

Unearthing the soil carbon food web with high resolution 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

Significance

We have limited understanding of soil carbon (C) cycling yet soil contains a large fraction of the global C pool. Microorganisms mediate most soil C cycling but have proven difficult to study due to the complexity of soil C biochemistry and the wide range of soil microorganisms participating in C reactions. We demonstrate temporal C use dynamics in discrete soil microbial taxa. Furthermore, we identified novel microorganisms involved in cellulose decomposition, the most globally abundant biopolymer. Further application of the method demonstrated in this paper will identify microbial taxa that mediate soil C transformations for more substrates and soils and increase our understanding of global soil C cycling.

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 CO₂ annually than anthropogenic emissions [3]. Global changes in atmospheric CO₂, 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].

To establish the relationship between community structure and soil function we must identify the *in situ* activity of specific soil microbes [7]. An estimated 80-90% of soil C cycling is mediated by microorganisms [8, 9] but exploring soil C processing is challenging due to soil's heterogeneous nature. The majority of microorganisms resist cultivation in the laboratory. Stable-isotope probing (SIP) links genetic identity and activity without cultivation and has been used to expand our knowledge of microbial contributions to biogeochemical processes [10]. Successful applications of SIP have identified organisms which mediate processes performed by a narrow set of functional guilds such as methanogens [11] but SIP has been less applicable in soil C cycling studies due to limitations in resolving power as a result of simultaneous labeling of many different organisms. High throughput DNA sequencing technology, however, has enabled

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exploration of complex soil C-cycling patterns via SIP.

A temporal activity cascade occurs in natural microbial communities during plant biomass degradation in which labile C is degraded before polymeric C [12, 13]. This study’s aim was to observe C assimilation dynamics in the soil microbial community. Our experimental approach included the addition of a soil organic matter (SOM) simulant to soil microcosms where a single C component was substituted for its ^{13}C equivalent. Parallel incubations of soils amended with this C mixture allowed 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 SIP with high throughput DNA sequencing. Amplicon sequencing of 16S rRNA genes from gradient fractions of multiple density gradients made it possible to track C assimilation by 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 C composition of fresh plant biomass. The same mixture was added to all microcosms, however, for each series except the control, xylose or cellulose was substituted for its ^{13}C counterpart. Microcosm amendments are identified in figures by the following code: “13CXPS” refers to the amendment with ^{13}C -xylose (^{13}C Xylose Plant Simulant), “13CCPS” refers to the ^{13}C -cellulose amendment and “12CCPS” refers to the amendment that only contained ^{12}C (i.e. control). 5.3 mg C substrate mixture per gram of soil 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 per gram soil. 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. Changes in the bulk soil microcosm microbial community structure and membership correlated significantly with incubation time (Figure S7B, 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 correlate with bulk soil 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], Figure XX). Twenty-nine OTUs significantly changed in relative abundance with time (“BH” adjusted p-value <0.10, [17]) and of these 29 OTUs, 14 were labeled substrate responders (Figure S2). If sequences were grouped by taxonomic annotations at the class level, only four classes significantly changed in abundance, *Bacilli* (decreased), *Flavobacteria* (decreased), *Gamma proteobacteria* (decreased) and *Herpetosiphonales* (increased) (Figure S5).

Responder abundances summed at phylum level increased for ^{13}C -cellulose (Figure S8) 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 S8).

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.

We refer to OTUs that putatively incorporated ^{13}C into DNA originally from an isotopically labeled substrate as substrate “responders” (see Supplemental Note XX for “response” criteria). 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 ^{13}C -xylose responders changed with time. The numerically dominant ^{13}C -xylose responder phylum shifted from *Firmicutes* to *Bacteroidetes* and then to *Actinobacteria* across days 1, 3 and 7 (Figure 4, Figure 2).

Only 2 and 5 OTUs had incorporated ^{13}C from ^{13}C -cellulose at days 3 and 7, respectively. At days 14 and 30, 42 and 39 OTUs incorporated ^{13}C from ^{13}C -cellulose into biomass. A *Cellvibrio* and *Sandaracinaceae* OTU assimilated ^{13}C from ^{13}C -cellulose at day 3. Day 7 ^{13}C -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 ^{13}C 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 4).

Ecological strategies of ^{13}C responders. ^{13}C -xylose responders are generally more abundant members based on relative abundance in bulk DNA SSU rRNA gene content than ^{13}C -cellulose responders (Figure 3, p-value 0.00028). However, both abundant and rare OTUs responded to ^{13}C -xylose and ^{13}C -cellulose (Figure 3). Two ^{13}C -cellulose responders were not found in any bulk samples (“OTU.862” and “OTU.1312”, Table S1). Of the 10 most abundant responders, 8 are ^{13}C -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 1.8610x^{-06}). ^{13}C -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% ^{13}C DNA BD is 0.04 g mL^{-1} greater than the BD of its ^{12}C counterpart. DNA BD increases as its ratio of ^{13}C to ^{12}C increases. An organism that only assimilates C into DNA from a ^{13}C isotopically labeled source, will have a greater $^{13}\text{C}:\text{C}$ ratio in its DNA than an organism utilizing a mixture of isotopically labeled and unlabeled C sources (see supplemental note XX).

^{13}C -xylose responder estimated *rrn* gene copy number was inversely related time of first response (p-value $2.02\text{x}10^{-15}$, Figure S1). OTUs that first respond at later time points have fewer estimated *rrn* copy number than OTUs that first respond earlier (Figure S1).

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 sin-

gle experiment without cultivation. We identified 104 OTUs in an agricultural soil that incorporated ^{13}C from xylose and/or cellulose into biomass and characterized substrate specificity and C-cycling dynamics for these soluble and polymeric C degraders. Included in ^{13}C -xylose and ^{13}C -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 S12): 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 ^{13}C -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). Ecological metrics suggest ^{13}C -cellulose responsive OTUs grow slower (Figure 3, Figure S1), 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 higher *rrn* gene copy number. ^{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 S1) suggesting fast-growing microbes assimilated ^{13}C from xylose before slow growers.

Labile C responder ecological strategies were more varied than polymeric ecological strategies perhaps because ^{13}C labeled microorganisms did not primarily assimilate xylose but became labeled via predatory interactions and/or are saprophytes. 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 S6). It’s also clear that some of the non-*Firmicutes* ^{13}C -xylose responders are closely related to known predators (e.g. *Agromyces*) and *Bacteroidetes* have been previously implicated as predatory soil bacteria [20]. 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, aerobic spore-formers. Hence, predatory interactions between soil bacteria may be of importance for modelling soil C turnover.

Implications for soil C cycling models. Land management, climate, pollution and disturbance can all influence soil community composition CITE which in turn can influence biogeochemical process rates CITE. Assessing functional group diversity and establishing identities of functional group members is an important step in predicting how biogeochemical process rates can change with community composition CITE. We highlight three key results in our study with implications for soil C cycling models: (1) labile and polymeric C decomposers may have similar within group phylogenetic breadth, (2) soil biomass does not respond *en masse* to C additions, and (3) trophic interactions among soil bacteria may greatly influence soil C fate.

It is assumed that transformations carried out by functional guilds of “narrow” phylogenetic breadth can be influenced more significantly by compositional change than processes carried out by a large number of taxa (CITE Tresseder, Schimel). “Narrow” processes are thought to include nitrogen transformations such as nitrogen fixation and denitrification, and recalcitrant C decomposition (CITE). Labile C is considered a “broad” process comparatively (CITE), however, the phylogenetic breadth of active labile C and recalcitrant C decomposers in soil has not been observed directly. Our results are in conflict with the established paradigm that labile C degradation is a “broader” process than recalcitrant C degradation. In fact, we found more OTUs responded to ^{13}C -cellulose, 63, than ^{13}C -xylose, 49. Further, both ^{13}C -cellulose and ^{13}C -xylose responders were largely clustered at taxonomic levels broader than the OTUs established in this study (Figure S6) with *Proteobacteria* ^{13}C -responders being a possible exception for cellulose and xylose. The phylogenetic clustering of substrate response suggests that both cellulose and xylose decomposition are “narrow” processes as opposed to “broad” and it follows that labile C dynamics in soil may be influ-

enced similarly in magnitude to recalcitrant C dynamics in response to changes in community composition.

”However, most process-based models that incorporate microbes are based on simple microbial parameters or functions”

Biogeochemical process models are the specific mechanism by which process rates are predicted. Biogeochemical models of soil C cycling, however, often treat soil biomass with simple and few parameters CITE.

Trophic interactions in soil C cycling are often modelled at the taxonomic level of domain CITE. That is, models have considered C cycling between bacteria and protists (CITE), for example, but not C cycling between among bacteria. We observed a cascade in activity with xylose additions that suggests significant trophic interactions among soil bacteria. Although we cannot be sure the temporal nature of ^{13}C -xylose response observed in our study can be attributed to predatory interactions, we note that the activity peak of *Bacteroidetes* and *Actinobacteria* occurred with a concomitant decrease in *Firmicutes* ^{13}C -xylose responder relative abundance. Considering that *Agromyces* and certain *Bacteroidetes* types are likely soil predators (CITE) one parsimonious hypothesis for ^{13}C -labelling of *Bacteroidetes* and *Actinobacteria* with a corresponding decrease in abundance of ^{13}C -labelled *Firmicutes* is that the *Bacteroidetes* and *Actinobacteria* fed on the ^{13}C -labelled *Firmicutes*.

”We conclude that predicting the influence of declining species diversity on trophic-level dynamics and ecosystem processes is difficult, at least in food webs with a small initial number of species, unless the characteristics of species and the nature of their interactions are known.”

”Research questions of the highest urgency are the assignment of species to functional groups and determining the redundancy of species within functional groups”

”These priorities follow from the need to address the extent of any loss of functioning in soils, associated with intensive agriculture, forest disturbance, pollution of the environment, and global environmental change.”

”The soil biota considered at present to be most at risk are species-poor functional groups among macrofaunal shredders of organic matter, bioturbators of soil, specialized bacteria like nitrifiers and nitrogen fixers, and fungiforming mycorrhizas”

Key results:

Verrucomicrobia, Chloroflexi, Firmicutes, for instance

narrow versus broad processes, labile versus recalcitrant carbon

trophic levels are inter-domain or implied as such

- (1) diversity of functional groups – species poor, narrow processes
- (2) predators
- (3) different types for different substrates, not en masse

Three findings are particularly notable: (1) soil microbes that use cellulose are largely different than those that use xylose (Figure 1), (2) C from labile sources passes through phylogenetically coherent groups in succession (Figure XX), and, (3) a small subset of the total suite of soil microbes used cellulose or xylose in our microcosms. Our findings imply that environmental perturbation can affect decomposition of C substrates in different ways, phylogenetically coherent groups of predators may feed on opportunistic microbes that grow on labile C, and that the diversity of soil microorganisms does not respond *en masse* to C input. Predicting how environmental changes will influence ecosystem processes such as cellulose decomposition will require studies to assess what mechanisms – biotic or otherwise – are rate limiting, how different microbes allocate C resources, which microorganisms participate in specific C transformations, and whether a few key taxa or complementary, diverse assemblages participate in the process. Here, we focus on the diversity and identities within functional guilds of C-cycling soil microbes.

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 soil lineages participated in cellulose decomposition. Cellulose C degraders included members of the *Verrucomicrobia* (*Spartobacteria*), *Chloroflexi*, *Bacteroidetes* and *Planctomycetes*. *Spartobacteria* in particular are globally cosmopolitan soil microorganisms and are often the most abundant *Verrucomicrobia* order in soil CITE. Our results also suggest that members of the *Bacteroidetes* and *Actinobacteria* act in the cascade 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 dynamics are 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 [21]. 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 [22]. To prepare nucleic acid extracts for isopycnic centrifugation as previously described [23], 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 [24] 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-nonenriched DNA. Each gradient was loaded with approximately 5 µg of DNA and ultracentrifuged for 66 h at 55,000 rpm and room temperature (RT). Fractions of ~100 µL 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 µL s⁻¹ [25] 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 [23] to measure a volume of 5 µL. Then buoyant density was calculated from the refractive index as previously described [23] (see also SI). The collected DNA fractions were purified by repetitive washing of Acroprep filter wells with TE. Finally, 50 µL 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 [26], 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 $0.25 \mu\text{L}$ $5 \text{ U } \mu\text{l}^{-1}$ AmpliTaq Gold (Life Technologies, Grand Island, NY; N8080243), $2.5 \mu\text{L}$ 10X Buffer II (100 mM Tris-HCl, pH 8.3, 500 mM KCl), $2.5 \mu\text{L}$ 25 mM MgCl_2 , $4 \mu\text{L}$ 5 mM dNTP, $1.25 \mu\text{L}$ 10 mg mL^{-1} BSA, $0.5 \mu\text{L}$ $10 \mu\text{M}$ BA515F, $1 \mu\text{L}$ $5 \mu\text{M}$ BA806R, $3 \mu\text{L}$ H_2O , $10 \mu\text{L}$ 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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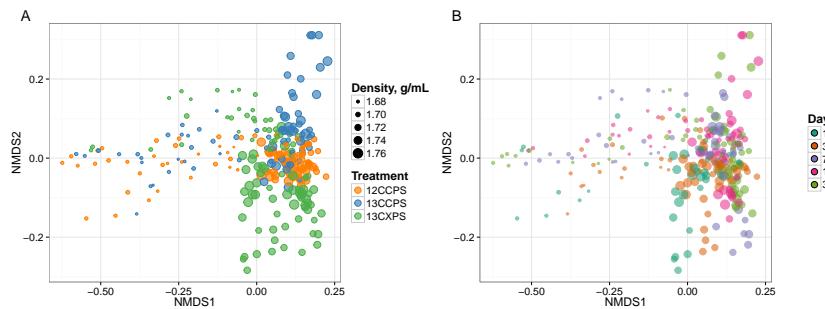


Fig. 1. NMDS analysis from weighted unifrac distances of 454 sequence data from SIP fractions of each treatment over time. Twenty fractions from a CsCl gradient fractionation for each treatment at each time point were sequenced (Fig. S1). Each point on the NMDS represents the bacterial composition based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

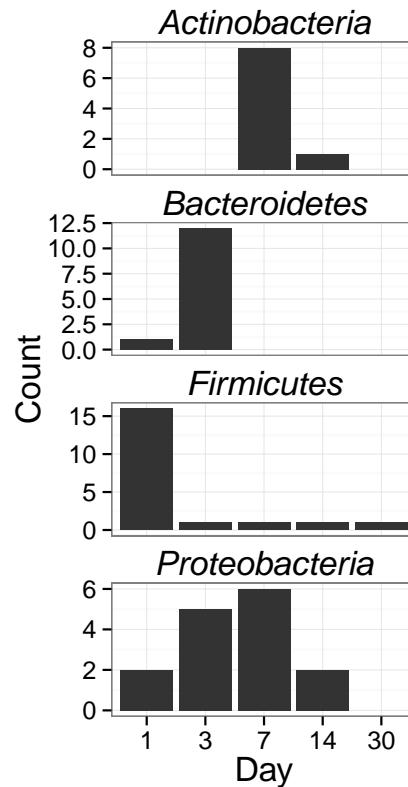


Fig. 2. Counts of ^{13}C -xylose responders in the *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria* at days 1, 3, 7 and 30.

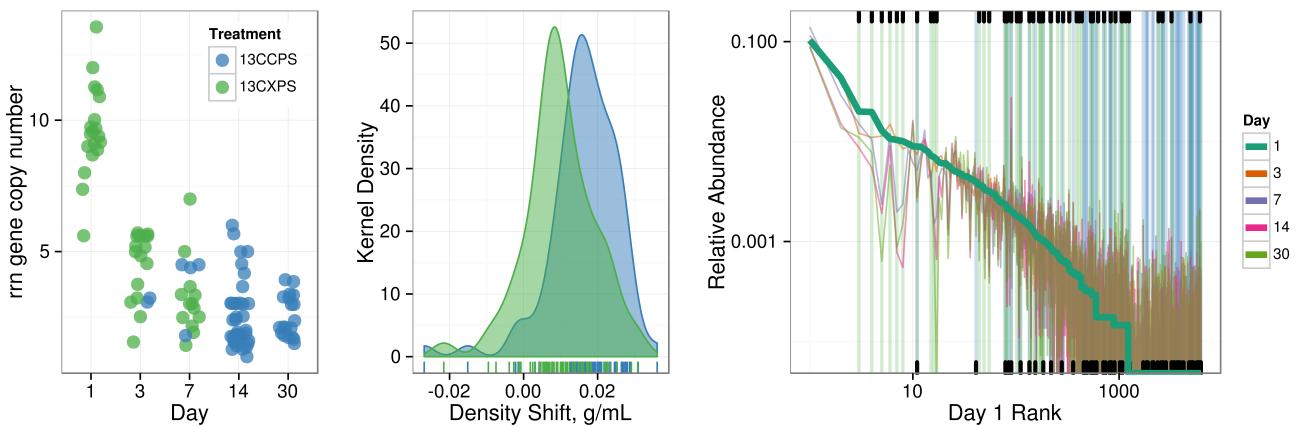


Fig. 3. ^{13}C -responder characteristics based on density shift (A) and rank (B). Kernel density estimation of ^{13}C -responder's density shift in cellulose treatment (blue) and xylose treatment (green) demonstrates degree of labeling for responders for each respective substrate. ^{13}C -responders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

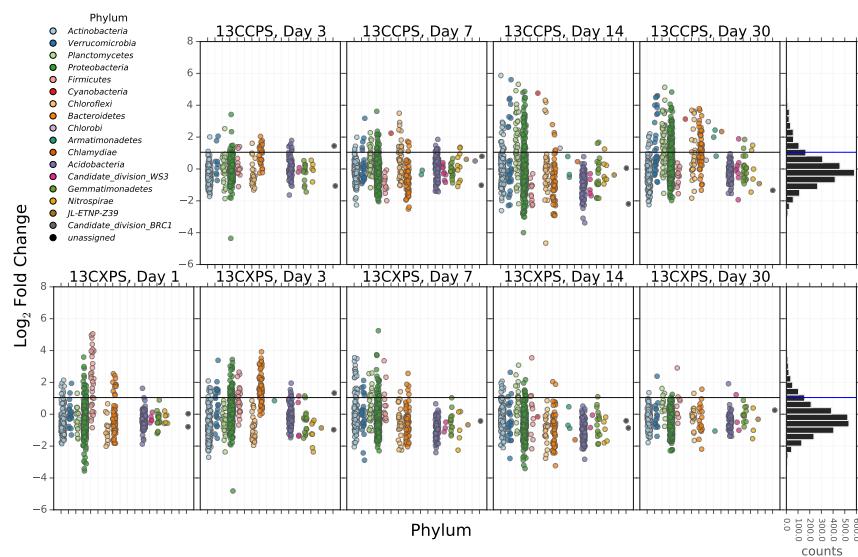


Fig. 4. Log₂ fold change of ^{13}C -responders in cellulose treatment (top) and xylose treatment (bottom). Log₂ fold change is based on the relative abundance in the experimental treatment compared to the control within the density range 1.7125–1.755 g ml⁻¹. Taxa are colored by phylum. ‘Counts’ is a histogram of log₂ fold change values.

Supplemental Figures and Tables

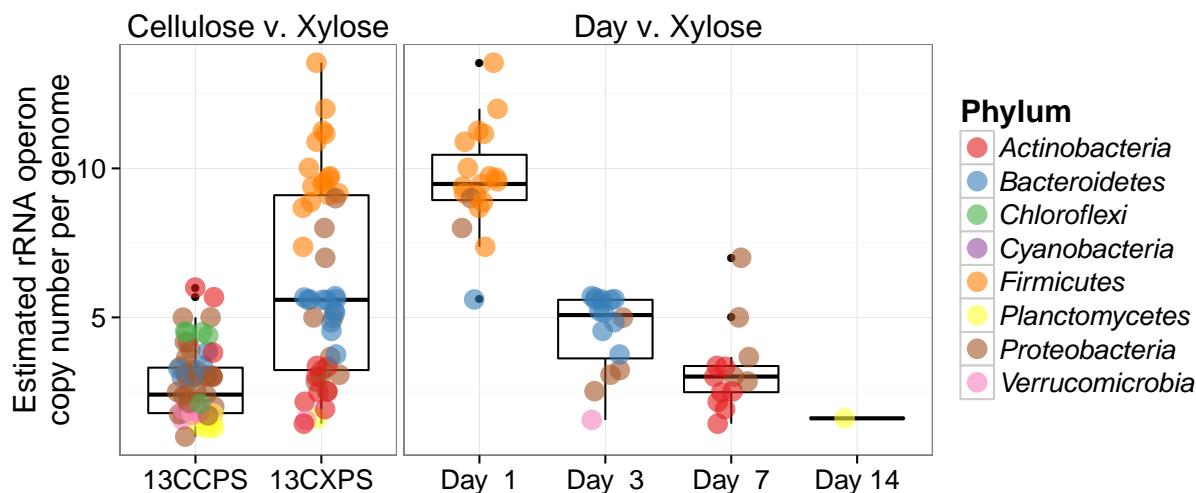


Fig. S1. Estimated rRNA operon copy number per genome for ^{13}C responding OTUs. Panel titles indicate which labeled substrate(s) are depicted.

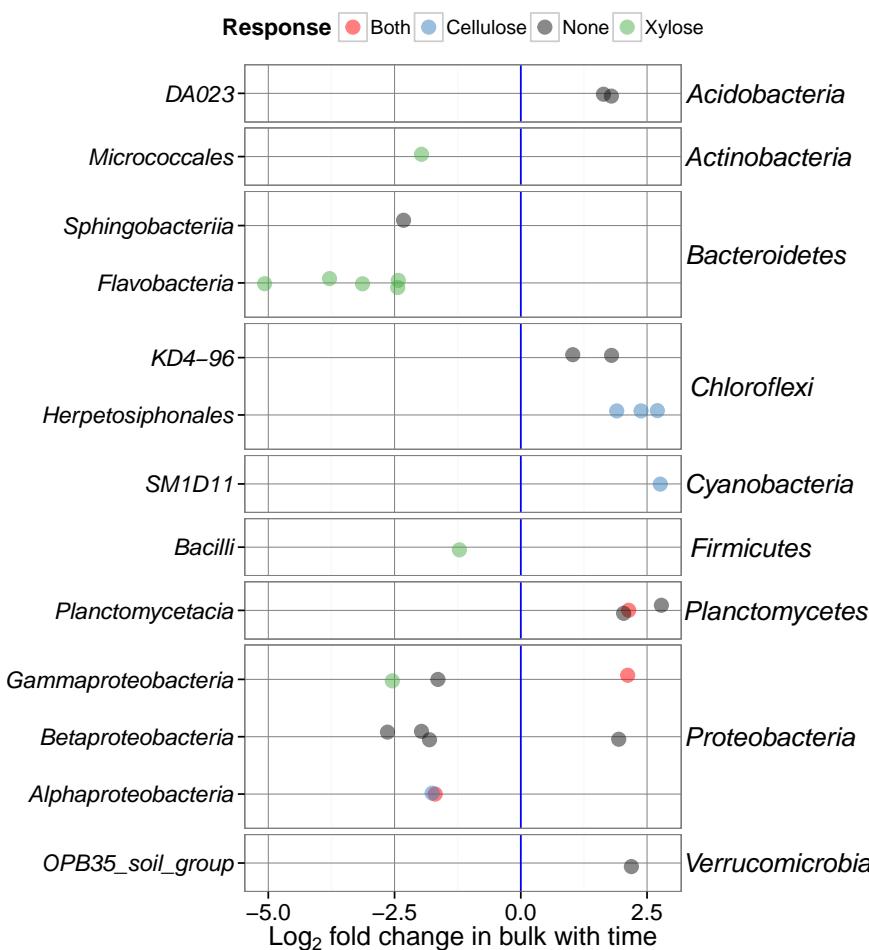


Fig. S2. Fold change time^{-1} for OTUs that changed significantly in abundance over time. One panel per phylum (phyla indicated on the right). Taxonomic class indicated on the left.

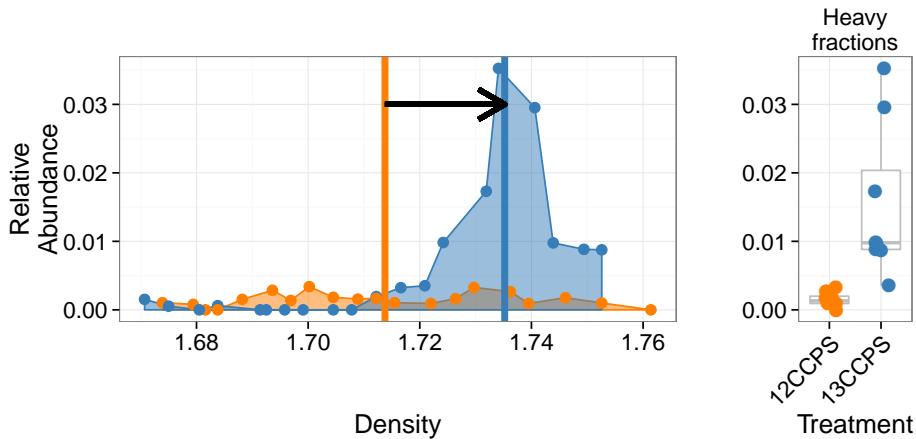


Fig. S3. Density profile for a single ^{13}C -cellulose “responder” OTU in the labeled gradient, blue, and the control gradient, orange. Vertical lines show center of mass for each density profile and arrow denotes the magnitude and direction of the BD shift upon labeling. Panel at right shows relative abundance values in the heavy fractions for each gradient.

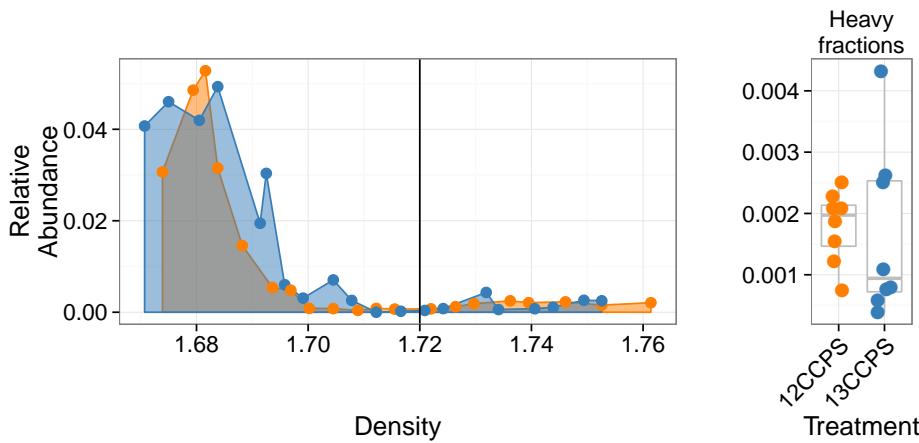


Fig. S4. Density profile for a single ^{13}C -cellulose “non-responder” OTU in the labeled gradient, blue, and the control gradient, orange. Vertical line shows where “heavy” fractions begin as defined in our analysis. Panel at right shows relative abundance values in the heavy fractions for each gradient.

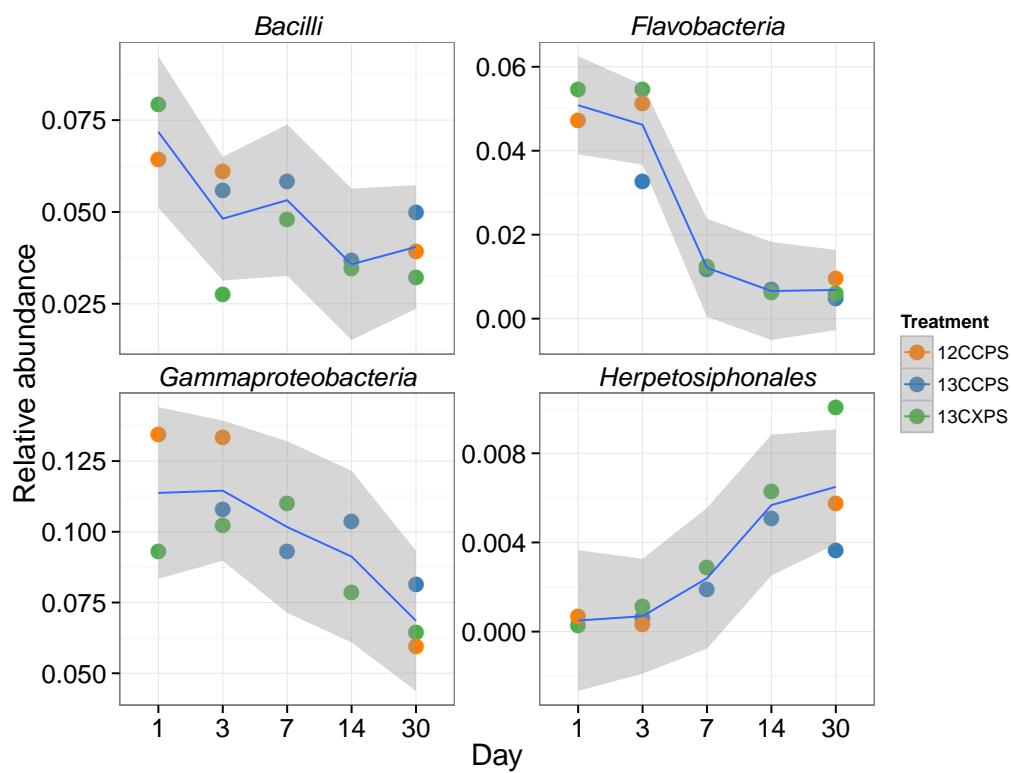


Fig. S5. Relative abundance versus day for classes that changed significantly in relative abundance with time.

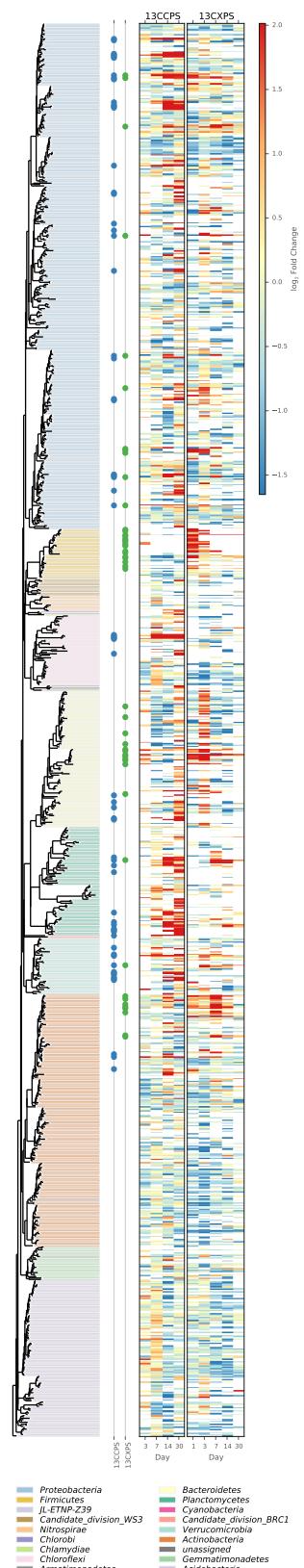


Fig. S6. Phylogenetic tree of sequences passing a user defined sparsity threshold (0.6) for at least one day of the time series. Branches are colored by phylum. ^{13}C -responders for cellulose (blue) and xylose (green) are indicated by a point beside the respective branch. Heatmap demonstrates \log_2 fold change of each taxa through the full time series for both treatments (cellulose, left; xylose, right).

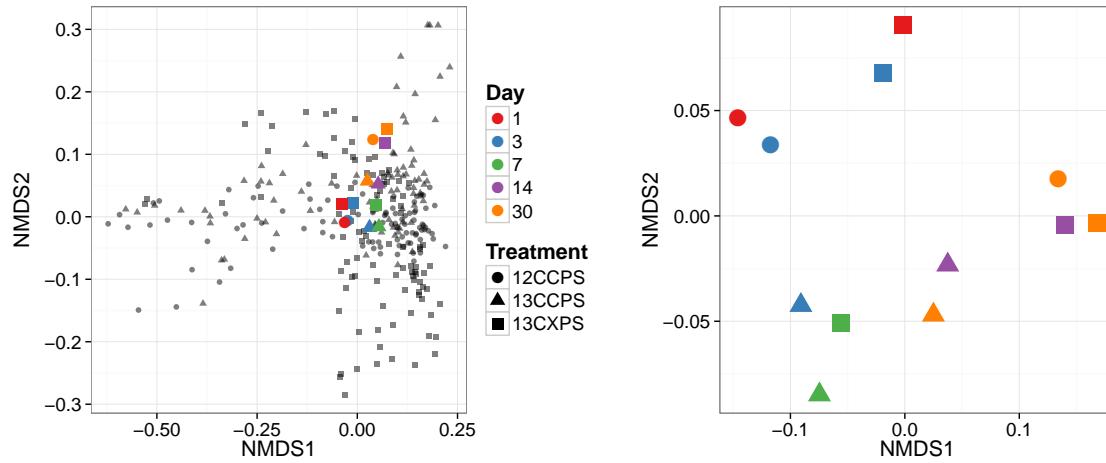
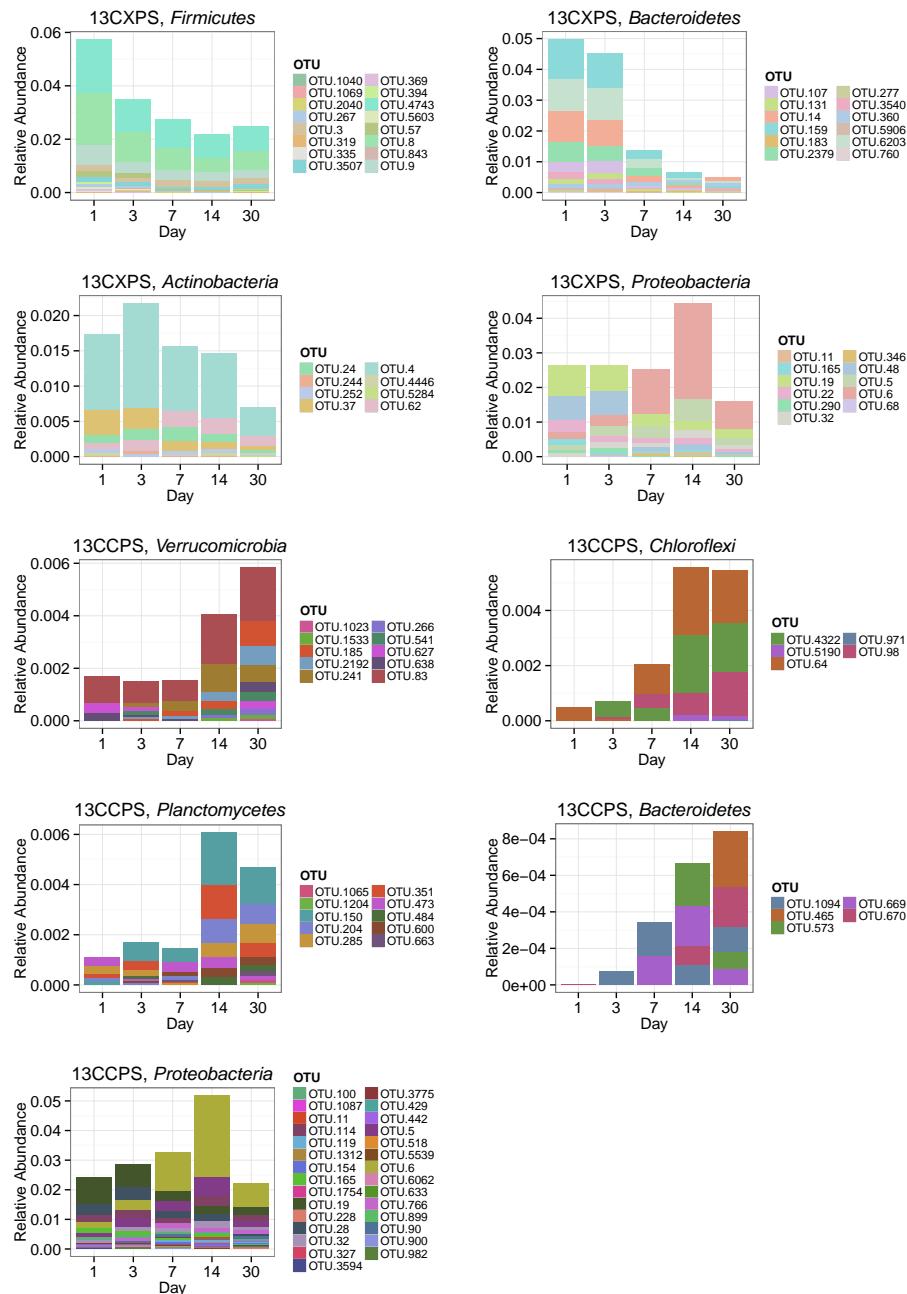


Fig. S7. Ordination of bulk gradient fraction phylogenetic profiles.

**Fig. S8.** Sum of bulk abundances with selected phylum for responder OTUs.

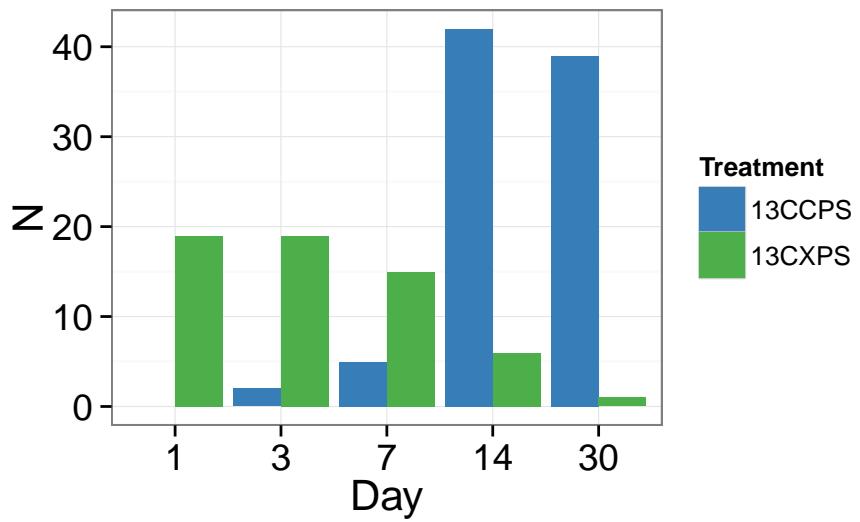


Fig. S9. Counts of responders to each isotopically labeled substrate (cellulose and xylose) over time.

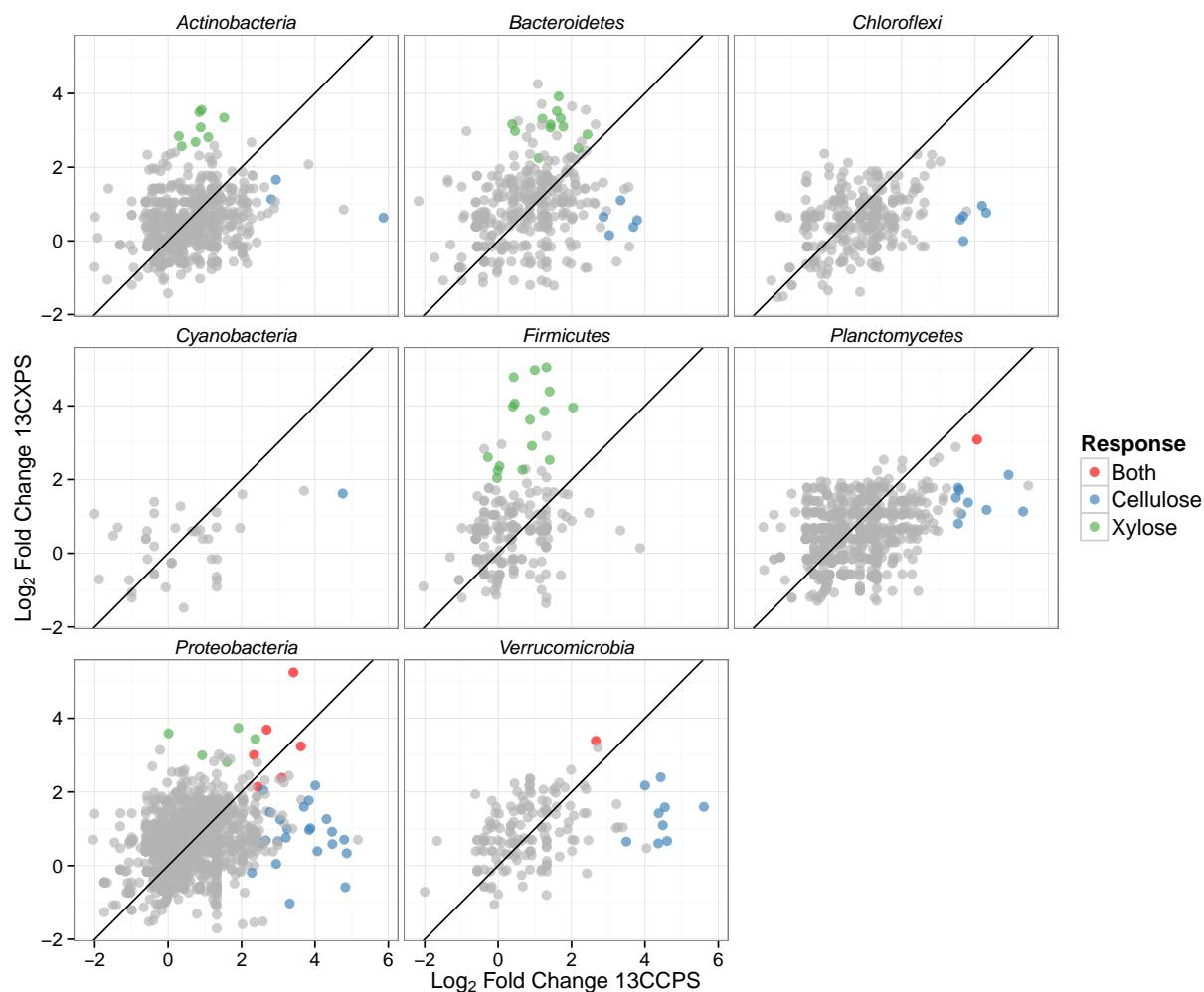


Fig. S10. Maximum \log_2 fold change in response to labeled substrate incorporation for each substrate and all OTUs that pass sparsity filtering in both substrate analyses. Points colored by response. Line has slope of 1 with intercept at the origin. OTUs falling in the top-right quadrant responded to both substrates while those in the top-left and bottom-right responded to ^{13}C -xylose and ^{13}C -cellulose, respectively.

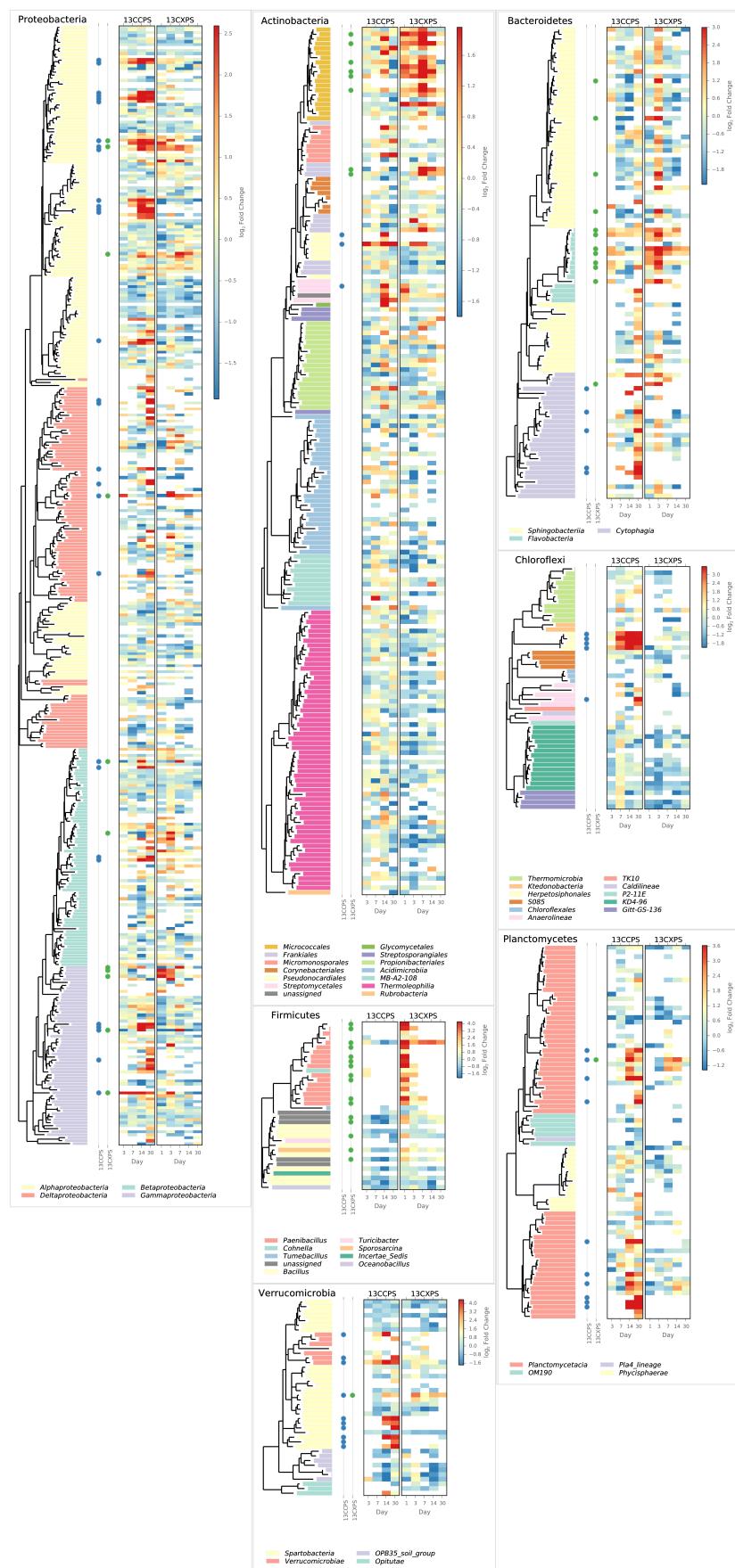


Fig. S11. Phylum specific trees. Heatmap indicates fold change between heavy fractions of control gradients versus labeled gradients. Dots indicate the position of “responders” to ^{13}C -xylose (green) or ^{13}C -cellulose (blue).

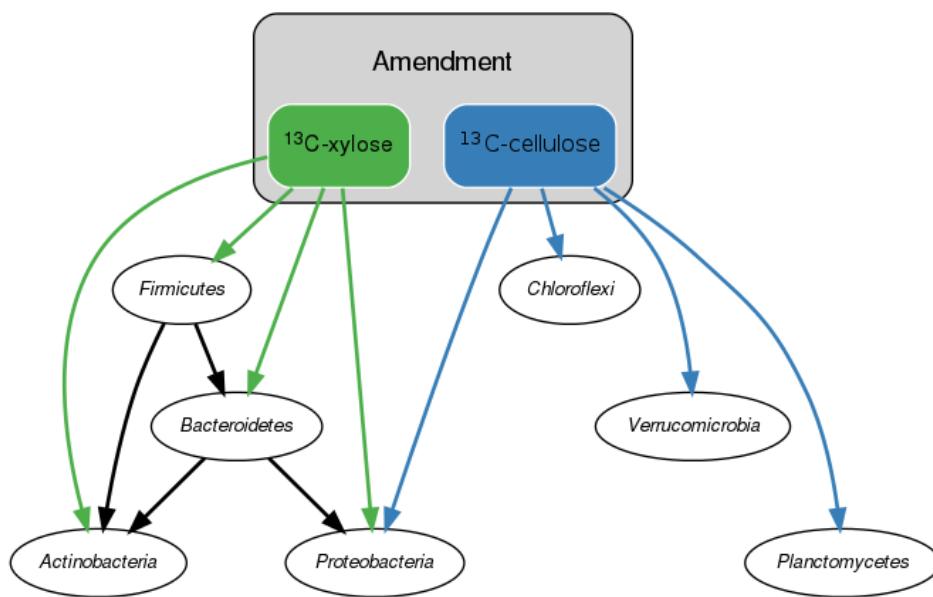


Fig. S12. Conceptual model of soil food web in this experiment.

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.100	2.66	14	<i>Pseudoxanthomonas sacheonensis</i> , <i>Pseudoxanthomonas dokdonensis</i>	100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.1023	4.61	30	No hits of at least 90% identity	80.54	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.1065	5.31	14	No hits of at least 90% identity	84.55	Planctomycetes Planctomycetacia Planctomycetales
OTU.1087	4.32	14	<i>Devsia soli</i> , <i>Devsia crocina</i> , <i>Devsia riboflavina</i>	99.09	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.1094	3.69	30	<i>Sporocytophaga myxococcoides</i>	99.55	Bacteroidetes Cytophagia Cytophagales
OTU.11	3.41	14	<i>Stenotrophomonas pavanii</i> , <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	Proteobacteria Gammaproteobacteria Xanthomonadales
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.119	3.31	14	<i>Brevundimonas alba</i>	100.0	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.120	4.76	14	<i>Vampirovibrio chlorellavorus</i>	94.52	Cyanobacteria SM1D11 uncultured-bacterium
OTU.1204	4.32	30	<i>Planctomyces limnophilus</i>	91.78	Planctomycetes Planctomycetacia Planctomycetales
OTU.1312	4.07	30	<i>Paucimonas lemoignei</i>	99.54	Proteobacteria Betaproteobacteria Burkholderiales
OTU.132	2.81	14	<i>Streptomyces spp.</i>	100.0	Actinobacteria Streptomycetales Streptomycetaceae
OTU.150	4.06	14	No hits of at least 90% identity	86.76	Planctomycetes Planctomycetacia Planctomycetales
OTU.1533	3.43	30	No hits of at least 90% identity	82.27	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.154	3.24	14	<i>Pseudoxanthomonas mexicana</i> , <i>Pseudoxanthomonas japonensis</i>	100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.165	3.1	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	<i>Asticcacaulis biprosthecium</i> , <i>Asticcacaulis benevestitus</i>	96.8	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.185	4.37	14	No hits of at least 90% identity	85.14	Verrucomicrobia Spartobacteria Chthoniobacterales
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.204	3.81	14	No hits of at least 90% identity	nan	Planctomycetes Planctomycetacia Planctomycetales

Table S1 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.2192	3.49	30	No hits of at least 90% identity	83.56	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.228	2.54	30	<i>Sorangium cellulosum</i>	98.17	Proteobacteria Deltaproteobacteria Myxococcales
OTU.241	2.66	14	No hits of at least 90% identity	87.73	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.257	2.94	14	<i>Lentzea waywayandensis</i> , <i>Lentzea flaviverrucosa</i>	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.266	4.54	30	No hits of at least 90% identity	83.64	Verrucomicrobia Spartobacteria Chthoniobacterales
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.285	3.55	30	<i>Blastopirellula marina</i>	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.32	2.34	3	<i>Sandaracinus amylolyticus</i>	94.98	Proteobacteria Deltaproteobacteria Myxococcales
OTU.327	2.99	14	<i>Asticcacaulis biprosthecum</i> , <i>Asticcacaulis benevestitus</i>	98.63	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.351	3.54	14	<i>Pirellula staleyi DSM 6068</i>	91.86	Planctomycetes Planctomycetacia Planctomycetales
OTU.3594	3.83	30	<i>Chondromyces robustus</i>	90.41	Proteobacteria Deltaproteobacteria Myxococcales
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.4322	4.19	14	No hits of at least 90% identity	89.14	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.442	3.05	30	<i>Chondromyces robustus</i>	92.24	Proteobacteria Deltaproteobacteria Myxococcales
OTU.465	3.79	30	<i>Ohtaekwangia kribbensis</i>	92.73	Bacteroidetes Cytophagia Cytophagales
OTU.473	3.58	14	<i>Pirellula staleyi DSM 6068</i>	90.91	Planctomycetes Planctomycetacia Planctomycetales
OTU.484	4.92	14	No hits of at least 90% identity	89.09	Planctomycetes Planctomycetacia Planctomycetales
OTU.5	2.69	14	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.518	4.8	14	<i>Hydrogenophaga intermedia</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.5190	3.6	30	No hits of at least 90% identity	88.13	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.541	4.49	30	No hits of at least 90% identity	84.23	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.5539	4.01	14	<i>Devosia subaequoris</i>	98.17	Proteobacteria Alphaproteobacteria Rhizobiales

Table S1 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.573	3.03	30	<i>Adhaeribacter aerophilus</i>	92.76	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.6	3.62	7	<i>Cellvibrio fulvus</i>	100.0	<i>Proteobacteria Gammaproteobacteria Pseudomonadales</i>
OTU.600	3.48	30	No hits of at least 90% identity	80.37	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.6062	4.83	30	<i>Dokdonella sp. DC-3, Luteibacter rhizovicinus</i>	97.26	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.627	4.43	14	<i>Verrucomicrobiaceae bacterium DC2a-G7</i>	100.0	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.633	3.84	30	No hits of at least 90% identity	89.5	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.638	4.0	30	<i>Luteolibacter sp. CCTCC AB 2010415, Luteolibacter algae</i>	93.61	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.64	4.31	14	No hits of at least 90% identity	89.5	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.663	3.63	30	<i>Pirellula staleyi DSM 6068</i>	90.87	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.669	3.34	30	<i>Ohtaekwangia koreensis</i>	92.69	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.670	2.87	30	<i>Adhaeribacter aerophilus</i>	91.78	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.766	3.21	14	<i>Devosia insulae</i>	99.54	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.83	5.61	14	<i>Luteolibacter sp. CCTCC AB 2010415</i>	97.72	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.862	5.87	14	<i>Allokutzneria albata</i>	100.0	<i>Actinobacteria Pseudonocardiales Pseudonocardiaceae</i>
OTU.899	2.28	30	<i>Enhygromyxa salina</i>	97.72	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.90	2.94	14	<i>Sphingopyxis panaciterrae, Sphingopyxis chilensis, Sphingopyxis sp. BZ30, Sphingomonas sp.</i>	100.0	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.900	4.87	14	<i>Brevundimonas vesicularis, Brevundimonas nasdae</i>	100.0	<i>Proteobacteria Alphaproteobacteria Caulobacterales</i>
OTU.971	3.68	30	No hits of at least 90% identity	78.57	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.98	3.68	14	No hits of at least 90% identity	88.18	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.982	4.47	14	<i>Devosia neptuniae</i>	100.0	<i>Proteobacteria Alphaproteobacteria Rhizobiales</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.1040	4.78	1	<i>Paenibacillus daejeonensis</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.107	2.25	3	<i>Flavobacterium sp. 15C3</i> , <i>Flavobacterium banpakuense</i>	99.54	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.11	5.25	7	<i>Stenotrophomonas pavanii</i> , <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.131	3.07	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	<i>Flavobacterium oncorhynchi</i> , <i>Flavobacterium glycines</i> , <i>Flavobacterium succinicans</i>	99.09	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.150	3.08	14	No hits of at least 90% identity	86.76	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.159	3.16	3	<i>Flavobacterium hibernum</i>	98.17	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.165	2.38	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	No hits of at least 90% identity	89.5	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.19	2.14	7	<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	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.2040	2.91	1	<i>Paenibacillus pectinilyticus</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.2379	3.1	3	<i>Flavobacterium pectinovorum</i> , <i>Flavobacterium sp. CS100</i>	97.72	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.24	2.81	7	<i>Cellulomonas aerilata</i> , <i>Cellulomonas humilata</i> , <i>Cellulomonas terrae</i> , <i>Cellulomonas soli</i> , <i>Cellulomonas xylinilytica</i>	100.0	<i>Actinobacteria Micrococcales Cellulomonadaceae</i>
OTU.241	3.38	3	No hits of at least 90% identity	87.73	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.244	3.08	7	<i>Cellulosimicrobium funkei</i> , <i>Cellulosimicrobium terreum</i>	100.0	<i>Actinobacteria Micrococcales Promicromonosporaceae</i>
OTU.252	3.34	7	<i>Promicromonospora thailandica</i>	100.0	<i>Actinobacteria Micrococcales Promicromonosporaceae</i>
OTU.267	4.97	1	<i>Paenibacillus pabuli</i> , <i>Paenibacillus tundrae</i> , <i>Paenibacillus taichungensis</i> , <i>Paenibacillus xylohexedens</i> , <i>Paenibacillus xylinilyticus</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.277	3.52	3	<i>Solibius ginsengiterrae</i>	95.43	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>

Table S2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.290	3.59	1	<i>Pantoea spp.</i> , <i>Klugvera spp.</i> , <i>Klebsiella spp.</i> , <i>Erwinia spp.</i> , <i>Enterobacter spp.</i> , <i>Buttiauxella spp.</i>	100.0	Proteobacteria Gammaproteobacteria Enterobacterales
OTU.3	2.61	1	[<i>Brevibacterium</i>] <i>frigoritolerans</i> , <i>Bacillus sp.</i> LMG 20238, <i>Bacillus coahuilensis</i> m4-4, <i>Bacillus simplex</i>	100.0	Firmicutes Bacilli Bacillales
OTU.319	3.98	1	<i>Paenibacillus xinjiangensis</i>	97.25	Firmicutes Bacilli Bacillales
OTU.32	3.0	3	<i>Sandaracinus amyloyticus</i>	94.98	Proteobacteria Deltaproteobacteria Myxococcales
OTU.335	2.53	1	<i>Paenibacillus thailandensis</i>	98.17	Firmicutes Bacilli Bacillales
OTU.346	3.44	3	<i>Pseudoduganella violaceinigra</i>	99.54	Proteobacteria Betaproteobacteria Burkholderiales
OTU.3507	2.36	1	<i>Bacillus spp.</i>	98.63	Firmicutes Bacilli Bacillales
OTU.3540	2.52	3	<i>Flavobacterium terrigena</i>	99.54	Bacteroidetes Flavobacteria Flavobacterales
OTU.360	2.98	3	<i>Flavisolibacter ginsengisoli</i>	95.0	Bacteroidetes Sphingobacteriia Sphingobacterales
OTU.369	5.05	1	<i>Paenibacillus sp.</i> D75, <i>Paenibacillus glycansilyticus</i>	100.0	Firmicutes Bacilli Bacillales
OTU.37	2.68	7	<i>Phycicola gilvus</i> , <i>Microterricola viridarii</i> , <i>Frigeribacterium faeni</i> , <i>Frondihabitans sp.</i> RS-15, <i>Frondihabitans australicus</i>	100.0	Actinobacteria Micrococcales Microbacteriaceae
OTU.394	4.06	1	<i>Paenibacillus pocheonensis</i>	100.0	Firmicutes Bacilli Bacillales
OTU.4	2.84	7	<i>Agromyces ramosus</i>	100.0	Actinobacteria Micrococcales Microbacteriaceae
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.4743	2.24	1	<i>Lysinibacillus fusiformis</i> , <i>Lysinibacillus sphaericus</i>	99.09	Firmicutes Bacilli Bacillales
OTU.48	2.99	1	<i>Aeromonas spp.</i>	100.0	Proteobacteria Gammaproteobacteria aaa34a10
OTU.5	3.69	7	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.5284	3.56	7	<i>Isopotericola nanjingensis</i> , <i>Isopotericola hypogaeus</i> , <i>Isopotericola variabilis</i>	98.63	Actinobacteria Micrococcales Promicromonosporaceae
OTU.5603	3.96	1	<i>Paenibacillus uliginis</i>	100.0	Firmicutes Bacilli Bacillales
OTU.57	4.39	1	<i>Paenibacillus castaneae</i>	98.62	Firmicutes Bacilli Bacillales
OTU.5906	3.16	3	<i>Terrimonas sp.</i> M-8	96.8	Bacteroidetes Sphingobacteriia Sphingobacterales
OTU.6	3.24	3	<i>Cellvibrio fulvus</i>	100.0	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.62	2.57	7	<i>Nakamurella flava</i>	100.0	Actinobacteria Frankiales Nakamurellaceae

Table S2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.6203	3.32	3	<i>Flavobacterium granuli</i> , <i>Flavobacterium glaciei</i>	100.0	<i>Bacteroidetes Flavobacteria Flavobacteriales</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.760	2.89	3	<i>Dyadobacter hamtensis</i>	98.63	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.8	2.26	1	<i>Bacillus niaci</i>	100.0	<i>Firmicutes Bacilli Bacillales</i>
OTU.843	3.62	1	<i>Paenibacillus agaragedens</i>	100.0	<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>

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