

DNA-SIP reveals functional guild diversity and membership for labile and recalcitrant C decomposition in soil

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Abstract

We identified microorganisms participating in xylose and/or cellulose decomposition in soil microcosms using nucleic acid stable isotope probing (SIP) coupled to next generation sequencing. 49 and 63 OTUs assimilated ^{13}C from xylose and cellulose into DNA, respectively. Microorganisms assimilated xylose-C at days 1, 3, and 7. Cellulose-C assimilation peaked at day 14 and was maintained at day 30. Many SIP-identified cellulose degraders are members of cosmopolitan but physiologically uncharacterized soil microbial lineages including *Spartobacteria*, *Chloroflexi* and *Planctomycetes*. ^{13}C from Xylose was initially assimilated by *Firmicutes* followed by *Bacteroidetes* and *Actinobacteria*. Trophic interactions may have caused this temporal pattern of incorporation. Soil C cycling models, however, often disregard bacterial trophic interactions. Fast growing substrate generalists assimilated xylose-C and slow growing substrate specialists assimilated cellulose-C. Xylose-C assimilators within time points clustered phylogenetically, and cellulose-C assimilators clustered phylogenetically overall. Knowledge of soil C cycling functional guild diversity, membership and activity will improve the predictive power of terrestrial C flux models.

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

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

ics by soil microbial taxa. Furthermore, we identified microorganisms involved in cellulose decomposition that were previously uncharacterized physiologically – cellulose is the most globally abundant biopolymer. Our results expand knowledge of soil functional guild diversity and activity which reveal soil structure-function relationships. This study is a departure from typical nucleic acid SIP studies that focus on listing the identities of heavy isotope labeled organisms. Our approach enables DNA-SIP to identify ^{13}C labeled microorganisms with greater resolution producing a better sampling of functional guilds. This not only allows us to connect function to genetic identity but also allows us to assess functional guild diversity and uncover ecological strategies. Further, we demonstrate how substrate specificity can be assessed from DNA-SIP data.

Introduction

Excluding plant biomass, there are 2,300 Pg of carbon (C) in soils worldwide which accounts for ~80% of the global terrestrial C pool [1, 2]. Fungi, archaea, and bacteria degrade plant biomass that reaches soil respiring the majority of plant biomass C producing 10 times more CO₂ annually than anthropogenic emissions [3]. Rising atmospheric CO₂ may stimulate plant growth and in turn increase plant biomass C input to soil [4]. Current climate change models concur on atmospheric and oceanic,

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Significance

We have a 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 C use dynam-

but not terrestrial, global C flux predictions [5]. Contrasting terrestrial C model predictions reflect how little is known about soil C cycling. We need to establish the roles and diversity of soil microbial community members involved with soil C cycling to reconcile inconsistencies in terrestrial C models [6, 7].

Functional guild membership and diversity establish the connections between soil functions and community structure [8]. Microorganisms mediate an estimated 80–90% of soil C cycling [9, 10] but the complexity of soil obfuscates microbial contributions to soil C cycling and the majority of microorganisms resist cultivation in the laboratory. Stable-isotope probing (SIP), however, links genetic identity and activity without cultivation and has expanded our knowledge of microbial contributions to biogeochemical processes [11]. Successful applications of SIP have identified organisms which mediate processes performed by functionally specialized microorganisms of limited diversity such as methanogens [12] but SIP has been less applicable in soil C cycling studies because simultaneous labeling of many different organisms has necessitated prohibitory resolving power. High throughput DNA sequencing technology, however, improves the resolving power of SIP enabling exploration of complex soil C-cycling processes.

This study aimed to observe labile C versus polymeric C assimilation dynamics in the soil microbial community. To soil microcosms we added a mixture of nutrients and C substrates that simulated the composition of plant biomass. All microcosms received the same C substrate mixture where the only difference between treatments was the identity of the isotopically labeled substrate. Specifically, we set up a series of microcosms with three treatments: in one treatment xylose was substituted for its ^{13}C -equivalent, in another cellulose was substituted for its ^{13}C -equivalent, and in the third treatment all substrates in the mixture were unlabeled. We harvested microcosms from each treatment at days 3, 7, 14 and 30 and additionally harvested microcosms receiving ^{13}C -xylose and unlabeled substrates on day 1. We chose to label xylose and cellulose to contrast labile C and polymeric C decomposition, respectively. Post incubation, we sequenced 16S rRNA genes from SIP density fractions with high throughput DNA sequencing technology. Our experimental design allowed us to observe the soil microbial community members that assimilated xylose-C and cellulose-C over time.

Results

Our experimental design allowed us to track the flow of xylose and cellulose C through the soil mi-

crobial community (Figure S1). 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, Figure S2). See Supplemental Note 1.9 for sequencing and density fractionation statistics. Microcosm treatments (see Methods) 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).

Soil microcosm microbial community changes with time. Changes in the bulk soil microcosm microbial community structure and membership correlated significantly with time (Figure S3, P-value 0.23, R^2 0.63, Adonis test [13]). 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 (Figure S3, P-value 0.003, “betadisper” function R Vegan package [14, 15]). Twenty-nine OTUs significantly changed in relative abundance with time (“BH” adjusted P-value < 0.10, [16]) and of these 29 OTUs, 14 were found to incorporate ^{13}C from labeled substrates into biomass (Figure S4). Four taxonomic classes significantly (adjusted P-value < 0.10) changed in abundance: *Bacilli* (decreased), *Flavobacteria* (decreased), *Gammaproteobacteria* (decreased) and *Herpetosiphonales* (increased) (Figure S5). Abundances grouped by phylum for OTUs that incorporated ^{13}C from cellulose increased with time whereas abundances grouped by phylum of OTUs that incorporated ^{13}C from xylose decreased over time although *Proteobacteria* abundance spiked at day 14 (Figure S6).

OTUs that assimilated ^{13}C into DNA. Within the first 7 days of incubation 63% of ^{13}C -xylose was respired and only 6% more was respired from day 7 to 30. At day 30, 30% of the ^{13}C from xylose remained in the soil. 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 1.7.4 for operational “response” criteria). There were 19, 19, 15, 6, and 1

¹⁹⁰ ^{13}C -xylose responders at days 1, 3, 7, 14, 30, respectively (Figure S2). The numerically dominant ^{13}C -xylose responder phylum shifted from *Firmicutes* to *Bacteroidetes* and then to *Actinobacteria* across days 1, 3 and 7 (Figure 2, Figure 3). ¹⁹⁵ *Proteobacteria* ^{13}C -xylose responders were found at days 1, 3, 7 but peaked at day 7 (Figure 3). Only 2 and 5 OTUs responded ^{13}C -cellulose at days 3 and 7, respectively. At days 14 and ²⁰⁰ 30, 42 and 39 OTUs responded to ^{13}C -cellulose. (Figure S2). *Proteobacteria*, *Verrucomicrobia*, and *Chloroflexi* had relatively high numbers of responders with strong response across multiple time points (Figure 2). *Verrucomicrobia* ^{13}C -cellulose responders were 70% *Spartobacteria*. *Chloroflexi* ²⁰⁵ responders were annotated as members of the *Herpetosiphonales* and *Anaerolineae* (Figure S10). *Cellvibrio*, a canonical soil cellulose degrader, was found to respond strongly to ^{13}C -cellulose in the ²¹⁰ microcosms. See Supplemental Note 2 for further counts of ^{13}C -responsive OTUs at greater taxonomic resolution.

Ecological strategies of ^{13}C responders. ^{13}C -xylose responders are generally more abundant ²¹⁵ members based on relative abundance in bulk DNA SSU rRNA gene content than ^{13}C -cellulose responders (Figure 4, P-value 0.00028, Wilcoxon Rank Sum test). However, ^{13}C -xylose and ^{13}C -cellulose responders included both abundant and rare OTUs (Figure 4). Two ^{13}C -cellulose responders were ²²⁰ 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.

²²⁵ Cellulose-responder-DNA buoyant density (BD) shifted further along the density gradient than xylose-responder-DNA BD in response to ^{13}C incorporation (Figure S7, Figure 4, P-value 1.8610×10^{-6} , Wilcoxon Rank Sum test). ²³⁰ ^{13}C -cellulose-responder-DNA BD shifted on average 0.0163 g mL^{-1} (sd 0.0094) whereas xylose responder BD 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 counter-²³⁵ part. 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}C to ^{12}C ratio in its DNA than an organism utilizing a mixture of isotopically labeled and unlabeled C sources (see ²⁴⁰ Supplemental Note 1.8). We predicted the *rrn* gene copy number for each OTU as described previously [17]. The estimated *rrn* gene copy number for ^{13}C -xylose responders was inversely related to the time ²⁴⁵ of first response for each OTU (P-value 2.02×10^{-15} , Figure S8). OTUs that did not respond at day 1

but did respond at day 3 and/or day 7 had fewer estimated *rrn* copy number than OTUs that responded at day 1 (Figure S8).

We assessed phylogenetic clustering of ^{13}C -responsive OTUs with the Nearest Taxon Index (NTI), the Net Relatedness Index (NRI) [18], and the consenTRAIT metric [19]. Briefly, positive NRI and NTI with corresponding low P-values indicates deep phylogenetic clustering whereas negative NRI with high P-values indicates taxa are overdispersed compared to the null model [20]. NRI and P-values for substrate responder groups suggest ^{13}C -xylose responders are overdispersed (NRI: -1.33, P: 0.90) while ^{13}C -cellulose responders are clustered (NRI: 4.49, P: 0.001). NTI values show that both ^{13}C -cellulose and ^{13}C -xylose responders are clustered near the tips of the tree (NTI: 1.43 (P: 0.072), 2.69 (P: 0.001), respectively). The consenTRAIT clade depth for ^{13}C -xylose and ^{13}C -cellulose responders was 0.012 and 0.028 16S rRNA sequence dissimilarity, respectively.

Discussion

Microbial response to isotopic labels. DNA-SIP can establish functional roles for thousands of phylotypes in a single experiment without cultivation. We identified 104 soil OTUs that incorporated ^{13}C from xylose and/or cellulose into biomass over ²⁷⁵ time. With this information we can build a conceptual model for the soil food web with respect to xylose and cellulose-C added to soil microcosms took the following path through the microbial food web (Figure S9): fast-growing *Firmicutes* spore formers first assimilated xylose C within 24 hours. Over the next 6 days, biomass from early-responding *Firmicutes* and the remaining xylose-C and was consumed by *Bacteroidetes*, *Actinobacteria*, and *Proteobacteria* phylotypes. Canonical cellulose degrading bacteria like *Cellvibrio* and members of cosmopolitan yet functionally uncharacterized soil phylogenetic groups like *Chloroflexi*, *Planctomycetes* and *Verrucomicrobia*, specifically the *Spartobacteria*, decomposed cellulose. Cellulose C incorporation into microbial biomass peaked at day 14 and extended through day 30.

Ecological strategies of soil microorganisms participating in the decomposition of organic matter. Models of soil C cycling rely on functional niches defined by soil microbiologists. In these models ecological strategies such as growth rate and substrate specificity are parameters for functional niche behavior [21]. Functional niches are commonly discovered by observing how community structure changes with changing conditions [22]. In this experiment, DNA-SIP revealed functional

niche membership. We also used DNA-SIP data to quantify substrate specificity which is related to the magnitude of DNA BD shift upon ^{13}C labeling (see Results). Moreover, we assessed growth rate of functional niche members by estimating niche member *rrn* gene copy number, a genomic feature reliably extrapolated from phylogeny that is indicative of how fast a microorganism grows [17, 23]. We found that ^{13}C -cellulose responsive OTUs are likely slow growing substrate specialists relative to ^{13}C -xylose responders (Figure 4, Figure S8). We also found that ^{13}C -xylose responsive OTUs that incorporated ^{13}C into biomass at day one grow faster than OTUs that responded later (Figure 4, Figure S8). If OTUs that first responded after day 1 consumed labeled OTUs that responded at day 1, this suggests that predators and/or saprophytes grow slower than microorganisms directly assimilating labile C and has implications for modelling trophic niches. We also note that ^{13}C -cellulose responders are generally lower abundance members of the bulk community than ^{13}C -xylose responsive OTUs (Figure 4), however, high *rrn* gene copy number may inflate ^{13}C -xylose-responder abundance.

NRI values quantify phylogenetic clustering [18] and have been used to assess clustering of soil OTUs that responded similarly to soil wet up [20, 24]. To our knowledge, assessing phylogenetic clustering of OTUs found to incorporate heavy isotopes into biomass during SIP incubations has not been attempted. We found that ^{13}C -cellulose and xylose responders are clustered and overdispersed, respectively. This suggests that the ability to degrade cellulose is phylogenetically conserved possibly reflecting the complexity of cellulose degradation biochemistry. The positive relationship between a physiological trait’s phylogenetic depth and its complexity has been noted previously [25] and the clade depth of ^{13}C -cellulose responders, 0.028 16S rRNA gene sequence dissimilarity, is on the same order as that observed for glycoside hydrolases which are diagnostic enzymes for cellulose degradation [26]. Overdispersion, as we saw for the ^{13}C -xylose responsive OTUs, may be indicative of a readily horizontally transferred trait and/or a trait that is broadly distributed phylogenetically, or, in this case may indicate that the overdispersed group includes more than one trait. It’s not clear which ^{13}C -xylose responsive organisms were labeled as a result of primary xylose assimilation (see below), and therefore it’s not clear if ^{13}C -xylose responsive OTUs in this experiment constitute a single ecologically meaningful group or multiple ecological groups. Temporally defined ^{13}C -xylose responder groups, however, were phylogenetically coherent (Figure S10, Figure 3). For example, most day 1 ^{13}C -xylose responders are members of the

Paenibacillus (see Supplemental Note 2). Notably, *Paenibacillus* have been previously implicated as labile C decomposers [27].

Intuitively we infer C cycling functional guild diversity from the distribution of diagnostic genes across genomes [26] or from screening culture collections for a particular trait [19]. For instance, the wide distribution of the glycolysis operon in microbial genomes is interpreted as evidence that many soil microorganisms participate in glucose turnover [7]. *In situ* functional guild diversity, however, can vary significantly from diversity assessed by functionally screening isolates and/or genomes. Xylose use in soil, for instance, may be less a function of catabolic pathway distribution across genomes and more a function of lifestyle. Phenomena such as seasonal change [28], and rainfall [24] cause nutrient and resource concentrations in soil to fluctuate. Therefore, fast growth and/or rapid resuscitation upon wet up [24] allow microorganisms to favorably compete for labile C resources. Life history ecological strategies tied to phylogeny like growth rate [22] may constrain the diversity of labile C assimilators even though the ability to use labile C is phylogenetically dispersed. DNA-SIP is useful for establishing *in situ* phylogenetic clustering and diversity of functional guilds because DNA-SIP can account for life history strategies by targeting active microorganisms. Additionally, snapshot estimates of community composition commonly inform soil-structure-function-relationship studies [22] but labile C decomposition might not be linked to snapshot community structure. Alternatively labile C decomposition might be linked specifically to community structure dynamics. That is, fast growing spore formers would not need to maintain high abundance to significantly mediate cycling of pulse delivered resources. This accentuates the importance of DNA-SIP for describing soil ecology as DNA-SIP assesses activity which can be decoupled from snapshot abundance.

Implications for soil C cycling models. Land management, climate, pollution and disturbance can influence soil community composition [7] which in turn influences soil biogeochemical process rates (e.g. [29]). Assessing functional group diversity and establishing identities of functional group members is necessary to predict how biogeochemical process rates will change with community composition [7, 30]. Aggregate biogeochemical processes that are the sum of many subprocesses involve a broad array of taxa and are assumed to be less influenced by community change than narrow processes that involve a single, specific chemical transformation by a narrow suite of microbial participants [7, 30]. Within an aggregate process such as C decomposition, subprocesses can be

further classified as broad or narrow [7]. In theory, “broad” and “narrow” functional guilds de-
 420 compose labile and recalcitrant C, respectively [7]. However, the diversity of active labile C and re-
 calcitrant C decomposers in soil has not been di-
 425 rectly quantified. Notably, we found more OTUs responded to ^{13}C -cellulose, 63, than ^{13}C -xylose,
 430 49. Also, it is possible that many ^{13}C -xylose responders are predatory bacteria or saprophytes as opposed to primary labile C degraders (see below). Cellulose and xylose decomposer functional guilds were non-overlapping in membership – of 104 ^{13}C -
 435 responders only 8 responded to both cellulose and xylose – and represented a small fraction of total soil community diversity (Figure 5). While xylose use is undoubtedly more widely distributed among microbial genomes than the ability to de-
 440 grade cellulose, the number of unique active cellulose decomposer OTUs outnumbered the number of unique active xylose utilizer OTUs.

Trophic interactions and/or functional groups tuned to different resource concentrations caused
 440 the activity succession from *Firmicutes* to *Bacteroidetes* and finally *Actinobacteria* in response to xylose addition. *Actinobacteria* (e.g. *Agromyces*) and *Bacteroidetes* have been previously implicated as predatory soil bacteria [31, 32], and, in our mi-
 445 crocosms *Bacteroidetes* and *Actinobacteria* activity peaked while *Firmicutes* ^{13}C -xylose responder relative abundance plummeted (Figure 2, Figure 3, Figure S6). Considering *Agromyces* and *Bac-
 450 teroidetes* phylotypes are likely soil predators, one parsimonious hypothesis for ^{13}C -labelling of *Bac-
 teroidetes* and *Actinobacteria* with a corresponding decrease in ^{13}C -labeled *Firmicutes* abundance is that *Bacteroidetes* and *Actinobacteria* fed on ^{13}C -
 455 labeled *Firmicutes*. Besides predation, mother cell lysis, the last step in sporulation, would release C from spore formers potentially to *Bacteroidetes* and *Actinobacteria*. If the temporal dynamics of
 ^{13}C -xylose incorporation are due to trophic interactions, predatory bacteria or saprophytes con-
 460 sumed many, if not most, fast-growing labile C degraders. Hence, soil C cycling models should include trophic interactions between soil bacteria but rarely do (e.g. [33]). When soil C models do account for predators/saprophytes, trophic inter-
 465 actions are predicted to significantly influence C:N ratios of SOM relative to litter C:N, and, recycle significant amounts of microbial biomass [21].

We propose two scenarios in the context of our results whereby community composition could af-
 470 fect C dynamics and fate. Genomic evidence shows cellulose degradation is a phylogenetically con-
 served trait [26]. Our study evaluates the phyloge-
 475 netic conservation of soil cellulose degradation in active microorganisms via DNA-SIP and our re-
 sults concur with genomic evidence. A decrease

in cellulose degrader abundance would diminish cellulose decomposition process rates as few soil microorganisms can fill the phylogenetically con-
 480 served cellulose degradation niche. Dispersed cel-
 lulose decomposers could renew ecosystem function, however. For labile C decomposition, the absence of fast growing spore formers would allow other microbes to assimilate labile C provided dispersal does not enable rapid recolonization. Primary labile C degraders in this study grow fast, and form spores and these distinct ecological strategies might indicate distinct C use dynamics and/or resource allocation. New labile C degraders may metabolize and allocate labile C differently thus changing labile C dynamics and fate. Further, labile C degrader substitution could affect biomass C turnover by predatory bacteria or saprophytes that feed on fast growing, spore forming labile C decomposers. On the other hand, spore formation enables dispersal [34] which would allow fast growing spore formers to continuously occupy the labile C decomposition niche. One proposed mechanism for similar decomposition rates of labile C across soils varying in community composition is that labile C is decomposed by a diverse suite of soil microorganisms [7]. An alternative hypothesis for consistent labile C process rates across different soils is that labile C degraders disperse readily. Notably, other lineages implicated in rapid labile C turnover include members of the *Actinobacteria* [24] and many soil *Actinobacteria* form hyphae that facilitate dispersal [35]. The two hypotheses are not mutually exclusive, but our results and previous studies suggest that environmental conditions unfavorable to fast-growing spore-formers and/or quickly resuscitated, hyphal *Actinobacteria* may impact labile C dynamics and fate.

Conclusion. Microorganisms sequester atmospheric C and respire SOM influencing climate change
 515 on a global scale but we do not know which microorganisms carry out specific soil C transformations. In this experiment microbes from physiologically uncharacterized but 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* or-
 520 der in soil [36]. Fast-growing *Firmicutes* spore formers assimilated labile C in our microcosms. *Bac-
 teroidetes* and *Actinobacteria* phylotypes, previ-
 525 ously implicated as predators, may have fed on the fast growing *Firmicutes*. Our results suggest that, cosmopolitan *Spartobacteria* may degrade cellulose on a global scale, bacterial tropic interactions can significantly impact soil C cycling, and life history

ecological strategies such as fast growth constrain functional guild diversity for labile C decomposi-
tion.
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Methods

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

540 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-
545 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 [37]. Mixture contained 38% cellulose, 23% lignin, 20% xylose, 3% arabinose, 1% galac-
550 tose, 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
555 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-
560 cellulose which was not sampled at day 1, n = 10. Other details relating to substrate addition can be found in SI. Microcosms were sampled de-
structively (stored at -80°C until nucleic acid pro-
cessing) at days 1 (control and xylose only), 3, 7,
565 14, and 30.

Nucleic acids were extracted using a modified Griffiths protocol [38]. To prepare nucleic acid extracts for isopycnic centrifugation as previously described [39], DNA was size selected (>4kb) using
570 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 [40] for a total of five ¹²C-control, five ¹³C-
575 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 sepa-
580 rate 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-
585 CsCl-gradient buffer solution in the centrifugation tube with water using a syringe pump at a flow rate of 3.3 μL s⁻¹ [41] into AcroprepTM 96 filter plate (Pall Life Sciences 5035). The refractive in-

dex of each fraction was measured using a Reichart AR200 digital refractometer modified as previously described [39] to measure a volume of 5 μL. Then buoyant density was calculated from the refractive index as previously described [39] (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.
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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 [42], 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 μL 5 U μl⁻¹ AmpliTaq Gold (Life Technologies, Grand Island, NY; N8080243), 2.5 μL 10X Buffer II (100 mM Tris-HCl, pH 8.3, 600 500 mM KCl), 2.5 μL 25 mM MgCl₂, 4 μL 5 mM dNTP, 1.25 μL 10 mg mL⁻¹ BSA, 0.5 μL 10 μM BA515F, 1 μL 5 μM BA806R, 3 μL H₂O, 10 μL 1:30 DNA template) in triplicate. Samples were normalized either using Pico green quantification and manual calculation or by SeqalPrepTM 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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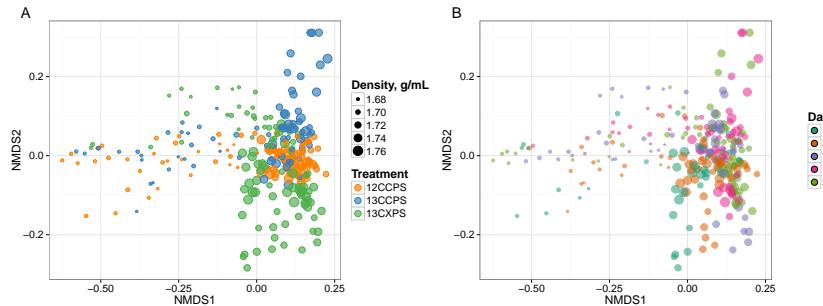


Fig. 1. NMDS analysis from weighted unifrac distances of 454 sequence data from SIP fractions of each treatment over time. Twenty fractions from a CsCl gradient fractionation for each treatment at each time point were sequenced (Fig. S1). Each point on the NMDS represents the bacterial composition based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

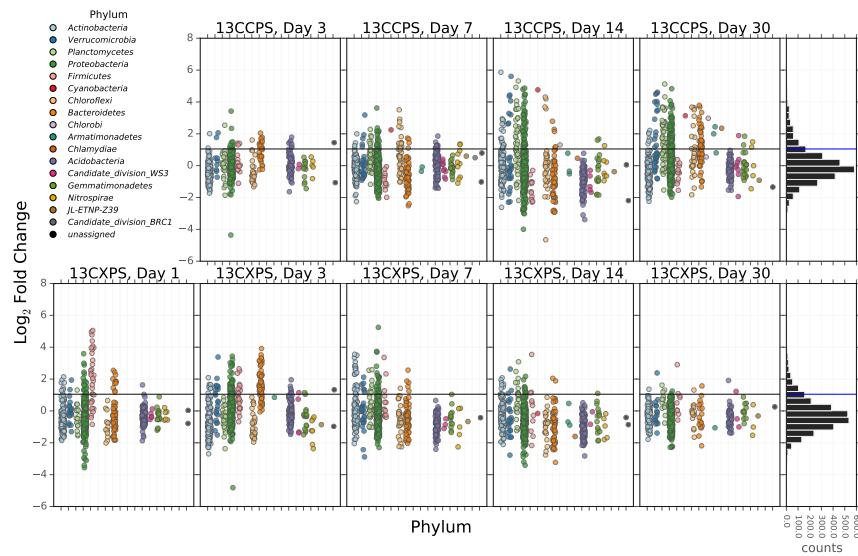


Fig. 2. Log₂ fold change of ¹³C-responders in cellulose treatment (top) and xylose treatment (bottom). Log₂ fold change is based on the relative abundance in the experimental treatment compared to the control within the density range 1.7125–1.755 g ml⁻¹. Taxa are colored by phylum. ‘Counts’ is a histogram of log₂ fold change values.

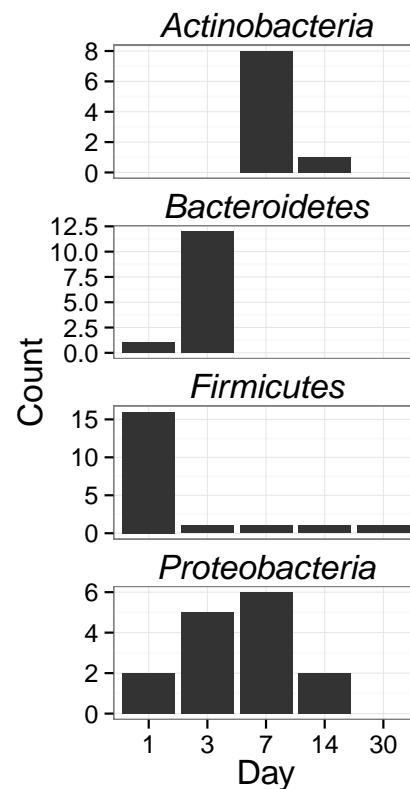


Fig. 3. Counts of ^{13}C -xylose responders in the *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria* at days 1, 3, 7 and 30.

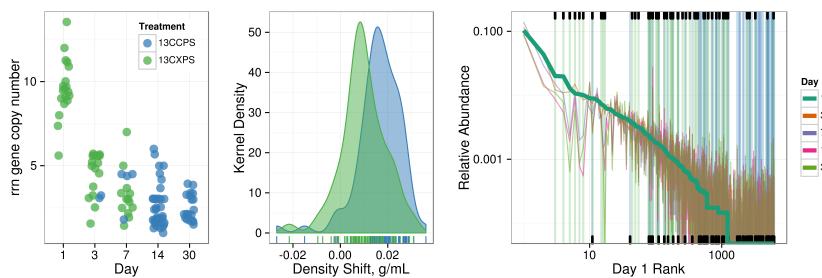


Fig. 4. ^{13}C -responder characteristics based on density shift (A) and rank (B). Kernel density estimation of ^{13}C -responder's density shift in cellulose treatment (blue) and xylose treatment (green) demonstrates degree of labeling for responders for each respective substrate. ^{13}C -responders in rank abundance are labeled by substrate (cellulose, blue; xylose, green). Ticks at top indicate location of ^{13}C -xylose responders in bulk community. Ticks at bottom indicate location of ^{13}C -cellulose responders in bulk community. OTU rank was assessed from day 1 bulk samples.

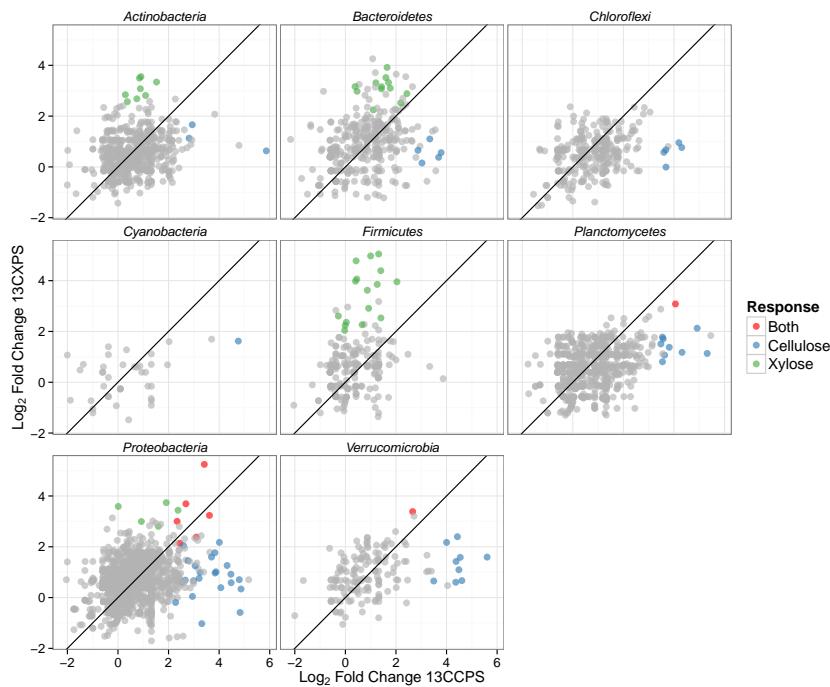


Fig. 5. Maximum log₂ fold change in response to labeled substrate incorporation for each substrate and all OTUs that pass sparsity filtering in both substrate analyses. Points colored by response. Line has slope of 1 with intercept at the origin. OTUs falling in the top-right quadrant responded to both substrates while those in the top-left and bottom-right responded to ¹³C-xylose and ¹³C-cellulose, respectively.