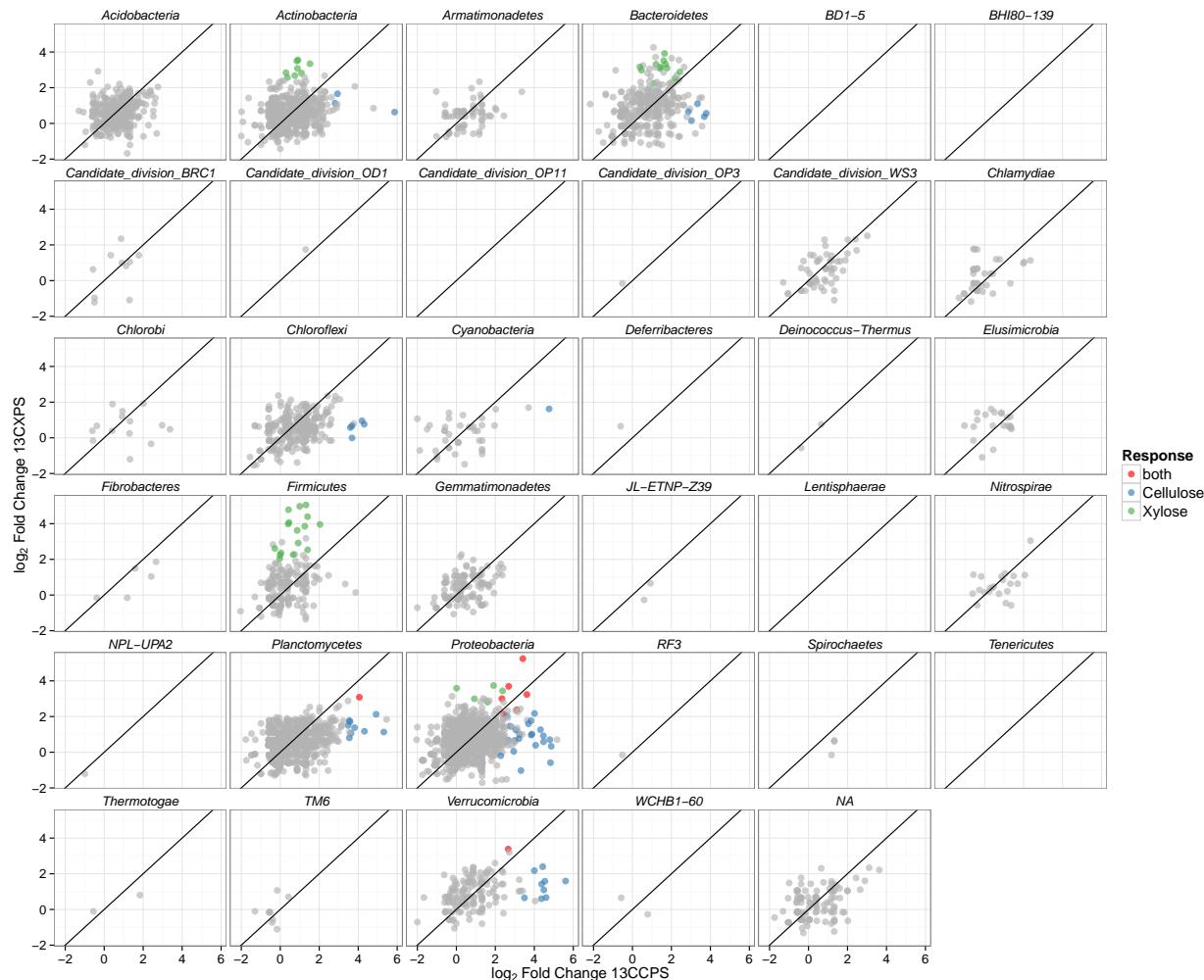


Fig. S11. Maximum \log_2 fold change in response to labeled substrate incorporation for each substrate and all OTUs that pass sparsity filtering in both substrate analyses. Points colored by response. Line has slope of 1 with intercept at the origin. OTUs falling in the top-right quadrant responded to both substrates while those in the top-left and bottom-right responded to ^{13}C -xylose and ^{13}C -cellulose, respectively.



Fig. S12. Phylum specific trees. Heatmap indicates fold change between heavy fractions of control gradients versus labeled gradients. Dots indicate the position of “responders” to ¹³C-xylose (green) or ¹³C-cellulose (blue).

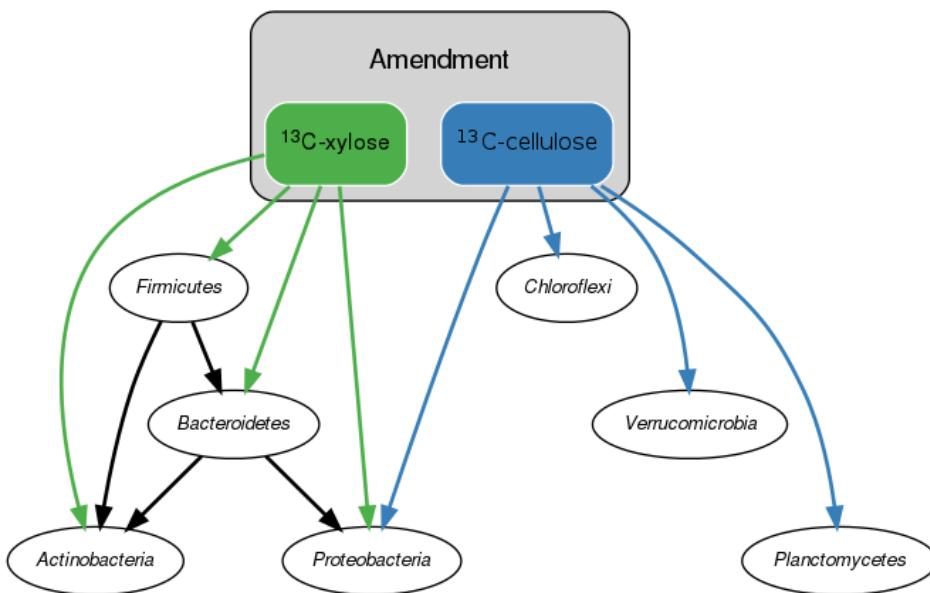


Fig. S13. Conceptual model of soil food web in this experiment.

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

OTU ID	Fold change ^a	Day ^b	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.862	5.87	14	<i>Allokutzneria albata</i>	100.0	<i>Actinobacteria Pseudonocardiales Pseudonocardiaceae</i>
OTU.257	2.94	14	<i>Lentzea waywayandensis, Lentzea flaviverrucosa</i>	100.0	<i>Actinobacteria Pseudonocardiales Pseudonocardiaceae</i>
OTU.132	2.81	14	<i>Streptomyces spp.</i>	100.0	<i>Actinobacteria Streptomycetales Streptomycetaceae</i>
OTU.465	3.79	30	<i>Ohtaekwangia kribbensis</i>	92.73	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.1094	3.69	30	<i>Sporocytophaga myxococcoides</i>	99.55	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.669	3.34	30	<i>Ohtaekwangia koreensis</i>	92.69	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.573	3.03	30	<i>Adhaeribacter aerophilus</i>	92.76	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.670	2.87	30	<i>Adhaeribacter aerophilus</i>	91.78	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.971	3.68	30	No hits of at least 90% identity	78.57	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.64	4.31	14	No hits of at least 90% identity	89.5	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.4322	4.19	14	No hits of at least 90% identity	89.14	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.98	3.68	14	No hits of at least 90% identity	88.18	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.5190	3.6	30	No hits of at least 90% identity	88.13	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.120	4.76	14	<i>Vampirovibrio chlorellavorus</i>	94.52	<i>Cyanobacteria SM1D11 uncultured-bacterium</i>
OTU.1065	5.31	14	No hits of at least 90% identity	84.55	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.484	4.92	14	No hits of at least 90% identity	89.09	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1204	4.32	30	<i>Planctomyces limnophilus</i>	91.78	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.150	4.06	14	No hits of at least 90% identity	86.76	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.663	3.63	30	<i>Pirellula staleyi DSM 6068</i>	90.87	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.473	3.58	14	<i>Pirellula staleyi DSM 6068</i>	90.91	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.285	3.55	30	<i>Blastopirellula marina</i>	90.87	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.351	3.54	14	<i>Pirellula staleyi DSM 6068</i>	91.86	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.600	3.48	30	No hits of at least 90% identity	80.37	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.900	4.87	14	<i>Brevundimonas vesicularis, Brevundimonas nasdae</i>	100.0	<i>Proteobacteria Alphaproteobacteria Caulobacterales</i>
OTU.1754	4.48	14	<i>Asticcacaulis biprosthecum, Asticcacaulis benevestitus</i>	96.8	<i>Proteobacteria Alphaproteobacteria Caulobacterales</i>
OTU.119	3.31	14	<i>Brevundimonas alba</i>	100.0	<i>Proteobacteria Alphaproteobacteria Caulobacterales</i>

Table S1 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.327	2.99	14	<i>Asticcacaulis biprosthecum,</i> <i>Asticcacaulis benevestitus</i>	98.63	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.982	4.47	14	<i>Devosia neptuniae</i>	100.0	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.1087	4.32	14	<i>Devosia soli</i> , <i>Devosia crocina</i> , <i>Devosia riboflavina</i>	99.09	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.5539	4.01	14	<i>Devosia subaequoris</i>	98.17	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.3775	3.88	14	<i>Devosia glacialis</i> , <i>Devosia chinhatensis</i> , <i>Devosia geojensis</i> , <i>Devosia yakushimensis</i>	98.63	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.429	3.7	30	<i>Devosia limi</i> , <i>Devosia psychrophila</i>	97.72	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.766	3.21	14	<i>Devosia insulae</i>	99.54	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.165	3.1	14	<i>Rhizobium skieniewicense</i> , <i>Rhizobium vignae</i> , <i>Rhizobium larrymoorei</i> , <i>Rhizobium alkalisoli</i> , <i>Rhizobium galegae</i> , <i>Rhizobium huautlense</i>	100.0	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.28	2.59	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.19	2.44	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
OTU.90	2.94	14	<i>Sphingopyxis panaciterrae</i> , <i>Sphingopyxis chilensis</i> , <i>Sphingopyxis sp. BZ30</i> , <i>Sphingomonas sp.</i>	100.0	Proteobacteria Alphaproteobacteria Sphingomonadales
OTU.518	4.8	14	<i>Hydrogenophaga intermedia</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.1312	4.07	30	<i>Paucimonas lemoignei</i>	99.54	Proteobacteria Betaproteobacteria Burkholderiales
OTU.114	2.78	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.633	3.84	30	No hits of at least 90% identity	89.5	Proteobacteria Deltaproteobacteria Myxococcales
OTU.3594	3.83	30	<i>Chondromyces robustus</i>	90.41	Proteobacteria Deltaproteobacteria Myxococcales
OTU.442	3.05	30	<i>Chondromyces robustus</i>	92.24	Proteobacteria Deltaproteobacteria Myxococcales
OTU.228	2.54	30	<i>Sorangium cellulosum</i>	98.17	Proteobacteria Deltaproteobacteria Myxococcales

Table S1 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.899	2.28	30	<i>Enhygromyxa salina</i>	97.72	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.6	3.62	7	<i>Cellvibrio fulvus</i>	100.0	<i>Proteobacteria Gammaproteobacteria Pseudomonadales</i>
OTU.6062	4.83	30	<i>Dokdonella sp. DC-3, Luteibacter rhizovicinus</i>	97.26	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.154	3.24	14	<i>Pseudoxanthomonas mexicana, Pseudoxanthomonas japonensis</i>	100.0	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.100	2.66	14	<i>Pseudoxanthomonas sacheonensis, Pseudoxanthomonas dokdonensis</i>	100.0	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.1023	4.61	30	No hits of at least 90% identity	80.54	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.266	4.54	30	No hits of at least 90% identity	83.64	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.541	4.49	30	No hits of at least 90% identity	84.23	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.185	4.37	14	No hits of at least 90% identity	85.14	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.2192	3.49	30	No hits of at least 90% identity	83.56	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.1533	3.43	30	No hits of at least 90% identity	82.27	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.83	5.61	14	<i>Luteolibacter sp. CCTCC AB 2010415</i>	97.72	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.627	4.43	14	<i>Verrucomicrobiaceae bacterium DC2a-G7</i>	100.0	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.638	4.0	30	<i>Luteolibacter sp. CCTCC AB 2010415, Luteolibacter algae</i>	93.61	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>

^a Maximum observed \log_2 of fold change.^b Day of maximum fold change.

Table S2: ^{13}C -xylose responders BLAST against Living Tree Project

OTU ID	Fold change ^a	Day ^b	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.4446	3.49	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	Actinobacteria Frankiales Nakamurellaceae
OTU.62	2.57	7	<i>Nakamurella flava</i>	100.0	Actinobacteria Frankiales Nakamurellaceae
OTU.24	2.81	7	<i>Cellulomonas aerilata</i> , <i>Cellulomonas humilata</i> , <i>Cellulomonas terrae</i> , <i>Cellulomonas soli</i> , <i>Cellulomonas xylolytica</i>	100.0	Actinobacteria Micrococcales Cellulomonadaceae
OTU.4	2.84	7	<i>Agromyces ramosus</i>	100.0	Actinobacteria Micrococcales Microbacteriaceae
OTU.37	2.68	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	Actinobacteria Micrococcales Microbacteriaceae
OTU.5284	3.56	7	<i>Isoptericola nanjingensis</i> , <i>Isoptericola hypogaeus</i> , <i>Isoptericola variabilis</i>	98.63	Actinobacteria Micrococcales Promicromonosporaceae
OTU.252	3.34	7	<i>Promicromonospora thailandica</i>	100.0	Actinobacteria Micrococcales Promicromonosporaceae
OTU.244	3.08	7	<i>Cellulosimicrobium funkei</i> , <i>Cellulosimicrobium terreum</i>	100.0	Actinobacteria Micrococcales Promicromonosporaceae
OTU.760	2.89	3	<i>Dyadobacter hamtensis</i>	98.63	Bacteroidetes Cytophagia Cytophagales
OTU.14	3.92	3	<i>Flavobacterium oncorhynchi</i> , <i>Flavobacterium glycines</i> , <i>Flavobacterium succinicans</i>	99.09	Bacteroidetes Flavobacteria Flavobacteriales
OTU.6203	3.32	3	<i>Flavobacterium granuli</i> , <i>Flavobacterium glaciei</i>	100.0	Bacteroidetes Flavobacteria Flavobacteriales
OTU.159	3.16	3	<i>Flavobacterium hibernum</i>	98.17	Bacteroidetes Flavobacteria Flavobacteriales
OTU.2379	3.1	3	<i>Flavobacterium pectinovorum</i> , <i>Flavobacterium sp. CS100</i>	97.72	Bacteroidetes Flavobacteria Flavobacteriales
OTU.131	3.07	3	<i>Flavobacterium fluvii</i> , <i>Flavobacterium bacterium HMD1033</i> , <i>Flavobacterium sp. HMD1001</i>	100.0	Bacteroidetes Flavobacteria Flavobacteriales
OTU.3540	2.52	3	<i>Flavobacterium terrigena</i>	99.54	Bacteroidetes Flavobacteria Flavobacteriales
OTU.107	2.25	3	<i>Flavobacterium sp. 15C3</i> , <i>Flavobacterium banpakuense</i>	99.54	Bacteroidetes Flavobacteria Flavobacteriales
OTU.277	3.52	3	<i>Solibius ginsengiterrae</i>	95.43	Bacteroidetes Sphingobacteriia Sphingobacteriales
OTU.183	3.31	3	No hits of at least 90% identity	89.5	Bacteroidetes Sphingobacteriia Sphingobacteriales
OTU.5906	3.16	3	<i>Terrimonas sp. M-8</i>	96.8	Bacteroidetes Sphingobacteriia Sphingobacteriales
OTU.360	2.98	3	<i>Flavisolibacter ginsengisoli</i>	95.0	Bacteroidetes Sphingobacteriia Sphingobacteriales

Table S2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.369	5.05	1	<i>Paenibacillus sp. D75,</i> <i>Paenibacillus glycansilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.267	4.97	1	<i>Paenibacillus pabuli,</i> <i>Paenibacillus tundrae,</i> <i>Paenibacillus taichungensis,</i> <i>Paenibacillus xylanexedens,</i> <i>Paenibacillus xylanilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.1040	4.78	1	<i>Paenibacillus daejeonensis</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.57	4.39	1	<i>Paenibacillus castaneae</i>	98.62	<i>Firmicutes Bacilli Bacillales</i>
OTU.394	4.06	1	<i>Paenibacillus pocheonensis</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.319	3.98	1	<i>Paenibacillus xinjiangensis</i>	97.25	<i>Firmicutes Bacilli Bacillales</i>
OTU.5603	3.96	1	<i>Paenibacillus uliginis</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.1069	3.85	1	<i>Paenibacillus terrigena</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.843	3.62	1	<i>Paenibacillus agarexedens</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.2040	2.91	1	<i>Paenibacillus pectinilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.3	2.61	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.335	2.53	1	<i>Paenibacillus thailandensis</i>	98.17	<i>Firmicutes Bacilli Bacillales</i>
OTU.3507	2.36	1	<i>Bacillus spp.</i>	98.63	<i>Firmicutes Bacilli Bacillales</i>
OTU.8	2.26	1	<i>Bacillus niaci</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.4743	2.24	1	<i>Lysinibacillus fusiformis</i> , <i>Lysinibacillus sphaericus</i>	99.09	<i>Firmicutes Bacilli Bacillales</i>
OTU.9	2.04	1	<i>Bacillus megaterium</i> , <i>Bacillus flexus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.22	2.8	7	<i>Paracoccus sp. NB88</i>	99.09	<i>Proteobacteria Alphaproteobacteria Rhodobacterales</i>
OTU.5	3.69	7	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	<i>Proteobacteria Betaproteobacteria Burkholderiales</i>
OTU.346	3.44	3	<i>Pseudoduganella violaceinigra</i>	99.54	<i>Proteobacteria Betaproteobacteria Burkholderiales</i>
OTU.32	3.0	3	<i>Sandaracinus amyloyticus</i>	94.98	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.68	3.74	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.290	3.59	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 Gammaproteobacteria Enterobacteriales</i>
OTU.11	5.25	7	<i>Stenotrophomonas pavani</i> , <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.48	2.99	1	<i>Aeromonas spp.</i>	100.0	<i>Proteobacteria Gammaproteobacteria aaa34a10</i>
OTU.241	3.38	3	No hits of at least 90% identity	87.73	<i>Verrucomicrobia Spartobacteria Chthoniobacteriales</i>

^a Maximum observed \log_2 of fold change.^b Day of maximum fold change.