*Clostridium difficile* colonizes alternative nutrient niches during infection across distinct murine gut communities

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### Abstract

*Clostridium difficile* infection (CDI) has become the largest single cause of hospital-acquired infection in the United States. CDI susceptibility is most frequently associated with previous antibiotic exposure, which disrupt the gut bacterial community. This has been described for multiple antibiotic classes which result in distinct gut communities, each presenting separate metabolic challenges to *C. difficile*. We hypothesized that *C. difficile* adapts its physiology to nutrient availability within differentially susceptible gut environments. Utilizing an *in vivo* model of CDI, we demonstrated that *C. difficile* highly colonized the cecum of mice receiving one of three individual antibiotic pretreatments. We found levels of spore and toxin production varied between each group, both processes partially regulated by environmental nutrient concentrations. To more closely investigate metabolic responses of *C. difficile* during infection, we performed transcriptomic analysis of the pathogen from cecal content of infected mice. This revealed expression variation in numerous catabolic pathways for various carbon sources. To assess which substrates *C. difficile* was exploiting, we developed a transcriptomic-enabled genome-scale metabolic model of *C. difficile* and a metabolite scoring algorithm that leveraged network architecture. With this platform, we identified carbon sources used by *C. difficile* asymmetrically between infection models. These results were validated through correlation with untargeted mass spectrometry analysis from each condition. Our results supported the hypothesis that *C. difficile* indeed metabolized alternative carbon sources across colonized environments. These data also highlighted conserved elements of *C. difficile*'s metabolic strategy, specifically consumption of host-derived aminoglycans and Stickland fermentation substrates.

### Importance

In this study we demonstrate that not only does *C. difficile* alter pathogenesis between differentially sensitized hosts, but also exploits separate nutrient niches across environments. Our results support that *C. difficile* possesses a highly plastic nutrient niche space, allowing it to successfully infect distinct communities. This work also provides evidence that *C. difficile* virulence may be driven by accessibility of specific carbon sources during infection. This work could lead to the discovery of targeted measures to prevent *C. difficile* colonization including potential pre- or probiotic therapies. Our metabolite importance calculation workflow also provides a platform to the study of nutrient requirements of pathogens in the context of infection or even patterns of substrate utilization in communities of bacteria.

### Introduction

Infection by the Gram-positive, spore-forming bacterium *Clostridium difficile* has increased in both prevalence and severity across numerous countries during the last decade (1). In the United States, *C. difficile* was estimated to have caused >500,000 infections and resulted in ~$4.8 billion worth of acute care costs in 2014 (2). *C. difficile* infection (CDI) causes an array of toxin-mediated symptoms ranging from abdominal pain and diarrhea to the more life-threatening conditions pseudomembraneous colitis and toxin megacolon. Prior treatment with antibiotics is the most common risk factor associated with susceptibility to CDI (3), by disrupting the gut microbiota (4). Multiple distinct antibiotic have been shown to induce susceptibility *C. difficile* to colonization in a mouse model (5–7). Each resulted in unique gut bacterial communities that were all equally receptive to *C. difficile* colonization. Others have also shown that many of select antibiotic classes also alter the gut metabolome, increasing the concentrations of some *C. difficile* growth substrates (6, 8–10). Taken together these results are a strong indication that the healthy gut microbiota inhibits the growth of *C. difficile* through limitation of substrates it needs to grow. The ability of an intact gut community to exclude *C. difficile* colonization is suggestive of the nutrient-niche hypothesis in which an organism must be able to utilize a subset of available resources better than all competitors to colonize the intestine (11, 12).

Based on genomic and *in vitro* growth characteristics, *C. difficile* appears able to fill multiple nutrient niches. *C. difficile* has a relatively large and mosaic genome, it is amenable to a variety of growth substrates, and is able to colonize a diverse array of hosts suggesting that that it is a bacterial generalist (13–15). Several forms of *C. difficile* carbon metabolism have also been shown to contribute to pathogenesis regulation. *In vitro* transcriptomic analyses suggests that high concentrations of easily metabolized carbon sources, such as glucose or amino acids, inhibit toxin gene expression and sporulation (16, 17). Other previous transcriptomic studies of *C. difficile* have mainly focused on *in vitro* changes (18, 19), with limited work characterizing transcription during colonization of germfree mice (20, 21). Although these analyses are informative, they are either primarily directed toward the expression of virulence factors or lack the context of the gut microbiota which *C. difficile* must compete against for substrates. Metabolomic analyses have also been used to assay changes in bacterial metabolism as they relate to CDI (6, 10); however, these methods are unable to a highlight specific organisms in the milieu, more closely resembling echoes of total community metabolism instead of currently active processes in any one species. In contrast to these approaches, *in vivo* *C. difficile* transcriptomic investigations from specific pathogen free (SPF) animals may provide unique insight into its active metabolic pathways in a more realistic model of infection. Genome-scale metabolic models have proven useful for accurately determining a given organism's nutritional requirements in different scenarios (22). Integrating transcriptomic data with genome-scale metabolic modeling has previously aided in identifying the most active aspects of an organism’s metabolism and which substrates are preferred (22–24). Transcription-driven approaches of the nature can then be further improved through combination with global metabolomic analysis in order validate modeling-based conclusions. Applying this collection techniques to study *C. difficile* colonization allowed us to directly test the nutrient-niche hypothesis.

### Results

**Levels of *C. difficile* sporulation and toxin activity vary among different communities.** Due to the connection between metabolism, sporulation, and toxin production in *C. difficile*, we measured sporulation and toxin production at 18 hours post infection in each group. There was not a significant difference in the number of vegetative cells between any susceptible condition tested (Fig. 1A). All antibiotic treated (Table 1; Fig. S1) specific pathogen free (SPF) and germfree (GF) animals were colonized to ~1×108 colony forming units (c.f.u.) per gram of content, while untreated SPF mice maintained colonization resistance to *C. difficile*. Despite having the same number of vegetative *C. difficile* cells, large differences were detected in the density of *C. difficile* spores. Significantly more spores (*P* = 0.005, 0.008, & 0.003) were detected in ex-GF mice than in the antibiotic treated mice (Fig. 1B). The spore densities in both streptomycin and clindamycin-pretreated mice were also generally higher than that in cefoperazone-pretreated mice. There was significantly more toxin activity in ex-GF animals than any other colonized group (all *P* < 0.002), but toxin titer also varied between antibiotic treatment groups (Fig. 1C). Although similar toxin activity was found in both the cefoperazone and clindamycin-pretreated groups, toxin titer was below the limit of detection in most streptomycin-pretreated animals. These results indicated that *C. difficile* colonized different communities to a consistently high level, but that the density of spores and toxin titer varied by treatment.

***C. difficile* differentially expresses metabolic pathways between colonized environments.** To more closely investigate the responses of *C. difficile* to colonizing distinct susceptible gut environments, we performed whole transcriptome analysis of *C. difficile* during infection of the antibiotic treatment models. As *C. difficile* represents <3.3% of the bacterial load in any ceca of the antibiotic-pretreated SPF mice (Fig. S2C), a high degree of sequencing depth per sample was required to yield sufficient quantities of reads contributed by *C. difficile*. This prohibited our ability to sequence each experimental replicate individually and made it necessary to pool samples within each treatment group, and allowed for some degree of conservation of replicates for downstream analysis. Since these circumstances were unavaoidable, we treated this as normalizing for the average expression of *C. difficile* in each environment. Microarray-based gene expression measurement was not a viable alternative as the amount of background orthologous transcription from other bacterial species would contribute greatly to non-specific binding and eliminate true *C. difficile* signal. Upon sequencing, approximately 300 million total raw paired-end reads were collected per pooled sample with an average of ~160 thousand reads attributed to *C. difficile* following all curation steps (refer to Methods). This corresponded to an average of ~40x coverage across the *C. difficile* str. 630 reference genome. While this value may be low compared to some transcriptional studies of *in vitro* bacterial monoculture or *in vivo* ex-GF monoassociation (20, 25), it is not feasible to reach higher coverage in the context of a diverse bacterial community. These levels have been shown to be largely acceptable for similar analyses due to the focus on large-scale differences in specific annotated genes (26). Microarray-based gene expression analysis was not a viable alternative as the amount of background transcription from other bacterial species would cause background non-specific binding of orthologous transcript and eliminate any true *C. difficile* signal.

We first attempted to measure differential expression of specific genes associated with *in vivo* phenotype changes reported in previous studies (Fig. S3), however no clear trends were evident through this analysis. Through this analysis, it became evident that many global transcriptional regulators with ties to metabolism were differentially expressed between conditions (Fig. S3D). This further indicated that *C. difficile* may adapt its metabolism to the environment it is colonizing. Toward this point, we focused on specific gene families known to contribute to certain forms of *C. difficile* metabolism (Table S1), and went on to calculate the percentage of total expression between antibiotic-pretreated conditions for each gene. We then identified the condition in which each gene was most highly transcribed and adjusted the size of the corresponding point relative to that value (Fig. 2A). Overall, this demonstrated that genes involved in amino acid catabolism had the greatest amount of expression. Included were enzymes involved in Stickland fermentation as well as several general peptidases. These results indicated that catabolizing environmental amino acids may be important for the growth of *C. difficile* during infection. We then performed analysis of each category individually strongly differentiated the three conditions from one another. In addition to high levels of expression, we found that the genes associated with amino acid catabolism were also expressed at nearly consistent levels across the conditions (Fig. 2B). This was in agreement with their high level of overall expression. Genes for the metabolism of the host-derived aminoglycans N-acetylglucosamine and N-acetylmannosamine were expressed at consistent levels across each treatment group as well (Fig. 2C). Along similar lines with related molecules, a number of genes for processing certain monosaccharides into glycolysis, as well as catabolism of the disaccharides trehalose and cellibiose were expressed relatively evenly between each condition (Fig. 2D & 2E). Combined, these findings suggested that catabolism of amino acids and specific carbohydrates are core components of the *C. difficile* nutritional strategy during infection.

Aside from those gene sets that were equally expressed across conditions, there were large differences in expression of certain pathways between groups of mice. We chose to assess sugar transport systems because they have been associated with adaptive expression of phosphotransferase systems (PTS) and ABC transporters with many known differences in substrate specificities (21). The genes classified as PTS transporters were overrepresented in both clindamycin and streptomycin-pretreated mice (Fig. 2F), while ABC sugar transporters were overrepresented in the cefoparazone-pretreated mice (Fig. 2G). The most stark differences were seen in transcription for genes involved in sugar alcohol catabolism (Fig. 2H). Expression of these genes was entirely absent from clindamycin-pretreated mice and expression of genes for mannitol utilization were overrepresented in cefoparazone-pretreated mice and expression of genes for sorbitol utilization were overrepresented in streptomycin-pretreated mice. Concordant patterns also emerged in genes associated with fermentation end steps and disaccharide degradation. Short chain fatty acids (SCFAs) and alcohols are the end products of both carbohydrate and amino acid fermentation in *C. difficile* through separate pathways with shared terminal steps. Transcripts for genes involved in *C. difficile* butyrate/butanol metabolism were more abundant in clindamycin-pretreated mice (Fig. 2I). Alpha/beta-galactosidase genes were also overrepresented in clindamycin-pretreated mice, suggesting increased disaccharide consumption in this condition. Monosaccharide catabolism includes genes for not only the integral steps of glycolysis, but also several genes that mediate entry points of monosaccharides to this pathway. Transcripts for several genes in this group were overrepresented in cefoparazone-pretreated mice, however genes that catalyze the committed step of glycolysis were overrepresented in streptomycin-pretreated mice. Overall, these results supported the hypothesis that *C. difficile* adapted its metabolism across different susceptible environments.

**Genome-scale metabolic model structure underscores known *C. difficile* biology.** To further investigate which metabolites were differentially utilized between conditions, we represented the metabolic network of *C. difficile* as a directed bipartite graph using the genome and biochemical reaction annotations available in KEGG (2016). Enzymes and metabolites were represented by nodes, and their interactions by directed connecting edges (Fig. 3A). The complete network of *C. difficile* str. 630 that we created contains 447 enzymes and 758 metabolites, with 2135 directed edges. To validate our metabolic network, we analyzed network topology by calculating two metrics of centrality, betweenness centrality (BC) and closeness centrality (CC), to assess for those nodes which are critical to the structure of the metabolic network and if these patterns reflect known patterns in *C. difficile* or bacterial metabolism (Table S2). BC is the quantity of shortest paths connecting all other member nodes of a network that pass through a given node. In biological terms, this refers to the amount of influence a given hub has on the overall flow of metabolism through the network (27). Similarly, CC is instead a calculation for the reciprocal sum of the lengths of those shortest paths quantified by the BC. This value demonstrates how essential a given node is the the overall structure of the metabolic network (28). Together, these metrics allowed for the assessment of how much a network reflects known principles of highly central biological processes.

Combining both analyses to find those nodes that are not only central control points, but also important to the structure of the entire network, we found 5 of the top 10 enzymes according to both BC and CC were most critical to metabolism based on topology (2-dehydro-3-deoxyphosphogluconate aldolase, aspartate aminotransferase, pyruvate-flavodoxin oxidoreductase, formate C-acetyltransferase, and 1-deoxy-D-xylulose-5-phosphate synthase). Many of these enzymes participate in core processes including glycolysis, the pentose phosphate pathway, or the citric acid cycle. Upon analysis of the other 15 high-scoring enzymes, the majority are also distinct components of these pathways as well as several for the metabolism of amino acids (Table S2) Similarly, the intersection of those substrates with high both BC and CC values revealed 6 metabolites as central nodes to the metabolism of *C. difficile* (pyruvate, acetyl-CoA, 2-oxoglutarate, D-4-hydroxy-2-oxoglutarate, D-glyceraldehyde 3-phosphate, and L-glutamate). Not only are these members of glycolysis and the citric acid cycle, but pyruvate, acetyl-CoA, and L-glutamate contribute to numerous intracellular pathways as forms of biological "currency" (29). Notably absent from the most well-connected metabolites were molecules like ATP or NADH. Their exclusion is likely a byproduct of the KEGG LIGAND reference used for network construction, which excludes cofactors from most biochemical reactions. While this may be a limitation of certain analyses, our study was not affected as the primary interest was in those substrates acquired from the environment. These results collectively validated our model of *C. difficile* str. 630 as a platform for studying metabolism.

**Metabolite importance algorithm reveals adaptive nutritional strategies of *C. difficile* during infection of distinct environments.** Moving into analysis of the *C. difficile* metabolic network, we sought to utilize transcriptomic data to infer which metabolites *C. difficile* is most likely to obtain from its environment in each condition. To accomplish this we mapped normalized transcript abundances to the enzyme nodes in the network. As transcription and translation are coupled in bacteria, we hypothesized that we could incorporate whole transcriptome sequencing results into the metabolic model to impute active metabolism. Several models of bacterial protein expression determinants also suggest that intracellular concentration of mRNA is the strongest predictor for abundance of the corresponding protein products (30). We were therefore confident in utilizing normalized transcript abundance as a proxy for enzyme levels. The importance of each metabolite was measured as the log2-transformed difference between the average transcript levels of enzymes that use the metabolite as a substrate and those that generate it as a product (Fig. 3B). A metabolite with a high importance score was most likely obtained from the environment because the expression of genes for enzymes that produce the metabolite were low. Given that separate sequencing efforts for each individual mouse in each group was impossible, we instead adopted a Monte Carlo-style simulation to achieve some degree of statistical validation to our findings. We first calculated metabolite importance scores for 10,000 iterations of random transcript abundance reassignment of all enzyme nodes in the network. Next we used these distributions to calculate a 95% confidence interval for each metabolite and create comparators that represent random noise (31). This ultimately allowed for computing a probability of given metabolite being excluded from its associated null hypothesis score distribution (Fig. 3C). All downstream analysis was performed using those metabolites that met this criteria.

Applying these methods to the *C. difficile* transcriptomic data collected from the *in vivo* CDI models, we sought to identify patterns of growth substrate importance within each infected condition. To first identify the core metabolites that are most essential to *C. difficile* in any condition, we first ranked the scores of all 758 metabolites in the metabolic network within each condition. Using these rankings we then cross-referenced the highest 40 scoring metabolites from each treatment group, recalculated the median importance across all conditions, and reported the top five consistenly high scoring metabolites (Fig. 4A). The host-derived aminoglycan N-acetylglucosamine (GlcNAc) was found to the have the highest median importance of all shared metabolites, which has been shown to be a readily available source of carbon and nitrogen utilized by *C. difficile*, entering into glycolysis. We also confirmed the *C. difficile* str. 630 could metabolize GlcNAc for growth (Fig. 4C) using specialized minimal media for *C. difficile* (32). The Stickland fermentation substrate proline was also found to be important in all conditions tested. *C. difficile* is auxotrophic for several amino acids including proline, which prevented testing it directly for *in vitro* growth changes despite providing for modest growth in carbohydrate negative controls. Both glycolysis and Stickland fermentation have been demonstrated by *C. difficile* *in vivo* during GF mouse mono-associated studies (20), but never before in the context of a complex community of potential competitors. This indicated that these metabolites may be an integral component of the nutrient niche for *C. difficile* in any infection condition.

We then moved on to assess differential patterns of metabolite importance across environments and implemented a subtractive approach using the metabolite rankings from the previous analysis. This resulted in those metabolites that were distinctly important to *C. difficile* in the respective environments, which we then reported the top five from each (Fig. 4B). All groups of metabolites contained at least one known carbon source for *C. difficile* (6, 12, 33), which we also validated in our strain (Fig. 4C). While host diet is likely the source of sorbitol, mannitol, and salicin, N-acetylneuraminate is another aminoglycan derived from the host mucin layer (34). Previously, the concentration of this molecule was shown to be increased through liberation by other bacterial species to the benefit of *C. difficile* (33), however our results contest that *C. difficile* utilizes it for growth even in the absence of other bacterial species. Succinyl-CoA was of distinct importance in clindamycin-pretreated mice, and is the direct precursor to succinate which *C. difficile* takes from the gut microbiota to utilize for growth (9). These results suggested that this relationship may only exist in certain types of perturbed gut environments. We also noted that *C. difficile* colonized in ex-GF were more likely to acquire numerous amino acids from the environment (Table S3), as opposed to their synthesis presumably due to reduced competition. These results supported the ability of our network algorithm to identify likely growth substrates and that *C. difficile* adapted its metabolism toward specific nutrients across environments.

***In vivo* metabolomic analysis supports that *C. difficile* consumes metabolites indicated by metabolic modeling.** To support conclusions from transcriptional network-based analysis we employed untargeted ultra-performance liquid chromatography and mass spectrometry (UPLC-MS) to measure the relative *in vivo* concentrations of metabolites in the conditions investigated, with special attention to those highlighted by large importance scores (Metabolon, Durham NC). Using these results, we first assessed variability in the datasets generated for this study with replicates. The goal was to infer possible consistency within transriptomic sequencing efforts without similar replication. Extremely low and consistent sample variance was found in across all 16S and metabolomic replicates (Fig. S5). Since species abundance partially determines enzyme abundance, which in turn partially controls changes in the metabolome, these data reassured us that our conclusions for transcriptional differences were reliable.

With respect the modeling results, we measured whether important metabolites from network analysis were increased in relative concentration in their corresponding susceptible environments compared to untreated SPF mice (Fig. S6). Looking first toward N-acetylglucosamine since it was the most consistently important shared metabolite (Fig. 4A), we found that its relative concentration was actually significantly decreased in all susceptible conditions tested (Fig. S6A; all *P* <= 0.002). A similar trend was also seen in salicylate (Fig. S5F; all *P* <= 0.045), a product of salacin cleavage (salicin was not included in the panel). We also found that N-acetylneuraminate (Fig. S6B), mannitol/sorbitol (Fig. S6G), and galactitol (Fig. S6H) were significantly increased in only cefoperazone-pretreated SPF and GF mice (all *P* < 0.05). Only Stickland fermentation substrates proline (all *P* < 0.002) and trans-4-hydroxyproline (all *P* < 0.002) were found to be significantly increased in all susceptible environments tested (Fig. S6C & S6E). Glycine (Fig. S6D) was found to also be consistently increased, with significant differences in cefoperazone-pretreated SPF and GF mice (*P* = 0.005 & 0.005).

We then determined that concentrations of important metabolites decreased during *C. difficile* infection compared to mock infection, implying their consumption by the pathogen. Both groups of host-derived aminoglycans, N-acetylglucosamine/N−acetylgalactosamine (Fig. 5A) and N-acetylneuraminate (Fig. 5F), were only significantly decreased in the presence of *C. difficile* in ex-GF mice (*P* < 0.67 & 0). No significant relationship was seen in either galactitol (Fig. 5C) or mannitol/sorbitol (Fig. 5D) (*P* > 0.059 & 0.388). The slight increase in the concentration of salicylate (Fig. 5E) may be interpreted as due to increased cleavage of salicin by *C. difficile*, but requires further investigation. As side note, acetate was found to be important in all conditions except ex-GF mice (Table S3) and has been shown to be consumed by *C. difficile* during Stickland fermentation (35). We found that *C. difficile* colonization indeed led to a significant decrease in the levels of acetate (Fig. S7C; *P* = 0.0121858). Together, these findings provided some validation for our metabolite importance algorithm as a method for predicting metabolites that are most likely consumed by a bacteria in a given environment, not just growth substrates. In accordance with the previous analysis, we found that proline (Fig. 5A) and trans-4-hydroxyproline (Fig. S7B) were significantly decreased in every *C. difficile* colonized environment (all *P* < 0.013). Glycine was concordantly decreased in each condition following infection (Fig. S7A), with significant change in cefoperazone-pretreatment (*P* = 0.217). These results strongly supported the hypothesis that amino acids are a primary energy source of *C. difficile* during infection.

### Discussion

Galactitol was also tested as it was important in streptomycin-pretreated animals, however it demonstrated nearly identical growth patterns to no carbohydrate control (Table S4).

These data also suggested a potential hierarchy in carbon source preference, but requires additional investigations to state conclusively.

Our results collectively support the hypothesis that *C. difficile* adjusts its metabolism to fit growth substrate availability in susceptible gut environments. The specific carbon sources identified as important to *C. difficile* across environments provided for substantial growth *in vitro* and decreased in concentration *in vivo* after the pathogen colonized. Increased availability is presumably the result of concomitant decreases in the population of one or more competitors for those resources. Some important substrates did not follow similar trends in the metabolome, but it does not necessarily imply that *C. difficile* cannot make use of them. It could simply mean that they are in large excess or their rate of consumption could be slow. Further research is required to explore these interactions. Our method is also able to identify consistent trends in metabolism across environments. The finding that Stickland fermentation substrates were consistently among the highest scoring shared metabolites and that they consistently decreased in concentration upon *C. difficile* colonization strongly indicated that these metabolites are central to the nutritional strategy of *C. difficile*. It stands to reason that catabolism of amino acids would be a highly conserved strategy for *C. difficile* since they provide not only carbon and energy, but are also a source for nitrogen which is a limited resource in the mammalian lower GI tract (36). This same principle could extend to host-derived aminoglycans from the mucus layer. Concentrations of N-acetylglucosamine were consistently decreased when groups of bacteria with the capacity to cleave it from mucus were either diminished or absent entirely (37). N-acetylneuraminate was only found to be highly important in ex-GF mice when no other competitors are present. This could suggest that *C. difficile* is less competitive for these desirable nutrients, but can only really access them when competition is at a minimum.

Based on the evidence presented, resistance to colonization by *C. difficile* could be due to an inability of the pathogen to outcompete a collection of metabolic specialists in an intact community and separate classes of antibiotics differentially eliminate subsets of these groups. This concept may potentially explain the success of fecal microbial transplant in eliminating *C. difficile* infection. The wholesale installation of a diverse range of specialized metabolic strategies might be enough to outcompete *C. difficile* from previously sensitive gut environments. This may be particularly true with competitors for fermentable amino acids as our data also suggests that these are critical to *C. difficile* overall *in vivo* metabolic strategy. A previous study generated a mutant *C. difficile* in proline reductase, which allows proline to enter Stickland fermentation, to evaluate how necessary proline is for growth (38). *C. difficile* was able to grow without defect due to hydroxyproline, a non-proteinogenic amino acid, replacing proline in Stickland fermentation by circumventing the proline reductase dependent step of the pathway. As hydroxyproline shares the exact same relationship in concentrations as proline (Fig. S7B), it stands to reason that *C. difficile* is utilizing both during the infection conditions tested. As glycine (Fig. S7A) can also similarly be utilized, the redundancy in this pathway strongly supports how imperative this type of metabolism is to *C. difficile* during infection.

Our modeling approach also may allow for the identification of emergent properties for the metabolism of *C. difficile* during infection. One example could be the appearance of CO2, an apparent metabolic end product, in the list of shared important metabolites. While this may be a shortcoming of the annotation, one group has posited that *C. difficile* may actually be autotrophic under certain conditions and could explain our results (39). This may highlight that our method not only identify growth substrates, but also reports metabolites that are being removed from the environment. Although our modeling results are consistent with previously published work on the metabolism of *C. difficile*, there are potential limitations of this approach. Ultimately, the metabolite importance calculation is dependent on correct and existing gene annotation. In this regard it has been shown that the pathway annotations in KEGG are robust to missing elements (40), however this does not completely eliminate the possibility for this type of error. Due to the topology of the metabolic network, we were also unable to integrate stoichiometry for each reaction which may effect rates of consumption or production. In spite of these assumptions, the method outlined here underscores known elements of *C. difficile* biology and our subsequent *in vivo* metabolomic analysis supported predictions of nutrient niche plasticity. Only through integrative multi-omic analysis of *C. difficile* infection employing genomics, transcriptomics, and metabolomics were we able to uncover a much clearer image of *C. difficile*'s metabolism during infection in the context of a complex community of bacteria. In conclusion, *C. difficile* was able to optimize its nutritional strategy for separate carbohydrates in each colonized gut environment. We also found that Stickland fermentation substrates and host-derived glycans were conserved elements of *C. difficile*'s nutrient niche across distinct gut communities. Our results implicate that further considerations are needed for the design or targeted prebiotic and probiotic therapies to prevent or eliminate of *C. difficile* from a colonized gut.

### Materials and Methods

**Animal care and antibiotic administration** Adapted from the previously described model (41), six-to-eight week-old SPF C57BL/6 mice were obtained from a single breeding colony maintained at the University of Michigan for all experiments. Six-to-eight week-old GF C57BL/6 mice were obtained from a single breeding colony maintained at the University of Michigan and fed Laboratory Rodent Diet 5001 from LabDiet for all experiments. All animal protocols were approved by the University Committee on Use and Care of Animals at the University of Michigan and carried out in accordance with the approved guidelines. Specified SPF animals were administered one of three antibiotics; cefoperazone, streptomycin, or clindamycin (Table 1). Cefoperazone (0.5 mg/ml) and streptomycin (5.0 mg/ml) were administered in distilled drinking water *ad libitum* for 5 days with 2 days recovery with untreated distilled drinking water prior to infection. Clindamycin (10 mg/kg) was given via intraperitoneal injection 24 hours before time of infection.

***C. difficile* infection and necropsy** *C. difficile* strain 630 spores were prepared from a single large batch whose concentration was determined a week prior to challenge for all experiments. On the day of challenge, 1×103 *C. difficile* spores were administered to mice via oral gavage in phosphate-buffered saline (PBS) vehicle. Subsequent quantitative plating for c.f.u. was performed to ensure correct dosage. Infection negative control animals were given an oral gavage of 100 μl PBS at the same time as those mice administered *C. difficile* spores. 18 hours following infection, mice were euthanized by carbon dioxide asphyxiation. Necropsy was then performed and cecal content was split into three small aliquots (~100 μl). Two were flash frozen immediately for later DNA extraction and toxin titer analysis respectively. The third aliquot was quickly moved to an anaerobic chamber for c.f.u. quantification. The remaining content in the ceca (~1 ml) was emptied into a stainless steel mortar in a dry ice/ethanol bath using 1 ml of sterile PBS. This process was repeated for each mouse within a treatment group to pool content into a single large sample (9 mice across 3 cages) to compensate for cage effects as much as possible while maximizing sequencing depth. The content was then finely ground and stored at -80° C for subsequent RNA extraction.

***C. difficile* cultivation and quantification** Cecal samples were weighed and serially diluted under anaerobic conditions (6% H, 20% CO2, 74% N2) with anaerobic PBS. Differential plating was performed to quantify both *C. difficile* spores and vegetative cells by plating diluted samples on CCFAE plates (fructose agar plus cycloserine, cefoxitin, and erythromycin) at 37° C for 24 hours under anaerobic conditions (42). It is important to note that the germination agent taurocholate was omitted from these plates to quantify only vegetative cells. In parallel, undiluted samples were heated at 60° C for 30 minutes to eliminate vegetative cells and leave only spores (43). These samples were serially diluted under anaerobic conditions in anaerobic PBS and plated on CCFAE with taurocholate at 37° C for 24 hours. Plating was simultaneously done for heated samples on CCFAE to ensure all vegetative cells had been eliminated.

***C. difficile* toxin titer assay** To quantify the titer of toxin in the cecum, a Vero cell rounding assay was performed (44). Briefly, filtered-sterilized cecal content was serially diluted 1:5 in PBS. As a control for toxin-mediated cell rounding the cecal content was diluted a further 1:2 by the addition of an equal volume of goat anti-toxin serum (T5000; TechLab). Vero cells were grown to a confluent monolayer in DMEM (Dulbecco's Modified Eagle's medium), supplemented with 10% heat-inactivated fetal bovine serum and 1% penicillin-streptomycin. The cells then were transferred to a conical tube and centrifuged at 1,000 rpm for 5 minutes to pellet the cells. The old media was removed and the cells were re-suspended in fresh media to a final concentration of 1×105 cells per 90μL. 90μL of the cell suspension were seeded in each well of a 96-well plate and incubated at 37° C in a 5% CO2 humidified incubator for 4 hours. Following the incubation, cecal samples were added to the Vero cells and the plate was incubated overnight at 37° C. Plates were viewed after 24 hours at 10x magnification for cell rounding. The cytotoxic titer was defined as the log10 transformed reciprocal of the highest dilution that produced rounding in 80% of the cells. A more detailed protocol with product information can be found at: <https://github.com/jlleslie/Intraspecific_Competition/blob/master/methods/Verocell_ToxinActivity_Assay.Rmd>

**16S rRNA gene sequencing** DNA was extracted from approximately 50 mg of cecal content from each mouse using the PowerSoil-htp 96 Well Soil DNA isolation kit (MO BIO Laboratories) and an epMotion 5075 automated pipetting system (Eppendorf). The V4 region of the bacterial 16S rRNA gene was amplified using custom barcoded primers and sequenced as described previously using an Illumina MiSeq sequencer (45). All 63 samples were sequenced on a single sequencing run.

**Sequence curation** The 16S rRNA gene sequences were curated using the mothur software package (v1.36), as described previously (45). In short, paired-end reads were merged into contigs, screened for quality, aligned to SILVA 16S rRNA sequence database, and screened for chimeras. Sequences were classified using a naive Bayesian classifier trained against a 16S rRNA gene training set provided by the Ribosomal Database Project (RDP) (46). Curated sequences were clustered into operational taxonomic units (OTUs) using a 97% similarity cutoff with the average neighbor clustering algorithm. The number of sequences in each sample was rarefied to 2,500 per sample to minimize the effects of uneven sampling.

**RNA extraction, shotgun library preparation, and sequencing** To generate enough mRNA biomass contributed by *C. difficile*, we pooled cecal content from all mouse replicates into a single large isolation for each treatment group. Pooling was performed in a sterile stainless steel mortar resting in dry ice and a small amount of 100% ethanol. After all content for the given group was added, the sample was ground with a sterile pestle to a fine powder and scraped into a sterile 50 ml polypropylene conical tube. Samples were stored at -80° C until the time of extraction. Immediately before RNA extraction, 3 ml of lysis buffer (2% SDS, 16 mM EDTA and 200 mM NaCl) contained in a 50 ml polypropylene conical tube was first heated for 5 minutes in a boiling water bath (47). The hot lysis buffer was added to the frozen and ground cecal content. The mixture was boiled with periodic vortexing for another 5 minutes. After boiling, an equal volume of 37° C acid phenol/chloroform was added to the cecal content lysate and incubated at 37° C for 10 minutes with periodic vortexing. The mixture was the centrifuged at 2,500 x g at 4° C for 15 minutes. The aqueous phase was then transferred to a sterile tube and an equal volume of acid phenol/chloroform was added. This mixture was vortexed and centrifuged at 2,500 x g at 4° for 5 minutes. The process was repeated until aqueous phase was clear. The last extraction was performed with chloroform/isoamyl alcohol to remove acid phenol. An equal volume of isopropanol was added and the extracted nucleic acid was incubated overnight at -20° C. The following day the sample was centrifuged at 12000 x g at 4° C for 45 minutes. The pellet was washed with 0° C 100% ethanol and resuspended in 200 μl of RNase-free water. Following the manufacturer's protocol, samples were then treated with 2 μl of Turbo DNase for 30 minutes at 37° C. RNA samples were retrieved using the Zymo Quick-RNA MiniPrep according the manufacturer's protocol. Completion of the reaction was assessed using PCR for the V4 region of the 16S rRNA gene for 30 cycles (Kozich, 2013). Quality and integrity of RNA was measured using the Agilent RNA 6000 Nano kit for total prokaryotic RNA. The Ribo-Zero Gold rRNA Removal Kit Epidemiology was then used to deplete prokaryotic and eukaryotic rRNA from the samples according the manufacturer's protocol. Prior to library construction, quality and integrity as measured again using the Agilent RNA 6000 Pico Kit. Stranded RNA-Seq libraries were made constructed with the TruSeq Total RNA Library Preparation Kit v2, both using the manufacturer's protocol. The Agilent DNA High Sensitivity Kit was used to measure concentration and fragment size distribution before sequencing. High-throughput sequencing was performed by the University of Michigan Sequencing Core in Ann Arbor, MI. For all groups, sequencing was repeated across 4 lanes of an Illumina HiSeq 2500 using the 2x50 bp chemistry.

**Sequence curation, read mapping, and normalization.** Raw transcript sequencing read curation was performed in a two step process. Residual 5’ and 3’ Illumina adapter sequences were trimmed using CutAdapt (48) on a per library basis. Reads were quality trimmed using Sickle (Joshi, 2011) on the default settings. An average of ~300,000,000 total reads (both paired and orphaned) remained after quality trimming. Mapping was accomplished using Bowtie2 (49) and the default stringent settings. ~1,600,000 reads in sample each mapped to the annotated nucleotide gene sequences of *PeptoClostridium difficile* str. 630 from the KEGG: Kyoto Encyclopedia of Genes and Genomes (50). Optical and PCR duplicates were then removed using Picard MarkDuplicates (<http://broadinstitute.github.io/picard/>), leaving ~150,000 reads per sample for final analysis. The remaining mappings were converted to idxstats format using Samtools (51) and the read counts per gene were tabulated. Discordant pair mappings were discarded and counts were then normalized to read length and gene length to give a per base report of gene coverage. Unless indicated otherwise, each collection of reads was then 1000-fold iteratively subsampled to 90% of the lowest sequence total within each analysis, and a median expression value for each gene was calculated.

**Reaction Annotation & Bipartite Network Construction.** The metabolism of *C. difficile* str. 630 was represented as a directed bipartite graph with both enzymes and metabolites as nodes. Briefly, models were semi-automatically constructed using KEGG (2016 edition) ortholog (KO) gene annotations to which transcripts had been mapped. Reactions that each KEGG ortholog mediate were extracted from ko\_reaction.list located in /kegg/genes/ko/. KOs that do not mediate simple biochemical reactions (ex. mediate interactions of macromolecules) were omitted. Metabolites linked to each reaction were retrieved from reaction\_mapformula.lst file located in /kegg/ligand/reaction/ from the KEGG release. Those reactions that did not have annotations for the chemical compounds the interact with are discarded. Metabolites were then associated with each enzyme and the directionality and reversibility of each biochemical conversion was also saved. This process was repeated for all enzymes in the given bacterial genome, with each enzyme and metabolite node only appearing once. The resulting data structure was an associative array of enzymes associated with lists of both categories of substrates (input and output), which could then be represented as a bipartite network. The final metabolic network of C. difficile str. 630 contained a total of 1205 individual nodes (447 enzymes and 758 substrates) with 2135 directed edges. Transcriptomic mapping data was then re-associated with the respective enzyme nodes prior to substrate importance calculations. Betweenness-centrality and overall closeness centralization indices were calculated using the igraph R package found at <http://igraph.org/r/>.

**Metabolite Importance Calculation.** The substrate importance algorithm (Fig. 3a) favors metabolites that are more likely acquired from the environment (not produced within the network), and will award them a higher score (Fig. 4b & 6c). The presumption of our approach was that enzymes that were more highly transcribed were more likely to utilize the substrates they act on due to coupled bacterial transcription and translation. If a compound was more likely to be produced, the more negative the resulting score would be. To calculate the importance of a given metabolite (m), we used rarefied transcript abundances mapped to respective enzyme nodes. This was represented by to and ti to designate if an enzyme created or utilized m. The first step was to calculate the average expression of enzymes for reactions that either created a given metabolite (i) or consumed that metabolite (ii). For each direction, the sum of transcripts for enzymes connecting to a metabolite were divided by the number of contributing edges (eo or ei) to normalize for highly connected metabolite nodes. Next the raw metabolite importance score was calculated by subtracting the creation value from the consumption value to weight for metabolites that are likely acquired exogenously. The difference was log2 transformed for comparability between scores of individual metabolites. This resulted in a final value that reflected the likelihood a metabolite was acquired from the environment. Untransformed scores that already equaled to 0 were ignored and negative values were accounted for by transformation of the absolute value then multiplied by -1. These methods have been written into a single python workflow, along with supporting reference files, and is presented as bigSMALL (BacterIal Genome-Scale Metabolic models for AppLied reverse ecoLogy) available in a public Github repository at <https://github.com/mjenior/bigsmall>.

**Transcriptome Randomization and Probability Distribution Comparison.** As sequencing replicates of *in vivo* transcriptomes was not feasible, we applied a Monte Carlo style simulation to distinguish calculated metabolite importances due to distinct transcriptional patterns for the environment measured from those metabolites that were constitutively important. We employed a 10,000-fold bootstrapping approach of randomly reassigning transcript abundance for enzyme nodes and recalculating metabolite importances. This approach was chosen over fitting a simulated transcriptome to a negative binomial distribution because it created a more relevant standard of comparison for lower coverage sequencing efforts. Using this method, each substrate node accumulated a random probability distribution of importance scores which were then used to calculate the median and confidence interval to generate a probability for each metabolite importance score to be the result of more than chance. This was a superior approach to switch randomization since the connections of the network itself was created through natural selection and any large-scale alterations would yield biologically uninformative comparisons(52).

**Measuring *in vivo* concentrations of acetate.** Cecal contents were flash frozen in liquid nitrogen at the time of necropsy and subjected to short chain fatty acid quantification analysis using GC-MS (gas chromatography–mass spectrometry) as described in the targeted metabolomics section of Theriot et al., 2014. All assays were performed at the Michigan Regional Comprehensive Metabolomics Resource Core in Ann Arbor, MI.

**Anaerobic *in vitro* *C. difficile* growth curves.** The carbon-free variation of *C. difficile* Basal Defined Medium (NCMM) was prepared as previously described (6). Individual carbohydrate sources were added at a final concentration of 5 mg/mL and pair-wise carbohydrate combinations were added at 2.5 mg/mL each (5 mg/mL total). A solution of the required amino acids was made separately and added when noted at identical concentrations to the same study. 245 μl of final media mixes were added to a 96-well sterile clear-bottom plate. A rich media growth control was also included, consisting of liquid Brain-Heart Infusion + 0.5% cysteine. All culturing and growth measurement were performed anaerobically in a Coy Type B Vinyl Anaerobic Chamber (3.0% H, 5.0% CO2, 92.0% N, 0.0% O2). *C. difficile* str. 630 was grown for 14 hours at 37° C in 3 ml BHI + 0.5% cysteine. Cultures were then centrifuged at 2000 rpm for 5 minutes and resulting pellets were then washed twice with sterile, anaerobic 1 × phosphate-buffered saline (PBS). Washed pellets were resuspended in 3 ml more PBS and 5 μl of prepped culture was added the each growth well of the plate containing media. The plate was then placed in a Tecan Sunrise plate reader, heated to 37° C. Plates were incubated for 24 hours with automatic optical density readings at 600 nm taken every 30 minutes. OD600 values were normalized to readings from wells containing sterile media of the same type at equal time of incubation. Growth rates and other curve metrics were determined by differentiation analysis of the measured OD600 over time in R to obtain the slope at each time point.

**Quantification of *in vivo* metabolite relative concentrations.** Metabolomic analysis performed by Metabolon (Durham, NC), a brief description of their methods is as follows. All methods utilized a Waters ACQUITY ultra-performance liquid chromatography (UPLC) and a Thermo Scientific Q-Exactive high resolution/accurate mass spectrometer interfaced with a heated electrospray ionization (HESI-II) source and Orbitrap mass analyzer at 35,000 mass resolution. Samples were dried then reconstituted in solvents compatible to each of the four methods. The first, in acidic positive conditions using a C18 column (Waters UPLC BEH C18-2.1x100 mm, 1.7 µm) using water and methanol, containing 0.05% perfluoropentanoic acid (PFPA) and 0.1% formic acid (FA). The second method was identical to the first but was chromatographically optimized for more hydrophobic compounds. The third approach utilized a basic negative ion optimized conditions using a separate dedicated C18 column. Basic extracts were gradient eluted from the column using methanol and water, however with 6.5mM Ammonium Bicarbonate at pH 8. Samples were then analyzed via negative ionization following elution from a hydrophilic interaction chromatography column (Waters UPLC BEH Amide 2.1x150 mm, 1.7 µm) using a gradient consisting of water and acetonitrile with 10mM Ammonium Formate, pH 10.8. The MS analysis alternated between MS and data-dependent MS n scans using dynamic exclusion. The scan range varied slighted between methods but covered 70-1000 m/z. Library matches for each compound were checked for each sample and corrected if necessary. Peaks were quantified using area under the curve.

**Statistical methods.** All statistical analyses were performed using R (v.3.2.0). Significant differences between community structure of treatment groups from 16S rRNA gene sequencing were determined with AMOVA in the mothur software package. Significant differences of Inv. Simpson diversity, c.f.u., toxin titer, and metabolite concentrations were determined by Wilcoxon signed-rank test with Benjamini-Hochberg correction. Undetectable points used the limit of detection for all statistical calculations. Significant differences for growth curves compared to no carbohydrate control (+ amino acids) were calculated using 2-way ANOVA with Benjamini-Hochberg correction. Significance for metabolite importance scores was determined as described above via comparison to Monte-Carlo simulations. Outlier metabolites in linear correlation analysis were identified with a 1.5 minimum cutoff for squared Studentized residual analysis of each individual generalized linear model.

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**Author Contributions** M.L.J. conceived, designed and performed experiments, analyzed data, and drafted the manuscript. J.L.L. performed experiments and analyzed data. V.B.Y. contributed to the manuscript. P.D.S. interpreted data and contributed the manuscript. The authors declare no conflicts of interest.

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### Figure Legends

**Table 1 | Antibiotics used during *C. difficile* infection models.**

**Figure 1 | *C. difficile* sporulation and toxin activity quantification after 18 hours of infection.** Nine mice were included in each treatment group. **(A)** Vegetative *C. difficile* c.f.u. per gram of cecal content (*P* = n.s.). **(B)** *C. difficile* spore c.f.u. per gram of cecal content. **(C)** Toxin titer from cecal content measured by activity in Vero cell rounding assay. Ex-GF mice displayed significantly more spore c.f.u. and toxin activity than all other groups (all *P* < 0.008). Untreated mice in A, B, & C had no detectable *C. difficile* or toxin activity (all *P* < 0.01). Dotted lines denote limits of detection (LOD), with undetectable points shown just below for clarity. Values for undetectable points were imputed as the LOD for calculation of significant differences which were identified by Wilcoxon signed-rank test with the Benjamini-Hochberg correction.

**Figure 2 | Ratios of *in vivo* expression for specfic *C. difficile* metabolic pathways across antibiotic-pretreated mice.** Each point in the ternary plot represents a unique gene from the annotated genome of *C. difficile* str. 630. Position reflects the ratio of median rarefied transcript abundance for that gene between the three colonized antibiotic pretreatment models. Genes from specific metabolic pathways of interest are highlighted with all other genes not included in these groups in gray. **(A)** Size of highlighted points represents the largest transcript abundance among the antibiotic pretreatments for each individual gene. Metabolic categories are also plotted separately in **(B-I)**. Genes, annotations, and normalized transcript abundances can be found in Table S1. Refer to Fig. S4 for additional explanation of figure interpretation.

**Figure 3 | Genome-scale bipartite metabolic modeling results using the transcriptome of *C. difficile* str. 630 in each colonized environment.** **(A)** Largest component from the bipartite genome-scale metabolic model of *C. difficile* str. 630. Enzyme node sizes reflect the levels of detectable transcript from each gene. Importance algorithm components: (I) average transcription of reactions consuming a metabolite, (II) average transcription of reactions producing a metabolite, and (III) difference of consumption and production. **(B)** The expanded window displays a partial example of D-fructose importance calculation. Values in the red nodes represent normalized transcript reads mapping to enzymes. **(C)** Example 10000-fold Mont-Carlo simulation results corresponding to a significant importance score for **m**.

**Figure 4 | Results from network-based metabolite importance calculation and *in vitro* *C. difficile* growth with important carbon sources.** Important metabolites included in this analysis were calculated at <5% probability to be a result of their associated random score distribution. **(A)** Median shared metabolites among the 50 highest scoring metabolites from each condition. **(B)** Distinctly important metabolites from each treatment group. The top 25 scoring metabolites from each group was cross-referenced against each other group resulting in metabolites that are differentially important between environments. **(C)** 18 hour *C. difficile* str. 630 *in vitro* growth curves validating identified growth nutrients from network analysis. All statistical comparison was performed in comparison to no carbohydrate control (*P* < 0.001). Significant differences between growth curves were calculated using 2-Way ANOVA with Benjamini-Hochberg correction.

**Figure 5 | Change in *in vivo* concentrations following *C. difficile* infection of important metabolites.** Comparison of relative concentrations of select metabolites from untargeted UPLC-MS analysis of *C. difficile* vs mock-infected mouse cecal content (n = 9 per group). **(A)** N−acetylglucosamine / N−acetylgalactosamine, **(B)** Proline, **(C)** Galactitol, **(D)** Mannitol / Sorbitol, **(E)** Salicylate, and **(F)** N−acetylneuraminate. Paired metabolites were quantified simultaneously as the only differ by chirality making differentiation impossible. Significant differences (*P* < 0.05) were determined using Wilcoxon signed-rank test with Benjamini-Hochberg correction when appropriate.

**Supplementary Figure 1 | Experimental time lines for mouse model pretreatments and *C. difficile* infection.** 9 wild-type C57BL/6 mice across 3 cages were included in each treatment group. **(A)** Streptomycin or **(B)** cefoperazone administered *ad libitum* in drinking water for 5 days with 2 days recovery with untreated drinking water before infection, **(C)** a single clindamycin intraperitoneal injection one day prior to infection, or **(D)** no antibiotic pretreatment (for both SPF control and GF mice). If no antibiotics were administered in the drinking water, mice were given untreated drinking water for the duration of the experiment beginning 7 days prior to infection. At the time of infection, mice were challenged with 1×103 *C. difficile* str. 630 spores at the time of infection. Sacrifice and necropsy was done 18 hours post-challenge and cecal content was then collected.

**Supplementary Figure 2 | Analysis of bacterial community structure resulting from antibiotic treatment.** Results from 16S rRNA gene amplicon sequencing from bacterial communities of cecal content in both mock-infected and *C. difficile* 630-infected animals 18 hours post-infection across pretreatment models. **(A)** Non-metric multidimensional scaling (NMDS) ordination based on ThetaYC distances for the gut microbiome of all SPF mice used in these experiments (n = 63). All treatment groups are significantly different from each other groups by AMOVA (*P* < 0.001). **(B)** Inverse Simpson diversity for each cecal community from the mice in (A). Cecal communities from mice not treated with any antibiotics are significantly more diverse than any antibiotic-pretreated condition by Wilcoxon signed-rank test (*P* < 0.001). **(C)** Representation of reads contributed by *C. difficile* in each sequenced condition. Shown in each group is the quantity of normalized reads contributed by either *C. difficile* or all other reads within that sequencing effort. The percents listed at the top of each group is the proportion of the total community composed of *C. difficile*. Significantly less were for *C. difficile* were detected in each condition, determined by Wilcoxon signed-rank test (*P* < 0.001).

**Supplementary Figure 3 | Select *C. difficile* gene set expression compared between treatment group.** Relative abundances of *C. difficile* transcript for specific genes of interest. **(A)** Transcription for select genes from the *C. difficile* sporulation pathway with the greatest variation in expression between the conditions tested. **(B)** Relative abundances of transcript for genes that encode effector proteins from the *C. difficile* pathogenicity locus. **(C)** Transcript abundances for genes associated with quorum sensing in *C. difficile*. **(D)** Transcript relative abundance of select sigma factors which expression or activity is influenced by environmental metabolite concentrations. Asterisks (\*) indicate genes from which transcript was undetectable.

**Supplementary Figure 4 | Additional explanation for Figure 2 interpretation.** Relative abundance of transcription for *C. difficile* 630 genes during infection across the 3 antibiotic pretreatment models used during this study. Points that are located closer to a corner are more highly transcribed in the condition associated with that corner compared to the others. As this shows a 3-dimensional data set in 2 dimensions, there is an amount of distortion proximal to each corner. Simply put for points that are nearer to an edge, a greater percentage of their total transcription was contributed by *C. difficile* colonizing those mice. **(A)** This point represents the transcription for a gene that is overrepresented in cefoperazone-pretreated mice. **(B)** This point represents a gene in which transcripts are equally detectable in all 3 conditions. **(C)** Transcripts for this gene are only underrepresented in only cefoperazone-pretreated mice, and are equally detectable in clindamycin and streptomycin-pretreated animals.

**Supplementary Figure 5 | Within-group median sample variance for community-level data with replication.** Shown are the median and interquartile range of the sample variance for all fields in each experimental group. This was done to demonstrate consistent measurements in multiple levels of data (n = 9 per group). **(A)** OTU abundances from 16S rRNA gene sequencing, sample variances for each OTU were calculated individually prior to summary statistic calculations. **(B)** Scaled intensities from untargeted metabolomic analysis, sample variances for each metabolite were calculated individually prior to summary statistic calculations. In both groups of calculations all median sample variances are >1, indicating extremely low levels of variability between samples of the same type.

**Supplementary Figure 6 | Relative *in vivo* concentrations of metabolites highlighted through network-based analysis in uninfected mice** Select metabolite concentrations using untargeted UPLC-MS quantification from cecal content of *C. difficile* susceptible mice compared to resistant controls. Samples were collected at the same 18 hour timepoint as the analyses performed in infection experiments (n = 9 mice per group). Highlighted carbohydrates included: **(A)** N−Acetylglucosamine / N−Acetylgalactosamine, **(B)** N−Acetylneuraminate, **(C)** Proline, **(D)** Glycine, **(E)** Salicylate, **(F)** Mannitol / Sorbitol, and **(G)** Galactitol. Significant differences (*P* < 0.05) were determined using Wilcoxon signed-rank test with Benjamini-Hochberg correction.

**Supplementary Figure 7 | Change in *in vivo* concentrations following *C. difficile* infection of additional select metabolites.** Comparison of concentrations for select metabolites from *C. difficile*-infected to mock-infected mouse cecal content 18 hours post-infection. **(A)** Glycine and **(B)** Trans-4-hydroxyproline were both quantified by untargeted UPLC-MS analysis. **(C)** Acetate concentrations were measured using GC-MS. Significant differences (*P* < 0.05) were determined using Wilcoxon signed-rank test with Benjamini-Hochberg correction.

**Supplementary Table 1 | Sets of genes included in Figure 2 with normalized abundances and annotations.**

**Supplementary Table 2 | Topology metrics for enzyme and metabolite nodes in the *C. difficile* str. 630 metabolic network.**

**Supplementary Table 3 | All metabolites with significant importantance scores in each colonized condition.**

**Supplementary Table 4 | Growth curve analysis for each tested carbon source.**

**Supplementary Table 5 | Outliers from generalized linear models of combined metabolome and metabolic network output analysis.**

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