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Host-Microbe Co-metabolism Dictates Cancer Drug Efficacy in C. elegans

Highlights

- Drug-microbe-host high-throughput screens reveal new mechanisms for cancer drugs
- Microbes integrate nutritional and drug cues regulating treatment efficacy in the host
- Ribonucleotide co-metabolism of cancer pro-drugs exists between host and microbe
- Imbalanced bacterial deoxynucleotides synergize 5-FU-induced autophagic cell death

In Brief

A three-way high-throughput screen involving host-microbe-drug interactions reveals that the beneficial impact of some drugs can be due to effects of drug-dependent alterations by gut microbe composition rather than direct action of the therapeutic itself.

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Host-Microbe Co-metabolism Dictates Cancer Drug Efficacy in C. elegans

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SUMMARY

Fluoropyrimidines are the first-line treatment for colorectal cancer, but their efficacy is highly variable between patients. We queried whether gut microbes, a known source of inter-individual variability, impacted drug efficacy. Combining two tractable genetic models, the bacterium E. coli and the nematode C. elegans, we performed three-way high-throughput screens that unraveled the complexity underlying host-microbe-drug interactions. We report that microbes can bolster or suppress the effects of fluoropyrimidines through metabolic drug interconversion involving bacterial vitamin B₆, B₉, and ribonucleotide metabolism. Also, disturbances in bacterial deoxy-nucleotide pools amplify 5-FU-induced autophagy and cell death in host cells, an effect regulated by the nucleoside diphosphate kinase ndk-1. Our data suggest a two-way bacterial mediation of fluoropyrimidine effects on host metabolism, which contributes to drug efficacy. These findings highlight the potential therapeutic power of manipulating intestinal microbiota to ensure host metabolic health and treat disease.

INTRODUCTION

Fluoropyrimidines are antimetabolite drugs primarily used to treat cancer. The archetype fluoropyrimidine, 5-fluorouracil (5-FU), is the principal therapy for colorectal cancer, the third most common cancer worldwide (Midgley and Kerr, 1999). 5-FU and its prodrugs, such as capecitabine, are uracil analogs that impede nucleotide biosynthesis, and hence cell division, by inhibiting thymidylate synthase (TS). Despite the widespread use of 5-FU-based chemotherapy, there is no universally accepted dose, and significant pharmacokinetic variations exist between individuals. As a result, adverse effects are frequent (diarrhea, nausea) and response rates sub-optimal (10% as monotherapy, 50% with combination therapies) (Longley et al., 2003). The observed inter-patient variation in 5-FU efficacy/toxicity has been attributed to several factors, including genetic polymorphisms in TS, dihydropyrimidine dehydrogenase, methylene THF reductase, and cytidine deaminase (Offer and Diasio, 2016). However, genetics alone does not explain differences in 5-FU tolerance between different continents suggesting environmental factors as key determinants in 5-FU action (O’Donnell and Dolan, 2009).

The influence of gut microbiota on 5-FU activity has not been explored. Gut microbes play an integral role in animal physiology, contributing to metabolism, influencing immunity, and modulating gut function. The thousands of species that make up the human microbiome surpass the host in terms of raw cell numbers, genomic diversity, and metabolic capability (Nicholson et al., 2012). Together, the host and its symbiotic microbiota (holobiont) act as a single evolutionary unit against environmental pressures (Rosenberg and Zilber-Rosenberg, 2011). Despite great advances in understanding the microbiome’s contribution to human health, one facet of the host-microbe relationship that remains undefined is the influence of microbiota on host-targeted drugs and the resulting contribution to host fitness. The consequences of not exploring these interactions at the holobiont level can be severe, as illustrated by the patient deaths due to the unanticipated microbial metabolism of the antiviral sorivudine to (E)-5-(2-bromovinyl)uracil, a suicide inhibitor of dihydropyrimidine dehydrogenase, a key host enzyme responsible for the detoxification of 5-FU (Okuda et al., 1997).

A significant barrier to exploring the host-microbiota relationship has been the complexity and diversity of the mammalian microbiome. The nematode C. elegans offers a simplified animal model with evolutionarily conserved features important for studying host-microbe interactions. Like humans, C. elegans have a symbiotic relationship with microbes, requiring them for nutrition, optimal development (Watson et al., 2014), and drug metabolism (Cabreiro et al., 2013).

Here, we employ an innovative host-microbe-drug model and high-throughput screening approaches to explore the role of microbes in modulating the effect of 5-FU and other fluoropyrimidines on C. elegans. We extensively define the microbial...
metabolic, genetic, and nutritional contributions to fluoropyrimidine activity on the host, revealing two distinct mechanisms by which bacteria modulate the efficacy of this class of anti-cancer drugs in vivo: (1) drug activation by bacterial ribonucleotide metabolism; and (2) influence of bacterial deoxynucleotide pools on the host response. We present a model that will be valuable for further probing host-microbe-drug interactions, highlighting how microbial metabolism can impact host fitness and survival in the context of pharmacotherapy.

RESULTS

Microbes Have a Large Impact on Fluoropyrimidine Action in C. elegans

We reasoned that gut microbes may contribute to the activity of 5-FU in the context of the holobiont. Fluoropyrimidines impede cell division and interfere with nematode fertility and development, allowing simple and robust readouts of drug activity on the host, such as the minimum inhibitory concentration (MIC) for egg hatching (SenGupta et al., 2013).

First, we compared 5-FU activity on worms fed five Escherichia coli laboratory strains commonly used in worm studies (Figure 1A) and observed up to 80-fold differences in 5-FU MICs (HB101, MIC = 8 \( \mu \)M versus BL21G, MIC = 0.1 \( \mu \)M, p < 0.001). The differences in host drug activity were independent of the bacterial strain serotype, as 5-FU efficacy was similarly variable between B strains (OP50 versus BL21G; 20-fold, p < 0.001) and within K-12 strains (BW25113 versus HT115; 8-fold, p < 0.001). This suggested that specific genotypic differences between the \( E. \) coli strains could be responsible for the observed variability in drug efficacy.

Interventions modifying bacterial metabolic activity can influence the effect of host-targeted drugs in \( C. \) elegans (Cabreiro et al., 2013). Accordingly, we cultured nematodes on bacteria killed by heat or UV treatment. 5-FU efficacy was greatly decreased in nematodes fed dead BW25113 (128-fold, Figure 1C) or OP50 (Figure S1A). Thus, bacterial enhancement of 5-FU activity on \( C. \) elegans requires live bacteria.

Next, we explored the microbial modulation of other clinically used fluoropyrimidines, including floxuridine (FUdR), flucytosine
(5-FC), capecitabine (CAP), and 5-fluoroorotic acid (5-FO). Fluoropyrimidine efficacy in C. elegans increased in the order CAP < 5-FC < 5-FO = FUdR = 5-FO. Within each drug treatment, the efficacy was highly dependent on the bacterial strain fed to the worms (e.g., 5-FU OP50 = 2 μM versus C. aquatica = 0.1 μM, p < 0.001; FUdR OP50 = 2 μM versus C. aquatica = 8 μM, p < 0.001) (Figures 1D and S1B–S1E). Therefore, as for 5-FU, the pharmacodynamics of these drugs in the host are bacteria dependent and drug specific.

A possible confounding factor for the differential effects of bacteria on worm MIC could be the absolute number of bacterial cells available and their digestion. To test whether there was a link between bacterial growth phenotype and modulation of drug efficacy in C. elegans, we quantified bacterial growth in the absence (Figure 1E) and presence (Figures 1F, S1F, and S1G) of 5-FU, and found no link with drug efficacy in C. elegans. Experiments with other fluoropyrimidines confirmed these observations (Figures S1H and S1I). Similarly, rates of bacterial consumption by worms do not explain 5-FU efficacy (Figure S1J).

The type of bacteria fed to C. elegans has a significant impact on host biology, including gene expression and metabolism (Watson et al., 2014). Expression of worm genes associated with pyrimidine metabolism, required for potential 5-FU conversion, was largely unaffected by the bacterial strain (Figure S1K). Therefore, bacterial modulation of 5-FU efficacy in C. elegans occurs by means other than bacterial regulation of nematode gene expression. Given that 5-FU disrupts pyrimidine metabolism homeostasis (Ser et al., 2016), we also investigated whether drug treatment induces metabolic changes in E. coli, which could contribute to the observed effects in the worm. Targeted metabolomics in worms or E. coli exposed to 1 μM 5-FU (the full inhibitory concentration for worm hatching) revealed that 5-FU did not affect bacterial metabolism as shown by principal component analysis (PCA), while inducing a significant metabolic shift in the worms (Figures 1G and S1L–S1M). These data imply distinct sensitivities to 5-FU action between host and microbe and support a regulatory effect of bacteria on drug efficacy in the host that is independent of altered bacterial metabolism caused by drug treatment.

Overall, we found that bacteria are key determinants of fluoropyrimidine efficacy on host metabolism and embryonic survival.

**Host-Microbe-Drug Screens Reveal Bacterial Regulators of Fluoropyrimidine Action**

We hypothesized that the bacterial uracil phosphoribosyltransferase upp mutant (Δupp), a gene previously used for cancer therapy (Koyama et al., 2000) and capable of metabolizing 5-FU in vitro, could influence the response of the host to treatment. As predicted, worms fed Δupp bacteria developed fully at concentrations of 5-FU that completely inhibited worms fed the control strain (Figure 2A), further suggesting an interspecies mediation of drug effects. Therefore, to investigate how E. coli impacts 5-FU action in C. elegans, we developed a three-way high-throughput host-microbe-drug screen using the E. coli non-essential gene knockout Keio library (Baba et al., 2006) (Figure 2B). The developmental response of C. elegans to 5-FU is dose dependent when fed control BW25113 (Figures S2A and S2B). Therefore, the worm response to the drug in the presence of each E. coli mutant was estimated as the MIC that arrests development at L1 larvae stage, allowing us to determine the relative contribution of each E. coli gene in mediating 5-FU effects in the host. 96 mutants were excluded from further investigation due to poor growth on nematode growth medium (NGM), undisrupted target gene, or impaired worm development in the absence of drug (Figure 2C; Table S2). A primary screen within a narrow range of drug concentrations (1–5 μM) revealed that ~80% of the total 3,813 E. coli mutants screened did not alter 5-FU effects in C. elegans (Figures 2C and S2C). 574 (15%) of the mutant strains allowed full development at 5 μM and were investigated further at a higher range of concentrations (5–100 μM). This secondary screen (Figures S2C) revealed that the top 5% (124 mutants) increased C. elegans resistance to drug to MICs >30 μM and the top 1% (35 mutants) to MICs >43 μM. Thus, we identified the subset of bacterial genes most significantly affecting 5-FU efficacy in the host.

Chemical perturbations in bacteria have been used to associate genes with phenotypes and function (Nichols et al., 2011). We therefore asked whether we could infer drug action on the host by evaluating the effect of 5-FU on bacteria alone. First, we investigated how gene deletions affect E. coli response to 5-FU, using changes in growth, measured by optical density (OD), as a readout of drug effects on the bacteria (Figures S2D and S2E). As expected, most deletions did not affect response to 5-FU treatment (rsq = 0.33, p < 2 × 10^-16; Figure S2D). One of the most significant resistant hits was ΔgcvA, which codes for the 5% of bacterial knockouts that confer the greatest MIC values in worms contained equal proportions of mutants with sensitive (e.g., ΔgcvA) and resistant (e.g., Δupp) growth interactions with 5-FU (Figure 2E). Altogether, bacterial growth or 5-FU effects on E. coli growth are not key determinants or predictors of 5-FU effects on host physiology. Moreover, when the three datasets are combined together (Figure 2D), this can be further inferred visually by the lack of a gradient in color top to bottom (correlation with 5-FU effects on bacterial growth) or left to right (correlation with bacterial growth alone). Indeed, the 5% of bacterial knockouts that conferred the greatest MIC values in worms contained equal proportions of mutants with sensitive (e.g., ΔgcvA) and resistant (e.g., Δupp) growth interactions with 5-FU (Figure 2E).

To determine which bacterial processes contribute to the effects of 5-FU on host physiology, we performed enrichment analysis of KEGG and EcoCyc pathways on the genes with strong 5-FU effects on C. elegans development (MIC >5 μM) (Figure 2F, see STAR Methods for details). Out of the significantly enriched pathways, 3 (pyridoxal-5-phosphate [PLP], chorismate, and folate biosynthesis) were involved in the production of 5,10-methylene tetrahydrofolate (CH2-THF), a cofactor for TS (thyA/TS; Figure 2G), the canonical target of 5-FU (Longley...
Figure 2. Chemical-Genomic Bacterial-Host Screens Identify Pathways for 5-FU Action Not Revealed by Bacterial-Drug Screens

(A) 5-FU inhibits worm development on control (BW25113) but not mutant E. coli (Δupp).

(B) Diagram of the three-way host-microbe-drug interaction screen.

(C) Screen design and Venn diagram of biologically relevant hits.

(D) 3D graph correlating effects of gene knockout on bacterial growth (x axis), effects of 5-FU on bacterial growth (y axis), and effects of knockout on worm growth inhibition by 5-FU (colored circles). Gray dashed fit line (correlation between 5-FU and knockout effects in bacteria) determines bacterial sensitivity to 5-FU (blue/green color gradient box). Error bars represent SD.

(E) Venn diagram of E. coli sensitive/resistant hits (FDR <0.05) with C. elegans 5% top hits for 5-FU treatment.

(F) KEGG (K) and EcoCyc (E) pathway enrichment for gene deletions, and their effects on C. elegans ranked by coverage. Knockouts with MIC >5 μM are hits. Violin plots display distribution of MIC values; Contour color, number of hits; interior color, pathway coverage. *FDR <0.05; **FDR <0.01.

(G) Metabolic network between chorismate, one-carbon, and vitamin B6 metabolism based on screen results.

See also Figure S2 and Table S2.
Surprisingly, pyrimidine metabolism was not significantly over-represented, suggesting that only key genes (e.g., *E. coli* epd, upp) contribute to the observed effects. Given the link between vitamin B₆, chorismate-folate, and pyrimidine metabolism, we next investigated how these bacterial biosynthetic pathways regulate 5-FU action in the host. Vitamin B₆ is a key cofactor involved in numerous enzyme-catalyzed reactions in all living systems. Unlike eukaryotes, *E. coli* is capable of synthesizing PLP, the active form of B₆, via both de novo and salvage pathways (Fitzpatrick et al., 2007) (Figure 3A). We therefore tested the impact of these two B₆ pathways in regulating 5-FU efficacy in the host. We found that impairing de novo PLP synthesis decreased 5-FU efficacy in the worm by 8- to 16-fold (p < 0.001; Figure 3B). By contrast, deletion of *pdxH* from the salvage pathway had no effect (Figure 3C). Knockout of *pdxH*, a gene at the intersection of both pathways, decreased 5-FU efficacy by 8-fold (p < 0.001; Figure 3C). Using liquid chromatography-tandem mass spectrometry (LC-MS/MS), we found that ∆*pdxH* mutants were also deficient in 5-FU efficacy (Figure 3C). Knockout of *pdxK*, a key kinase in the salvage pathway, improved 5-FU efficacy (Δ*pdxK* = 0.1 μM versus BW25113 = 0.25 μM, p < 0.001; Figure 3C). Altogether, our data imply a key role of bacterial PLP in the mediation of 5-FU effects on host physiology.

**E. coli** Vitamin B₆ Is Essential for 5-FU Efficacy in *C. elegans*

Given the link between vitamin B₆, chorismate-folate, and pyrimidine metabolism, we next investigated how these bacterial pathways regulate 5-FU action in the host. Vitamin B₆ is a key cofactor involved in numerous enzyme-catalyzed reactions in all living systems. Unlike eukaryotes, *E. coli* is capable of synthesizing PLP, the active form of B₆, via both de novo and salvage biosynthetic pathways (Fitzpatrick et al., 2007) (Figure 3A). We therefore tested the impact of these two B₆ pathways in regulating 5-FU efficacy in the host. We found that impairing de novo PLP synthesis decreased 5-FU efficacy in the worm by 8- to 16-fold (p < 0.001; Figure 3B). By contrast, deletion of *pdxH* from the salvage pathway had no effect (Figure 3C). Knockout of *pdxH*, a gene at the intersection of both pathways, decreased 5-FU efficacy by 8-fold (p < 0.001; Figure 3C). Using liquid chromatography-tandem mass spectrometry (LC-MS/MS), we found that ∆*pdxH* mutants were also deficient in 5-FU efficacy (Δ*pdxH* = 0.1 μM versus BW25113 = 0.25 μM, p < 0.001; Figure 3C). Altogether, our data imply a key role of bacterial PLP in the mediation of 5-FU effects on host physiology.

**Figure 3. Pyridoxal-5-Phosphate Is a Key Cofactor for the Mediation of 5-FU Effects**

(A) The de novo (blue, *E. coli*) and salvage pathway genes (green, *E. coli*; red, *C. elegans*) of B₆ metabolism. (B) Knockout of *B₆* de novo pathway enzymes in *E. coli* reduces 5-FU efficacy in worms. (C) *C. elegans* knockout of *pdxH* from the salvage pathway had no effect (Figure 3C). Interestingly, knockout of *pdxK*, a key kinase in the salvage pathway, improved 5-FU efficacy (Δ*pdxK* = 0.1 μM versus BW25113 = 0.25 μM, p < 0.001; Figure 3C). Using liquid chromatography-tandem mass spectrometry (LC-MS/MS), we found that ∆*pdxH* mutants were also deficient in 5-FU efficacy (Δ*pdxH* = 0.1 μM versus BW25113 = 0.25 μM, p < 0.001; Figure 3C). Altogether, our data imply a key role of bacterial PLP in the mediation of 5-FU effects on host physiology.

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Vitamins are important regulators of microbial metabolism but can also influence host metabolism. Therefore, we tested
whether PLP affects bacterial or host metabolism to regulate 5-FU efficacy. Supplementation with 1 mM pyridoxal (PL), a precursor of PLP through conversion by pyridoxal kinase (bacterial = \textit{pdxK} or worm = \textit{pdxJ}), fully rescued the effect of the \textit{ΔpdxJ} mutant and improved 5-FU efficacy (BW + PL = 0.1 \textmu M versus BW = 0.25 \textmu M, \( p = 0.006 \), Figure 3D). Similar effects were observed at 10 \textmu M PL (Figure S3B). Also, supplementation with PL fully rescued PLP and pyridoxine (PN) levels in the glycine cleavage system (GCS) (\textit{F57C9.1}) (Figures 3A and S3D), with reduced capacity to utilize B6 vitamers, was similar to wild-type (WT) worms when fed \textit{ΔpdxJ} and supplemented with PL (Figures S3E and S3D), suggesting that PL rescue is not mediated by worm metabolism. Consistent with this idea, worms grown on the PLP-deficient mutant \textit{ΔpdxJ} failed to show significant gene expression changes for enzymes involved in vitamin B6 folate metabolism, the glycine cleavage system, and nucleotide metabolism, which mediate the effects of 5-FU in eukaryotic cells (Ser et al., 2016) (Figure S3F). Taken together, these results support a role for bacterial PLP in the modulation of drug efficacy in the host via effects on microbial metabolism rather than direct effects on the host.

**Vitamin B6 Regulates One-Carbon Metabolism in Bacteria to Mediate 5-FU Effects on the Host**

One-carbon metabolism (OCM) plays an essential role in a myriad of biochemical processes. Out of the 43 enzymes in \textit{E. coli} that require PLP as a cofactor, ten were found in our screen as regulating the effects of 5-FU on host physiology, with five belonging to OCM (Figures 2G). In particular, PLP is essential for reactions involved in the production of CH2-THF (Longley et al., 2003), an important cofactor in pyrimidine synthesis by TS.

Glycine and serine metabolism are at the center of OCM, as major one-carbon donors in the production of CH2-THF (Locasale, 2013). We found that knockout of bacterial genes involved in the glycine cleavage system \( \text{gcv} \) or their transcriptional regulators \textit{gcvA} and \textit{gcvR} reduced 5-FU effects up to 8-fold (Figure 4A). PLP is a key cofactor in the two parallel reactions mediated by \textit{glyA} and \textit{gcvP} to produce CH2-THF, and therefore we queried whether PLP regulates 5-FU effects via the GCS. Accordingly, host 5-FU MICs were similar for worms fed the single mutants, \textit{ΔgcvP} and \textit{ΔpdxJ}, and the respective double mutant (Figure 4B). These results support GCS as the main pathway regulated by PLP to mediate the efficacy of 5-FU.

Next, we probed the role of CH2-THF in mediating 5-FU effects. First, we tested whether the inhibition of bacterial folate metabolism alters 5-FU efficacy on the host. Inhibition of the shikimate pathway that produces the folate precursor para-aminobenzoic acid (PABA; Figure S4A) decreased 5-FU efficacy up to 16-fold (Figure S4B). Also, impairing synthesis of the main precursors of CH2-THF, including tetrahydrofolate (THF) by \textit{ΔfolM} or \textit{ΔpurU} and 5,10-methenyl-THF (CH+–THF) by \textit{Δfauf}, reduced 5-FU efficacy by 8- to 16-fold (Figure 4C). In contrast, deletion of \textit{metF} resulted in increased drug efficacy (MIC = 0.1 \textmu M, \( p < 0.001 \), Figure 4C), possibly due to retention of CH2-THF within the folate cycle. Next, we performed LC-MS/MS analysis of bacterial folate metabolism in \textit{Δfauf} and \textit{ΔgcvP} mutants to investigate the impact of these genes on folate metabolism. Our data show a shift in folate metabolite pools with an increase...
in formyl-THF (CHO-THF; +33%, p < 0.0001) in Δfau, and THF (+25%, p < 0.0001) in ΔgcvP, with a decrease in the remaining folate forms (Figure 4D), confirming their role in the regulation of folate metabolism and consistent with our observations in GlcD-deficient mouse embryos (Pai et al., 2015). These findings suggest a redistribution of folates to maintain essential CH₂-THF pools required for cellular division. Altogether, the data indicate that bacterial folate metabolic status regulates the efficacy of 5-FU on the host.

In order to probe the activity of folate-dependent enzymes, we analyzed folate polyglutamation profiles. Folates are defined by a pteridine ring, PABA, and a variable number of glutamate moieties, which determine retention and bioavailability for enzymatic reactions (Kwon et al., 2008). Major differences in polyglutamation profiles were observed only for CH₂-THF (Figure 4E) but not other folate forms (Figure S4C). The decrease in the abundance of shorter polyglutamate chains of CH₂-THF in Δfau (n_glut = 3) and ΔgcvP (n_glut = 3, n_glut = 4) (Figure 4E) is consistent with the role of these genes in the mediation of 5-FU efficacy in the host (Figures 4A–4C), possibly by regulating the availability of CH₂-THF as a cofactor for TS. To confirm this, we used chemical interference by metformin, which dramatically alters polyglutamylation of CH₂-THF in E. coli (Cabreiro et al., 2013). Our data show that metformin treatment impairs 5-FU treatment by 16-fold, and this effect is partially rescued in a strain resistant to metformin but not 5-FU (OP50-MR) (Figure 4F). Indeed, bacterial growth data show that metformin is antagonistic to the effects of 5-FU (Figures S4D–S4F). Given that genetic polymorphisms in human methylene THF reductase (Offer and Diario, 2016) are associated with 5-FU efficacy in cancer treatment, we investigated the effect of ΔgcvP and Δdku mutations on host folate metabolism by LC-MS/MS. Our data show that these bacterial mutants do not regulate folate pools in the host (Figure S4G). Overall, our results indicate that disrupted folate metabolism in bacteria have a direct impact on 5-FU efficacy, without directly modulating host OCM.

**Fluoropyrimidines Hijack Bacterial Ribonucleotide Metabolism to Regulate Drug Efficacy on the Host**

Fluoropyrimidines are pro-drugs that require intracellular metabolic conversion to downstream active metabolites to induce DNA damage (Longley et al., 2003). Since TS links OCM and pyrimidine metabolism, we hypothesized that bacteria could influence drug cytotoxicity through metabolic interconversion, an effect possibly regulated by vitamin B₉. Cytosine deaminase (CodA), which converts cytosine to uracil, exists only in prokaryotes and has been used for suicide gene therapy against cancer for the delivery and conversion of 5-FC to 5-FU to cancer cells expressing bacterial codA (Koyama et al., 2000). We utilized this peculiarity to determine whether E. coli regulates drug efficacy independently of the host metabolic machinery by conducting a bioconversion assay (see STAR Methods for details, Figure 5A). 5-FC was effective at inhibiting worm hatching only if fed on WT bacteria but not ΔcodA or Δupp mutants (Figures 5A and 5B). Pre-incubation of 5-FC with control bacteria complemented the metabolic deficiency of ΔcodA and Δupp. Interestingly, the intermediate response observed for pre-incubation with ΔcodA suggests an alternative but less efficient pathway for conversion of this pro-drug (Figure 5B). LC-MS/MS analysis of fluoronucleotides supports these findings (Figure 5C). The amount of 5-FC was higher in ΔcodA relative to control (4.61-fold, p = 0.004; 1.7-fold, p = 0.044) with a concomitant decrease of 5-FU (4.4-fold, p = 0.018; 5.4-fold, p = 0.006) in pellets (intracellular) and supernatants (secreted), respectively. 5-fluorouridine 5'-monophosphate (5-FUMP) was also decreased in ΔcodA pellets (4.5-fold, p = 0.0008). Thus, bacteria can convert and secrete metabolized fluoronucleotides from 5-FC, which then target worm metabolism (Figure 1G).

Therefore, which bacterial genes are involved in the full bioconversion of fluoropyrimidines? To explore this, we first investigated the contribution of the salvage pathways of pyrimidine ribonucleotides (e.g., UMP and deoxyribonucleotides (e.g., thymidine) (Figure 5D). Impeding bacterial uptake of nucleobases and nucleosides reduced 5-FU action (Figure S5A). Inhibition of ribonucleotide metabolism through knockout of upp and/or udk had no role alone (ΔuppΔudk = 0.25 μM, p = 0.916) but synergistically with ΔpyrF to inhibit bacterial contribution of 5-FU effects on the host (Δupp = 2 μM; ΔuppΔudk = 32 μM; ΔudkΔupp = 32 μM, Figure 5E). As expected, knockout of the pyrimidine nucleotidase y jiG improved drug efficacy (Δy jiG = 0.1 μM, p = 0.014). We further investigated the link between pyrimidine supplementation, bacteria, and 5-FU effects on the host by feeding worms bacterial mutants of pyrimidine metabolism (Figure 5D). Supplementation of uridine (Figure S5B) and orotate (Figure S5C) dramatically reduced 5-FU efficacy (by 160- and 16-fold, respectively), an effect mediated by the ribonucleotide salvage pathway genes upp, udk, udp and the de novo pyrimidine pathway gene pyrE, but not pyrD, respectively (Figures S5B and S5C). Indeed, interfering with the deoxyribonucleotide salvage pathway increased 5-FU efficacy by rewiring nucleotide metabolism though the ribonucleotide salvage pathway (Δtkd = 0.1 μM, versus BW = 0.25 μM, p = 0.004; ΔtkdΔupp = 32 μM versus ΔudkΔupp = 32 μM, p = 1), a finding consistent with the observation that supplementation with thymidine slightly increases 5-FU efficacy in worms fed Δtkd bacteria (Figure S5D).

Next, we addressed the role of the de novo pathway. We observed that knockout of genes downstream (pyrE and pyrF) but not upstream (pyrD) of orotate strongly impaired 5-FU efficacy (ΔpyrE and ΔpyrF = 32 μM; ΔpyrD = 0.25 μM) (Figure 5F). In addition, bioconversion of 5-FO and excretion of metabolized fluoronucleotides can be performed by WT E. coli but not ΔpyrE (Figure S5E). We also found pathway specificity in the conversion of fluoronucleotides, as worms fed ΔpyrE did not modulate 5-FU effects (Figure S5C) or downstream metabolites of converted 5-FO (Figure S5E). Thus, bacterially mediated bioconversion and secretion of fluoropyrimidines is pathway specific (de novo for 5-FO and salvage ribonucleotide for 5-FU and 5-FC) and determines drug efficacy in the host. Furthermore, our data suggest that E. coli also acts as an integrator of nutritional metabolites to regulate the effects of fluoropyrimidines on host metabolism.

Therefore, we tested whether B₉ and B₉ act in concert with ribonucleotide metabolism to mediate drug transformation. Our data indicate that pdkJ and gcvP are negatively epistatic to upp, udk (Figure 5G). Also, supplementation of PL required intact ribonucleotide salvage to improve 5-FU efficacy (Figure S4H) and
Figure 5. Bacteria Complement C. elegans Metabolically to Mediate 5-FU Effects

(A) Diagram of the bioconversion experiment.
(B) Pre-conversion of 5-FC by bacteria enhances drug effects on the host.
(C) Control but not codA metabolize 5-FC and excrete 5-FU. BD-below detection in codA but not BW.
(D) Diagram of bacterial (fluoro)pyrimidine metabolism. Dashed arrows, more than one reaction.
(E) Opposite effects of salvage deoxyribonucleotide (Dtdk) and ribonucleotide (Dupp, DuDk, DuDp) metabolism in 5-FU efficacy.
(F) Bacterial de novo pyrimidine metabolism regulates the effects of 5-FO.
(G and H) B6 deficiency (G) and PL supplementation (H) regulate 5-FU effects through bacterial ribonucleotide metabolism.
(I) Bacterial conversion of 5-FU alters fluoropyrimidine profiles and availability in C. elegans.
(J) Knockout of host umps-1 mediates drug effects on worm development only in the absence of bacterial conversion of 5-FO.

Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. See also Figure S5. For statistics, see Table S5.
increased the transcription of pyrimidine metabolism genes (Figure S5F), and pdxJ regulates drug bioconversion (Figure S5G). Altogether our findings implicate this metabolic axis as central for fluoropyrimidine metabolism, and the regulation of nucleotide flux is mediated by vitamin B₆ and B₉.

Gut microbes are key players involved in the regulation of host physiology through metabolism of nutrients and xenobiotics (Spanogiannopoulos et al., 2016). Does co-metabolism of fluoropyrimidines occur in the worm E. coli holobiont? We performed fluoronucleotide LC-MS/MS analysis of worms and E. coli treated with 5-FU. Our data highlight distinct profiles both in worms and bacteria, an effect dependent on E. coli genotype (Figure 5I). In particular, 5-FUMP and 5-fluorouridine 5'-triphosphate (5-FUTP) were significantly decreased in ΔudpΔndkΔupp triple mutants and worms fed this strain (Figures S5H and S5I). Similar trends were observed for worms fed heat-killed bacteria, ΔpdbΔgcvP double mutants and control bacteria supplemented with uridine (Figures S5J and S5K), further supporting the role of bacterial ribonucleotide salvage metabolism in the conversion of fluoronucleotides to increase drug efficacy in the host. In order to probe this further, we utilized umps-1(zu456) loss-of-function worm mutants, which are incapable of converting orotate to UMP (Merry et al., 2014). Since umps-1(zu456) impairs fertility, we assayed worm larval development (which was not affected by the mutation; data not shown) as a proxy for drug efficacy. Indeed, umps-1(zu456) worms were only resistant to the effects of 5-FO when fed ΔpyrE bacteria (Figure 5J), but not to 5-FU (Figure S5L). Overall, our data suggest that host de novo pyrimidine metabolism does not contribute to fluoropyrimidine efficacy beyond its minor role in converting 5-FO at high drug concentrations and supports the notion that the holobiont functions as a single unit in the mediation of drug effects.

**Bacterial Deoxynucleotide Imbalance Increases 5-FU-Induced Autophagy and Cellular Death**

We found that knockout of bacterial ndk, the nucleoside diphosphate kinase from the deoxyribonucleotide salvage pathway, and yjjG from the ribonucleotide salvage pathway, improved efficacy of fluoropyrimidine treatment in worms (0.1 μM, p < 0.0001; Figures 5E, 5F, 6A, and 6G). Therefore, we probed whether ndk was acting in concert with the bacterial conversion of 5-FU to downstream fluoronucleotides to mediate the host response to drug. Surprisingly, knockout of ndk was not epistatic to pyrE in the mediation of 5-FO effects (Figure 6A), did not confer resistance to bacterial 5-FU (Figures 6B and 6A), and did not alter 5-FUTP or 5-FdUMP abundance in E. coli or C. elegans (Figures 6C and 6D), the two metabolites responsible for impeding cellular division by causing RNA and DNA damage, respectively (Longley et al., 2003). In contrast, knockout of yjjG (1) dramatically increased fluoronucleotide abundance in both organisms (Figures 6C and 6D), possibly by impeding diversion of 5-FU metabolism to the less toxic prodrug 5-fluorouridine (5-FUrd) (Figure 5D); (2) enhanced bacterial sensitivity to 5-FU (Figure 6B); and (3) required higher concentrations of uridine for rescuing 5-FU toxicity (Figure S6B). Altogether, these data suggest a distinct mode of action conferred by these two genes. To gain insight into the mechanism underlying such effects, we performed analysis of nucleotide metabolism by LC-MS/MS. This approach revealed discrete deoxynucleotide changes in Δndk, but not ΔyjjG or ΔpyrE (Figures 6E, S6C, and S6D). To investigate the role of microbial deoxynucleotides in modulating drug potency, we tested the function of the dCTP deaminase dcd, which, like ndk, alters dNTP pools (Figure 6F) (Maslowska et al., 2015). Knockout of dcd, like ndk, improved 5-FU efficacy on the host (Figure 6G) but did not alter the bacterial sensitivity to 5-FU (Figures 6B and S6A). Thus, bacterial deoxynucleotide imbalance mediated by ndk and dcd promotes cellular death by a distinct mechanism to increased fluoronucleotide pools in host cells (e.g., yjjG) (Figure 6D).

In C. elegans, overexpression of TS in the germline increases resistance to 5-FU effects (Kim et al., 2008). As a consequence of TS inhibition, DNA damage (Longley et al., 2003) and disruption of the cell cycle have previously been reported for mammalian cells treated with 5-FU (Ser et al., 2016). Similarly, we observed that folate metabolism was dysregulated in embryos, but not intact worms treated with 5-FU (Figures 6H and S6E), suggesting that TS in the germline is one of the likely targets of 5-FU in C. elegans. DNA damage caused by cancer drugs induces autophagy-mediated cell death in human cells (Zeng and Kinsella, 2011). Similarly, DNA damage checkpoint activation by 5-FU in C. elegans induces autophagy, measured by changes in lgg-1::GFP fluorescence, the worm ortholog of atg8/LC3 (SenGupta et al., 2013). Therefore, we investigated the role of bacteria in the activation of autophagy by 5-FU and found that autophagy was activated by 5-FU in a dose- and bacterial-dependent manner (Figure S6F). Also, Δndk and Δdcd but not ΔyjjG synergized the effects of 5-FU to induce autophagy (Figure 6I) despite similar effects on embryonic lethality (Figure 6G), further supporting a distinct mechanism to induce cell death in host cells. To probe the involvement of the DNA damage mismatch repair (MMR) pathway in the activation of autophagy (SenGupta et al., 2013), we tested the MMR-deficient mutant

**Figure 6. Bacteria Regulate 5-FU Effects in C. elegans by Two Distinct Mechanisms**

(A) Bacterial ndk effects on the efficacy of 5-FU are independent of 5-FU bioconversion mediated by pyrE.

(B) IC₅₀ values for bacterial growth with 5-FU.

(C and D) LC-MS/MS quantification of fluoropyrimidines in E. coli (C) and C. elegans (D) supplemented with 50 μM 5-FU.

(E) Volcano plot of nucleotide metabolism of bacterial mutants.

(F) Diagram of deoxynucleotide metabolism in E. coli. X = G or A.

(G) Bacterial deoxynucleotide imbalance caused by Δndk and Δdcd improves 5-FU effects.

(H) 5-FU alters folate metabolism homeostasis in embryos. Inset: effects of 5-FU on egg hatching of the analyzed samples.

(I) Activation of autophagy (Lgg-1::GFP reporter) in embryos by 5-FU is dependent on bacteria.

(J) Host ndk-1 is required for 5-FU-induced autophagy activation by bacterial deoxynucleotide imbalance.

(K) Bacterial ndk effects on 5-FU efficacy are mediated by the host ndk-1 gene.

Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. See also Figure S6. For statistics, see Table S6.
msh-6(pk2504)). We found that msh-6 improved resistance to 5-FU, as previously reported (SenGupta et al., 2013), but this effect was dependent on bacterial metabolism, in particular, deoxynucleotide metabolism. msh-6 mutants were only resistant to 5-FU when fed HT115 (Figure S6G), but not BW25113 (Figure S6H) or Δndk (Figures S6G and S6H). Thus, imbalanced bacterial deoxynucleotide pools improve 5-FU efficacy in the host independently of the MMR. So, how is autophagy activated by bacterial deoxynucleotide pools in the context of 5-FU treatment? Given the role of ndk in regulating deoxynucleotide metabolism, we tested whether the worm ortholog ndk-1 plays a role in mediating these effects. Efficient knockdown of ndk-1 by RNAi (Figure S6I) reduced fertility (data not shown) but did not contribute to 5-FU effects on the host (Figures 6J and 6K). ndk-1 RNAi solely decreased the activation of autophagy (Figure 6J) and abolished the improvement in 5-FU efficacy conferred by knockout of bacterial ndk (Figure 6K). Thus, host ndk-1 regulates effects of microbial deoxynucleotides to modulate drug potency. This implies another role for NDK rather than its direct involvement in the metabolism of fluoropyrimidines. Overall, we show that bacteria mediate two modes of cellular death in the host either by an increase of RNA-damaging FUTP (e.g., ΔyjG) or by sensitizing the DNA-damaging effects of 5-FU (e.g., Δndk, Δcd).

**DISCUSSION**

In this study, we have demonstrated how microbes and dietary cues modulate the efficacy of fluoropyrimidines on the C. elegans host.

**Chemical-Holobiont Screens for Drug Effects on Host Physiology**

Historically, pharmacology has solely considered host biology when developing new therapeutics, which may contribute to the high degree of failure observed for drugs undergoing clinical trial. While it is accepted that gut microbiota are capable of altering drug pharmacodynamics (Spanogiannopoulos et al., 2016), probing the complex relationships between host, microbe, and drug has proved difficult. Here, we used a nematode-microbe model to unravel the contribution of bacterial genes in host responses to anti-cancer drugs by testing a combination of bacterial genetics, dietary sources, and chemical compounds. The advantages of the metabolically and evolutionarily conserved C. elegans model are clear: the convenience of sustaining animals on defined bacterial populations, together with the ease of genetic manipulations and biochemical analysis in both organisms, allows rigorous investigation of host-microbe interactions by rapid screening that is not possible in higher models. This system may be of particular use for pre-clinical screening of drug interactions in the context of host and microbe, a task usually studied in vitro or by analyzing candidate compounds using in vitro fecal models (Spanogiannopoulos et al., 2016), or for designing bacteria for drug delivery, a prospect for future personalized medicine. While our screening approach

![Figure 7](image-url)
of incorporating the host as a biological readout validated findings obtained by more traditional microbial high-throughput genetic and chemical genetic approaches, we provide striking insights into host-microbe interactions that could not be uncovered by studying microbes in isolation.

Another advantage of our approach is the evolutionarily conserved effects of 5-FU on host metabolism, at similar physiological drug concentrations to that observed in human plasma after treatment or at concentrations capable of inhibiting TS in colon cancer cells (Ser et al., 2016). In fact, similar metabolic changes were observed in the serum of tumorous mice treated with 5-FU (Ser et al., 2016) and worms treated with 5-FU. Changes in metabolites from pyrimidine (e.g., uracil, orotate), one-carbon (e.g., methionine, homocysteine, L-serine), and carnitine metabolism (e.g., L-acetylcarnitine, isovalerylcarnitine) were observed (Figures S1K and S1L). Most importantly, the model proved valuable in identifying key biological processes at the host-microbe interface (bioconversion and host-microbe metabolic complementation for drugs), bacterial pathways responsible for drug efficacy (e.g., ribonucleotide (Garcia-Gonzalez et al., 2017 [this issue of Cell]), vitamin B₆, and OCM), and dietary cues affecting drug metabolism (e.g., pyrimidines) (Figure 7E).

**Role of the Microbiota in Modulating Fluoropyrimidine Efficacy**

We report that bacterial activation of fluoropyrimidines by direct metabolic conversion is critical for optimal drug efficacy in worms. Given that the microbiota is a key determinant of host health and a source of inter-individual variability (Nicholson et al., 2012), and given the highly conserved nature of nucleotide metabolism across bacterial taxa (Peregrín-Alvarez et al., 2009), our results raise the possibility that microbes might similarly influence the action of 5-FU and predict cancer therapy outcomes in patients. In recent years, there have been several reports of microbial influence on drug efficacy (reviewed by Spano Giovanni et al., 2016), some in the context of cancer therapy. For example, gut microbes have been reported to reactivate the cancer drug irinotecan, causing toxicity. Also, gut microbes isolated from human feces are capable of converting 5-FC to 5-FU, but whether this phenomenon contributes to drug efficacy in the host has never been tested until now. Similarly, we demonstrate that *E. coli* can convert not only 5-FC, but also other clinically relevant fluoropyrimidine prodrugs such as 5-FU and capectabine. Importantly, worm responses to fluoropyrimidines were strongly contingent on their microbes, with pharmacodynamics varying by as much as 40-fold on different bacterial strains and disruption of bacterial metabolism leading to changes as great as 256-fold. We have revealed that inhibition of bacterial ribonucleotide metabolism drastically antagonizes drug efficacy, while inhibition of deoxyribonucleotide metabolism improves it, an effect also regulated by dietary pyrimidines. Similar mechanisms have been observed in mammals, where dietary arginine regulates the inactivation of the cardiac drug digoxin by the gut microbe *E. lenta* (Haiser et al., 2013).

Here, we have discovered that the *C. elegans*-*E. coli* holobiont acts together as a single unit in the context of drug metabolism, showing biochemical complementation for the mediation of fluoropyrimidine effects on host physiology (Figure 7G).

**Role of Diet and Drugs in Fluoropyrimidine Efficacy**

Interventions that disrupt the microbiota, such as antibiotics, impair the response of tumors to CpG-oligonucleotide immunotherapy and platinum chemotherapy (Iida et al., 2013). Additionally, unforeseen interactions between the antiviral drug sorivudine and 5-FU prodrugs have led to patient deaths due to microbiome-drug interactions (Okuda et al., 1997). Consistent with these findings, our data show that the anti-diabetic drug metformin, which possesses anti-cancer properties, inhibits bacterial OCM, thereby reducing 5-FU efficacy in *C. elegans*. Given the interaction of metformin with the human microbiota (Cabreiro, 2016), these results raise the possibility that co-therapies for cancer might yield undesired outcomes if host-microbe-drug interactions are not taken into account.

In addition to drugs, we observed that dietary nutrients (e.g., pyrimidines, vitamin B₆) can alter the efficacy of 5-FU. Vitamins produced by gut microbes (e.g., vitamin B₆) are a determining factor in shaping microbial communities (Degnan et al., 2014). Likewise, our data show that in bacteria, B₆ regulates ribonucleotide flux via modulation of OCM.

**Bacteria as Regulators of 5-FU-Induced Cell Death: A Double-Edged Sword**

The magnitude and balance of deoxynucleotide pools are important for replication fidelity (Maslowska et al., 2015). Here, we show that alterations in deoxynucleotide pools caused by mutations in *dcd* and *ndk* do not sensitize bacterial mutants to the DNA damage agent 5-FU but increase efficacy of treatment in the host. Our results illustrate that the holobiont metabolic complementation occurs at two levels in the context of drugs: (1) in their bioconversion and by regulating the availability of RNA-damaging fluoronucleotides such as FUTP to the host, and (2) in the supply of regulatory metabolites that synergize with 5-FU-induced DNA damage. Consistent with our observations, it was previously reported that bacterial nucleotide metabolism regulates *C. elegans* germline proliferation (Chi et al., 2016).

Cancer treatments can activate either pro-survival or pro-death autophagy activity in tumor cells, an effect dependent on the cellular context (Zeng and Kinsella, 2011), but this mechanism is not fully understood. Our data suggest a divergent role for dNTP pool imbalance between prokaryotes and eukaryotes and a mechanism where deoxynucleotide pools from non-self to self can amplify autophagy-mediated cell death inflicted by fluoropyrimidines on eukaryotic cells. In contrast, increased dNTP pools desensitize human cancer cells to rapamycin-induced autophagy (Chen et al., 2014). Altogether, these findings implicate dNTP pools in the regulation of autophagy by drugs, a mechanism of relevance to cancer biology and human health.

Our chemical-genomic-holobiont screening approaches highlight that bacteria play key roles in the efficacy of a drug in an animal model and illustrate a critical missing component in our understanding of the mechanistic basis of drugs in the treatment of disease. In humans, the identification of gut microbiota members responsible for these mechanisms and their regulation by dietary supplements could have a dramatic impact on treatment outcome.
STAR METHODS

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SUPPLEMENTAL INFORMATION

Supplemental Information includes seven figures and seven tables and can be found with this article online at http://dx.doi.org/10.1016/j.cell.2017.03.040.

AUTHOR CONTRIBUTIONS


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# STAR METHODS

## KEY RESOURCES TABLE

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### Chemicals, Peptides, and Recombinant Proteins

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### Critical Commercial Assays

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### Experimental Models: Organisms/Strains

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(Continued on next page)
CONTACT FOR REAGENT AND RESOURCE SHARING

Further information and requests for reagents may be directed to, and will be fulfilled by the Lead Contact Filipe Cabreiro (f.cabreiro@ucl.ac.uk).

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Nematode and Bacterial Strains

*C. elegans* strains N2 Bristol, GH636 *umps-1(zu456)III*, GC833 *gip-1(ar202)III*, NL2099 *nrf-3(pk1426)III*, NL2511 *msh-6(pk2504)* and DA2123 adIS2122[lgg-1p::GFP::lgg-1 + rol-6 (su1006)] were obtained from the Caenorhabditis Genetics Center (CGC). The *E. coli* Keio Knockout Collection (Baba et al., 2006) (odd numbered strains) was obtained from the National BioResource Project. Other bacterial strains obtained from the Coli Genetic Stock Center, and bacterial strains created for this study are listed in Table S1.

Both bacterial and nematode mutants were re-confirmed by PCR or snPCR using primers listed in Table S1.

Software and Algorithms

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Nematode Culture Conditions

Worms were maintained and raised at 20°C, unless otherwise stated, on nematode growth medium (NGM). Where indicated molten molten agar was supplemented with fluoropyrimidines (0.01, 0.05, 0.1, 0.25, 0.5, 1, 2, 4, 8, 16, 32, 64 μM), nucleotides (200 μM, 2 mM) and B6 vitamins (10 μM, 1 mM). Maintenance of the GH636 strain was achieved on NGM plates supplemented with 100 mM uridine. For UV and heat treatment of bacteria, an overnight culture of the indicated bacterial strain grown at 37°C was centrifuged at 5000 rpm for 30 min at 4°C, then resuspended in phosphate buffered saline (PBS) at a final OD600 = 24. For UV treatment, bacteria were irradiated for 30 min on a CL-1000 Ultraviolet Crosslinker (UVP) containing bulbs irradiating at 254 nm; for heat treatment, bacteria were incubated for 30 min at 70°C in a water bath. For RNAi experiments, worms were kept for two generations on NGM plates.
containing 1 mM IPTG (isopropyl β-D-1-thiogalactopyranoside) seeded with E. coli HT115(DE3) or HT115(DE3) Δndk expressing RNAi constructs in the pL4440 feeding vector. RNAi clones were verified by sequencing and efficacy of knockdown was determined by qRT-PCR (Figures S3D and S6I).

**Bacterial Strain Construction**

Bacterial strains used and generated in this study are shown in the Key Resources Table. E. coli single deletion mutants were obtained from the Keio collection (Baba et al., 2006). Strains with multiple mutations were constructed by removing the kanamycin resistant marker from single Keio clones by transformation with pCP20 and subsequent transfer of kanamycin-resistant-tagged mutations via P1vir phage-mediated transduction. All bacterial mutants were confirmed by colony PCR using the primers detailed in Table S1. In general, binding sites of the -cseq-F and -R primers are located up- and down-stream of the mutation site, respectively, and were used to confirm kanamycin-sensitive mutants, while the K1, which binds to the kanamycin resistance gene, was used in conjunction with the appropriate -cseq-F primer to confirm kanamycin-resistant mutants.

For the generation of BW25113-GFP strains we used bacterial clones containing promoter-fused plasmids from the library of transcriptional fusions of gfp from the Uri Alon lab. The MG1655 strains containing promoter-fused plasmids for udk, ndk, and upp genes (see Key Resources Table plasmid list) were selected from the library and each plasmid was extracted using a GenElute Plasmid Miniprep Kit (Sigma Aldrich). The resulting plasmid DNA was confirmed by PCR, using the -cseq-F primer and the Primer 1 from pUA66 as a reverse primer (Table S1). Following confirmation, each plasmid was transformed into the BW25113 strain.

**METHOD DETAILS**

**Lifespan Analysis**

Axenic worm eggs were obtained by treating healthy gravid WT adults with alkaline hypochlorite. Bleached eggs were allowed to develop until the L4 larval stage on HT115(DE3) L4440 or gld-1 RNAi E. coli at 25°C. Efficacy of gld-1 knockdown was confirmed by tumorigenicity of the gonads and by the absence of embryos/oocytes. Animals (gld-1 RNAi or glp-1 (gof)) were transferred to control and 5-FU treated plates seeded with BW25113 or BW25113 Δupp and maintained at 25°C for the whole duration of the lifespan. Worms were transferred to fresh plates every 4 days. Animals that did not display tumorous gonads were removed from the trial at day 1 of adulthood and the ones that showed protruded vulvas were censored. Survival was monitored every 1-2 days and worms were scored as dead if they did not respond to prodding with a platinum wire. Statistical analysis was performed by the log-rank test using JMP 11 software (SAS Institute).

**Hatching Assays**

Assays were performed in 12-well plates. C. elegans were raised from L1 stage on control (BW25113), other WT or mutant E. coli strains for 2 days at 20°C. Two L4-stage worms were transferred to each well containing seeded NGM agar supplemented with varying concentrations of 5-FU or other drugs. Adult worms were removed after a 24 hr incubation at 25°C. After another 24 hr incubation period, the hatching ratio was scored as the fraction (%) of developed larvae from the initially laid eggs, and presented as the mean ± SD from at least 3 independent biological replicates with at least 100 animals per data point. Statistical analysis was performed by group analysis one per row multiple t tests using Graphpad Prism 6 software.

**Developmental assay**

NGM agar plates containing the appropriate drug concentration were prepared, seeded, and incubated as described for the Host-Microbe-Drug Screen. Visual scoring of nematode development was based on a 5 level system, as follows:

0 = Complete ablation of development (i.e., arrested at L1 stage),
1 = L2/L3-sized
2 = L4/young adult-sized
3 = Fertile adults, no progeny
4 = Complete development, fertile adults with progeny (comparable to no drug control)

**C. elegans bacterial-consumption assays**

Bacteria grown overnight in LB-Miller broth were washed twice in NGM broth, normalized to OD_{595nm} = 3.1 and added to 96-well microtiter plates (100 µL/well, OD_{595nm}~0.6). Antibiotics (Carbenicillin, 100 µg/mL; Streptomycin, 100 µg/mL; Penicillin, 100 µg/mL) were included to inhibit bacterial growth. Synchronized L1 nematodes were added at 800-1000 animals per well. Plates were incubated at 25°C, 400 rpm and the absorbance at OD_{595nm} was measured at 16, 20, 24 and 28 hr using a Tecan Infinite Pro
M200 microplate reader and Magellan v7.2 software. Rates of consumption were expressed as the decrease in OD_595nm units per hour.

**C. elegans Fluorescence Microscopy**
Quantitation of 5-FU growth inhibition was achieved by using the constitutive and robust expression of the GFP::LGG-1 throughout all worm developmental stages and after freezing as a readout of worm size. L1 larvae were placed in 96-well plates containing 5-FU supplemented NGM and seeded with BW25113, BW25113 Δupp, and the respective complemented strains. After 48 hr incubation at 20°C, worms from each well were resuspended in PBS, transferred to a 96-well plate and frozen before imaging. GFP intensity as a measure of area was quantified as the pixel density in the entire cross sectional area of each worm from which the background pixel density was subtracted. 30 worms per condition in 3 biological replicates were imaged.

Alternatively, L1s were raised to the L4-stage on the appropriate bacterial strains, then transferred to 12-well plates containing 5-FU and respective controls to lay eggs for 24 hr at 25°C (similarly to the hatching assays). The levels of autophagy (GFP::LGG-1) in embryos were measured based on whole egg GFP intensity. At least 40 embryos per condition in 3 biological replicates were imaged.

For the effects of 5-FU on tumorous gonad size, day-4 adult gla-1 RNAi animals for each experimental drug and bacterial condition were fixed in 100% methanol for 5 min on ice. Samples were stained with 500 mg/mL DAPI for 15 min in the dark, followed by 3x M9 buffer washes, and placed on 2% agarose pads before imaging. Images were taken of the entire animal using the 10x objective. Tumor retraction was measured as the distance between the two arms of the gonad at the midpoint of the cross sectional area normalized to the distance between the two loops of the gonads. At least 45 worms per condition in 3 biological replicates were imaged.

All images were taken using a Zeiss Axioskop 2 Plus microscope with a DAPI filter cube (excitation: 358 nm; emission: 463 nm) or a GFP filter cube (excitation: 470 nm; emission: 525 nm), an Hamamatsu ORCA-ER digital camera, and further analyzed using Velocity 6.3 software (PerkinElmer). Statistical analysis was performed by one-way ANOVA using GraphPad Prism 6 software.

**Quantitative RT-PCR**
Transcriptional measurements of *C. elegans* were performed in synchronized L4 hermaphrodites fed on diverse bacterial strains and conditions. For total RNA extraction, worms were disrupted in TRI Reagent (Zymo Research) with lysing matrix D (MP Biomedicals), and flash-frozen in liquid nitrogen, then stored at ~80°C overnight. After a thaw-freeze-thaw procedure, samples were homogenized using ThermoMixer C (Eppendorf) at 2000 rpm for 10 min at 4°C. Total RNA were extracted using Direct-zol MiniPrep (Zymo Research) and purified of DNA by in-column DNase I treatment. RNA quantification was achieved using Qubit® RNA HS Assay Kit (Thermo Fisher Scientific). cDNA synthesis was performed using iScript Reverse Transcription Supermix (Bio-Rad). Quantitative PCR was performed with PrecisionPLUS 2x qPCR MasterMix (PrimerDesign) using a LightCycler® 480 Real-Time PCR system (Roche). Primer sequences for each gene (Table S1) were previously optimized over a linear range of cDNA concentrations. Relative transcriptional abundance of target genes was calculated using the ΔCt method and was normalized to averaged mRNA levels of the housekeeping gene cdc-42. At least 3 independent biological replicates for each condition were measured per gene. Statistical significance was obtained using one-way ANOVA tests (for comparison between 4 groups) or unpaired t tests (comparison between two groups) performed in GraphPad Prism 6 software.

**1-Carbon Metabolism Analysis**
For bacterial sample collection and metabolite extraction, 3-day old bacterial lawns of BW25113 or mutants grown at 20°C supplemented NGM and seeded with BW25113, BW25113 Δupp, and the respective complemented strains. After 48 hr incubation at 20°C, worms from each well were resuspended in PBS, transferred to a 96-well plate and frozen before imaging. GFP intensity as a measure of area was quantified as the pixel density in the entire cross sectional area of each worm from which the background pixel density was subtracted. 30 worms per condition in 3 biological replicates were imaged.

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**1-Carbon Metabolism Analysis**
For bacterial sample collection and metabolite extraction, 3-day old bacterial lawns of BW25113 or mutants grown at 20°C on standard NGM plates were scraped using a 24 cm cell scraper and transferred to an eppendorf tube and snap frozen in liquid nitrogen. The bacterial pellet was kept at ~80°C until required.

For worm samples, approximately 1000 synchronized L1 stage larvae were grown at 20°C on standard NGM plates seeded with 3-day old BW25113 or mutant bacteria. L4 larvae were collected for analysis or transferred to fresh NGM plates containing 5-FU and incubated at 25°C for an additional 24 hr before collection. Worms were washed thoroughly using dH_2O to remove bacteria and snap frozen in liquid nitrogen. The worm pellet was kept at ~80°C until required.

For egg samples, approximately 5000 synchronized 1-day adult worms per condition (control and 1 μM 5-FU) were axenized using alkaline hypochlorite. Bleached eggs were placed in M9 buffer for 3 hr to recover from bleaching. An aliquot was kept for determining Folate measurements by LC-MS/MS were performed as previously described (Cabreiro et al., 2013). Mass spectrometric data were analyzed as in (Pai et al., 2015) using MassLynx Software (Waters). Statistical analysis was performed by one-way ANOVA using the Graphpad Prism 6 software.
**Vitamin B<sub>6</sub> Analysis**

For bacterial sample collection and metabolite extraction, 3-day old bacterial lawns grown on standard NGM or supplemented with 1.0 mM pyridoxal at 20°C were washed from plates using 1x PBS. The bacteria were washed three times in 1x PBS to remove potential contaminating pyridoxal from the NGM medium and centrifuged at for 30 min at 4,000 rpm, 4°C. The bacterial pellet was snap frozen in liquid nitrogen and kept at −80°C until required. At least 4 biological replicates were collected for each condition.

The bacterial pellets were resuspended in 50 μL dH<sub>2</sub>O and lysed by subjecting the sample to 5 freeze-thaw cycles using a methanol-dry ice bath and a 37°C waterbath. The resulting lysates were pelleted for 5 min at 5,000 rpm, 4°C, and the supernatants collected. Proteins were precipitated by mixing 10 μL of bacterial lysate supernatant with 0.15 N (final concentration) trichloroacetic acid (TCA, Sigma Aldrich) and spiked with deuterated internal standards (PMP, PNP, PLP: d<sub>3</sub>-PLP, PM: d<sub>3</sub>-PM, PN: d<sub>2</sub>-PN and PL: d<sub>3</sub>PL; all at a final concentration of 25 nM, Table S1) up to a total volume of 120 μL. Samples were vortexed for 30 s, left on ice in the dark for 60 min and centrifuged to pellet the precipitated protein. The resulting supernatant was transferred to a glass vial and kept at −20°C in the dark until sample analysis.

B<sub>6</sub> vitamers LC-MS/MS analysis was carried out using an adapted version of the protocol detailed in (Footitt et al., 2013). Stock solutions of all B<sub>6</sub> vitamers and deuterated internal standards were reconstituted using dH<sub>2</sub>O, stored at −80°C to prevent degradation, and kept on ice protected from light during laboratory handling. A Waters Acquity H-Class UPLC system was connected to a Waters Xevo TQ-S triple quadrupole mass spectrometer in multiple reaction monitoring and positive ionisation mode. A Waters Acquity UPLC HSS T3 column (1.8 μm, 2.1 x 50 mm) with a 1.8 μm Acquity UPLC HSS T3 guard column was used for reversed-phase chromatographic separation along with a mobile phase consisting of A: 3.7% acetic acid (Sigma Aldrich) in H<sub>2</sub>O with 0.02% heptfluorobutyric acid (HFBA, Sigma Aldrich) and B: 100% methanol (Fisher Scientific). A gradient elution over 6.5 min was used. Gradient and retention times of each compound are listed in Table S3. Mass spectrometer settings were as follows: capillary 2.50 kV, source temperature 150°C, desolation temperature 600°C, cone gas flow rate 150 L/hr, and desolation gas flow rate 1200 L/hr. The optimized cone voltages and collision energies for each compound are as detailed in Table S3.

Analyte concentrations were determined by taking the peak area ratio of each vitamer and comparing it to a deuterated internal standard (PMP, PNP, PLP compared to d<sub>3</sub>-PLP, PM to d<sub>3</sub>-PM, PN to d<sub>2</sub>-PN and PL to d<sub>3</sub>PL). All vitamers were well differentiated according to retention time, except for PLP and PNP which elute at a similar time however, these can be differentiated from each other by mass without cross-talk between ion pairs occurring. Calibration curves were constructed between 1.25 and 200 nM and shown to have linearity (r<sup>2</sup> > 0.99). All results were normalized to protein concentration determined by the Pierce BCA Assay Kit (Thermo Scientific) according to the manufacturer’s instructions. Statistical analysis was performed by one-way ANOVA using GraphPad Prism 6 software.

**100 Metabolite Method**

For bacterial samples, 3-day old bacterial lawns of BW25113 growing on NGM plates supplemented with 100 M 5-FU at 20°C were washed from plates using 1x PBS. The bacteria were washed three times in 1x PBS to remove bacteria, and snap frozen in liquid nitrogen. The worm pellet was kept at −80°C in the dark until sample analysis.

For bacterial sample collection and metabolite extraction, 3-day old bacterial lawns grown on standard NGM or supplemented with 1 mM pyridoxal at 20°C plates were washed from plates using 1x PBS. The bacteria were washed three times in 1x PBS to remove potential contaminating pyridoxal from the NGM medium and centrifuged at for 30 min at 4,000 rpm, 4°C. The bacterial pellet was snap frozen in liquid nitrogen and kept at −20°C until required. At least 4 biological replicates were collected for each condition.

The bacterial pellets were resuspended in 50 μL dH<sub>2</sub>O and lysed by subjecting the sample to 5 freeze-thaw cycles using a methanol-dry ice bath and a 37°C waterbath. The resulting lysates were pelleted for 5 min at 5,000 rpm, 4°C, and the supernatants collected. Proteins were precipitated by mixing 10 μL of bacterial lysate supernatant with 0.15 N (final concentration) trichloroacetic acid (TCA, Sigma Aldrich) and spiked with deuterated internal standards (PMP, PNP, PLP: d<sub>3</sub>-PLP, PM: d<sub>3</sub>-PM, PN: d<sub>2</sub>-PN and PL: d<sub>3</sub>PL; all at a final concentration of 25 nM, Table S1) up to a total volume of 120 μL. Samples were vortexed for 30 s, left on ice in the dark for 60 min and centrifuged to pellet the precipitated protein. The resulting supernatant was transferred to a glass vial and kept at −20°C in the dark until sample analysis.

For bacterial and supernatant analysis, samples were collected as explained in the Bioconversion Assay section and kept at −80°C until required. For worm sample collection and metabolite extraction, 3-day old bacterial lawns grown on solid media, bacteria were cultured and collected as explained in methods for 1-Carbon metabolism analysis. For bacteria grown on solid media, bacteria were cultured and collected as explained in methods for 1-Carbon metabolism analysis. The bacterial pellets were resuspended in 50 μL dH<sub>2</sub>O, spun down at 15,000 rpm at 4°C and flash frozen in liquid nitrogen. The bacterial pellet was kept at −80°C until required. For worm samples, approximately 4000 synchronized L1 stage larvae were grown at 20°C and kept on ice protected from light during laboratory handling. A Waters Acquity H-Class UPLC system was connected to a Waters Xevo TQ-S triple quadrupole mass spectrometer in multiple reaction monitoring and positive ionisation mode. A Waters Acquity UPLC HSS T3 column (1.8 μm, 2.1 x 50 mm) with a 1.8 μm Acquity UPLC HSS T3 guard column was used for reversed-phase chromatographic separation along with a mobile phase consisting of A: 3.7% acetic acid (Sigma Aldrich) in H<sub>2</sub>O with 0.02% heptfluorobutyric acid (HFBA, Sigma Aldrich) and B: 100% methanol (Fisher Scientific). A gradient elution over 6.5 min was used. Gradient and retention times of each compound are listed in Table S3. Mass spectrometer settings were as follows: capillary 2.50 kV, source temperature 150°C, desolation temperature 600°C, cone gas flow rate 150 L/hr, and desolation gas flow rate 1200 L/hr. The optimized cone voltages and collision energies for each compound are as detailed in Table S3.

**Analyte concentrations were determined by taking the peak area ratio of each vitamer and comparing it to a deuterated internal standard (PMP, PNP, PLP compared to d<sub>3</sub>-PLP, PM to d<sub>3</sub>-PM, PN to d<sub>2</sub>-PN and PL to d<sub>3</sub>PL). All vitamers were well differentiated according to retention time, except for PLP and PNP which elute at a similar time however, these can be differentiated from each other by mass without cross-talk between ion pairs occurring. Calibration curves were constructed between 1.25 and 200 nM and shown to have linearity (r<sup>2</sup> > 0.99). All results were normalized to protein concentration determined by the Pierce BCA Assay Kit (Thermo Scientific) according to the manufacturer’s instructions. Statistical analysis was performed by one-way ANOVA using GraphPad Prism 6 software.**

**Nucleotide and Fluoronucleotide Analysis**

For bacteria grown on solid media, bacteria were cultured and collected as explained in methods for 1-Carbon metabolism analysis. For bacteria and supernatant analysis, samples were collected as explained in the Bioconversion Assay section and kept at −80°C until further analysis.
For worm samples, approximately 5000 synchronized L1 stage larvae were grown at 20 °C on standard NGM plates seeded with 3-day old BW25113 or mutant bacteria. L4 larvae were collected for analysis or transferred to fresh NGM plates containing 5-FU and incubated at 25 °C for an additional 8 hr before collection. Worms were washed thoroughly using dH2O, frozen in liquid nitrogen and kept at −80 °C until further analysis.

3-4 biological replicates from each type of bacteria/worm/supernatant sample were collected for each condition. Each sample was spiked with an optimal concentration of the internal standards (200 μM of Cytidine-13C9,15N3, 5′-triphosphate and Uridine-13C9,15N2, 5′-triphosphate, 10 μM of caffeine, 250 μM of 5-Fluorouridine, Table S1). Bacteria and worm samples were resuspended in 100 μL 100% methanol and sonicated using 30 s intervals at 4 °C for a total of 2 min (bacterial samples) or 6 min (worm samples), at 100% amplitude using a high intensity ultrasonic water bath sonicator coupled to a cup horn (Q700 Qsonica). Subsequently, protein was removed by centrifuging lysed samples for 30 min at 13,000 rpm, 4 °C and collecting the resulting supernatant to fresh tubes. Samples were lyophilized and the resulting pellet was resuspended in 50 μL of ice-cold dH2O prior to sample injection and analysis. Supernatants were filtered through an Amicon Ultra (0.5 mL) centrifugal filter Ultracel 3K (Merck Millipore) for 20 min at 13,000 rpm, 4 °C. The resulting filtrate was collected and kept on ice prior to sample injection and analysis.

Nucleotide and fluoronucleotide analysis by LC-MS/MS was performed essentially as described in (Laourdakis et al., 2014) using the ion transitions, cone voltages, and collision energies described in Table S6. Analyte concentrations were determined by correlation of the MS signal of a given metabolite with the appropriate internal standard signal. The results obtained were normalized against protein concentration determined using a Qubit® Fluorometer, according to the manufacturer’s instructions. For each metabolite differences between strains were determined using linear modeling. Log2 transformed metabolite concentrations in Δndk, ΔyjG and ΔpyrE mutants were compared against the BW control. Significance of differences was evaluated within the linear models using pooled standard errors.

Bacterial Fluorescence Quantification

NGM plates ± pyridoxal (1 mM) were prepared and seeded with 150 μL overnight LB culture of BW25113 strain containing either a promoterless plasmid or the GFP promoter plasmid for ndk, udk, and upp genes (Key Resources Table). The plates were incubated for 3 days at 20 °C, then the bacteria were scraped off the plates and washed with 2 mL of 1x PBS into 2 mL eppendorf tubes. The resulting bacterial cultures were thoroughly mixed by vortexing and diluted 4-fold. 75 μL of each sample was added to a 96-well plate containing 75 μL 1x PBS. Bacterial OD was measured at 600 nm and GFP intensity was measured at excitation 470 nm, emission 525 nm using a Tecan Infinite Pro M200 plate reader with Magellan v7.2 software. 4 biological replicates were used for each measurement. Differences between strains were calculated between values determined as: [(GFP gene of interest/OD600nm)/GFP promoterless/OD600nm]. Statistical analysis was performed by one-way ANOVA using GraphPad Prism 6 software.

Bacterial MIC Assays

Bacteria grown overnight in LB-Miller broth were washed twice in NGM broth, normalized to OD600nm = 2 and added to 96-well microtiter plates at a final dilution of 1,000-fold in 200 μL NGM broth containing 2-fold serially diluted drug. Plates were incubated for 16 hr at 37 °C, 180 rpm and the absorbance at OD600nm was measured using a Tecan Infinite Pro M200 microplate reader and Magellan v7.2 software. GraphPad Prism 6 was used to create drug response curves and calculate the concentration of drug required for 50% growth inhibition (IC50) using a log(inhibitor) versus response - variable slope (four parameter) model, and perform statistical analysis of IC50 values by one-way ANOVA.

Bioconversion Assays

BW25113 or Keio mutant bacteria were cultured in LB-Miller broth overnight at 37° C. Cultures were spun down at 4000 rpm for 30 min, washed twice with PBS, then resuspended in 1 mL of PBS and the OD600nm determined using a standard spectrophotometer. Each sample was normalized to 12 OD units and centrifuged at 10,000 rpm for 10 min. Bacterial pellets were re-suspended in 1 mL of 5 mM 5-FO or 5-FC in 1X PBS and incubated overnight at 37° C, 650 rpm in the dark. Bacteria were spun down at 10,000 rpm for 5 min, and the resulting supernatants were filter sterilized (0.22 μm) and used for downstream experiments including hatching assays or mass spectrometry.

Host-Microbe-Drug Screen

Keio collection bacteria were grown for two generations in LB-Miller broth in 96-well, flat-bottomed microtiter plates at 37°C overnight. At this point, L1 nematodes were added per well, and incubated at 20°C for 72 hr. For the primary screen, L1 nematodes on each one of the 3813 knockouts were exposed to 5-FU concentrations (0, 1, 2.5, 5 μM). Mutants with inconsistent results were
rescreened. Bacterial clones on which nematodes developed at 5 μM 5-FU (574, 15% of total screened) were further tested in a secondary screen at a wider range of drug concentrations (0, 5, 10, 15, 20, 30, 40, 50, 75, 100 μM) with 3 biological replicates (Figure S2C, right panel). For each mutant, final MIC value was established as the minimum 5-FU concentration that hinders worm growth.

**Microbe-Drug Screen**

Bacterial clones from the worm secondary screen were screened in 5-FU bacterial growth-inhibition assays in 96-well microtiter plates. Mutants were grown in LB for one generation followed by growth in NGM broth for a second generation, before being inoculated in fresh NGM broth for the assay. Plates were incubated at 37°C, 180 rpm, and bacterial growth was measured at 24 hr by OD_{600nm} using a Tecan Infinite Pro M200 plate reader and Magellan v7.2 software. Bacterial OD values were corrected for media only blanks and averaged from 3 independent biological repeats ± SD.

**QUANTIFICATION AND STATISTICAL ANALYSIS**

**General**

Data were considered statistically significant when \( p < 0.05 \) by unpaired t tests, multiple t tests, one-way ANOVA or Benjamini-Hochberg FDR < 0.05 as indicated in the Figure, Figure labels or experimental methods. Asterisks denote corresponding statistical significance: *\( p < 0.05 \); **\( p < 0.01 \); ***\( p < 0.001 \). Data are presented as the mean ± SD from at least 3 independent biological replicates, unless stated otherwise in Figures, Figure labels or experimental methods. Statistical analysis was performed using GraphPad Prism 6 software, log-rank test in JMP 11 software (SAS Institute) or linear modeling in R, as indicated.

**High-Throughput Screens**

Data analysis was performed using the R statistical analysis software package v3.2.3 (https://www.r-project.org), unless stated otherwise. Linear modeling/regression was accomplished using R base function "lm," and function "glm" from "multvar" package. Outliers in linear regression analysis were identified using Bonferonni-adjusted outlier test from "car" package. Plots were generated using "ggplot" and "gplots" packages.

Information on *E. coli* knockouts from the Keio library and their annotations was acquired from (Baba et al., 2006). Additional gene annotations for *E. coli* K-12 were collected using R packages from Bioconductor v3.2: "org.EcK12.eg.db," "KEGGREST" and "GO.db." Information on genes with unknown function, enzymes using pyridoxal-5-phosphate (PLP) and metabolic pathways was acquired using PathwayTools and "pythoncyc" Python API software from EcoCyc. All software and databases were used at their most recent versions, as of 2016-08.

The relationship between *E. coli* growth ± 5-FU treatment (OD values) and *C. elegans* (MIC averages) was established using linear regression (Figures S2F and S2G). Outliers \( \Delta \text{atpH}, \Delta \text{purA}, \Delta \text{priA}, \Delta \text{yfgA}, \Delta \text{hyfF} \) and \( \Delta \text{aceE} \), with respective Bonferonni-adjusted significance: \( p = 1.8 \times 10^{-5}, p = 2.1 \times 10^{-4}, p = 2.1 \times 10^{-3}, p = 6.8 \times 10^{-3}, p = 0.01, p = 0.02 \) were excluded from the correlation estimation in both datasets. The bacterial growth in control and 5-FU treatment was correlated (Figure S2D). Analysis of knockout and 5-FU interaction in bacteria was performed using linear modeling on log2 transformed growth OD values (Figure S2E). Here, BW25113 (WT) growth without 5-FU was used as reference contrast in corresponding knockout and drug treatment factors. The interaction term shows the difference of combined KO and 5-FU effect from the sum of separate effects. Bacterial strains containing gene deletions that counteract 5-FU effect are considered resistant (antagonistic interaction), whereas strains with gene deletions that strengthen drug effect are considered sensitive (synergistic interaction). The interaction between 5-FU and knockout effect was found to be significantly correlated with the knockout effect itself \( (y = -0.06-0.35x, r^2 = 0.12, p = 2 \times 10^{-16}, \text{data not shown}) \). This indicates that in general the strains with more impaired growth are more resistant to 5-FU treatment. For example, 5-FU treatment causes 36% growth reduction in WT (OD\text{Control} = 0.28, OD\text{Treatment} = 0.18) and only 5% in \( \Delta \text{IdcA} \), which grows to ~31% of WT growth in control (OD\text{Control} = 0.08, OD\text{Treatment} = 0.07) and has no significant interaction with 5-FU treatment (\( p = 0.82, \text{FDR} = 0.88 \) (Table S2)). The interaction estimates in the linear model were adjusted against this trend to avoid confounding of these effects. The significance of effects in the linear model was estimated using pooled standard errors and Benjamini-Hochberg FDR correction for multiple testing (Table S2).

KEGG and EcoCyc pathway enrichment was estimated in terms of knockout effects on *C. elegans*. Knockouts with MIC values > 5 μM were considered hits and only pathways containing 5 or more corresponding genes were included in the analysis. The pyrimidine pathway was added for illustrative purposes. The significance of the pathway enrichment was calculated using the hypergeometric test, where the \( p \) value indicates the likelihood to encounter no less than the observed number of hits in the pathway (right-tail probability), given that the total number of hits is 574 out of 3813 screened knockouts. Coverage was defined as the ratio of hits over the total number of screened knockouts in a specific pathway.

Enrichment of KEGG pathways for compounds from the 100 metabolites study was evaluated using metabolite concentrations and the “Pathway analysis” tool on MetaboAnalyst 3.0.
Figure S1. Effects of Fluoropyrimidines on Bacterial Growth and C. elegans Egg Hatching, Related to Figure 1

(A) C. elegans fed heat or UV-killed OP50 show increased resistance to 5-FU. MIC Control = 2 μM; MIC UV = 16 μM; MIC Heat = 32 μM.

(B–E) Fluoropyrimidines show varying efficacy on worms fed E. coli K-12/B hybrid HB101, K-12 BW25113, E. coli B OP50 and Comamonas aquatica DA1877. Response to 5-FO (B), FUdR (C), capecitabine (D) and 5-FC (E).

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(F and G) Effects of 5-FU on (F) laboratory and (G) wild-type bacterial growth in NGM broth. No significant changes in IC₅₀ values were observed within bacterial strain serotype despite 8-fold changes in worm MICs (e.g., BW25113 versus HT115, Figures 1A, 2B, and 2F). Drug response curves were calculated using a log(inhibitor) versus response - variable slope (four parameter) model. *C. aquatica* grew poorly in NGM and was readily killed by 5-FU while *E. cloacae* grew the best on NGM with or without 5-FU (G), but both conferred low worm MICs (Figure 1B).

(H and I) Effects of fluoropyrimidines on (H) BW25113 and (I) OP50 bacterial growth in NGM broth. Note that *E. coli* is remarkably resistant to growth inhibition by 5-FC but capable of modulating the pharmacodynamics of 5-FC in the worm hatching assays (E).

(J) Rates of consumption of diverse bacterial strains by *C. elegans* over a period of 8 hr. Differences in bacterial consumption do not correlate with 5-FU efficacy.

(K) Expression of worm genes involved in fluoropyrimidine metabolism does not correlate with bacterial-induced changes in drug efficacy. For example, increases in uridine monophosphate kinase (*C29F7.3*) and uridine phosphorylase (*upp-1*) expression for HB101-fed nematodes does not correlate with the reduced drug efficacy observed for this strain (Figures S1B–S1E) compared to OP50, BW25113 and *C. aquatica*.

(L) Metabolite profiling in worms and *E. coli*, treated with 5-FU. BLOD = below level of detection. Only statistically significant changes in metabolite levels are displayed.

(M) KEGG pathway enrichment analysis for metabolomics in *E. coli* and *C. elegans*. Metabolite concentration comparisons were made against control conditions in appropriate species. Grey indicates that enrichment is non-significant (p > 0.05), white – enrichment could not be estimated. Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. For statistics see Table S1.
Figure S2. Chemical Genomic Bacterial Screens and Chemical Genomic Bacterial Host Screens, Related to Figure 2

(A) 5-FU inhibits development of worms fed control E. coli BW25113 but not Δupp mutants. This effect was reversed by gene complementation (pUpp). Worm size was obtained from fluorescence intensity measurements of the DA2123 worm strain.

(B) Representative GFP fluorescence images of DA2123 worms from (A) illustrating the effects of 5-FU on worm size.

(C) Cumulative distribution of C. elegans MIC values and variability (from 3 independent biological replicates) for 5-FU effects for each knockout with MIC > 5 μM.

(D) Bacterial growth (OD 600nm) of Keio knockouts in liquid NGM. Correlation between control and 50 μM 5-FU treatment. Linear fit (red) indicates general growth reduction by drug treatment (slope 0.44 < 1; p < 2.3 x 10^-5).

(E) Linear modeling applied for bacterial growth to determine antagonistic and synergistic hits in bacterial screen. Examples for WT, Δupp, ΔpaaF and ΔgcvA. Black arrows mark knockout effects in comparison to WT, purple arrows mark 5-FU treatment effect, gray bars indicate expected combined effect of knockout and 5-FU treatment. Significant interaction between knockout and 5-FU treatment is shown by green (antagonistic) and blue (synergistic) arrows.

(F and G) Correlation between C. elegans MIC values and E. coli growth OD600nm in NGM (F) or NGM + 50 μM 5-FU (G). Linear regression fit and covariation ellipse are marked in red. Knockouts that exhibit significant interaction with 5-FU (FDR < 0.05) are color-coded green (resistant) and blue (sensitive). Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. For statistics, see Table S2.
Figure S3. Effects of Bacterial Vitamin B₆ Metabolism on 5-FU Efficacy, Related to Figure 3

(A) Vitamin B₆ pools are altered in ΔpdxH mutant E. coli measured by LC-MS/MS. PLP = Pyridoxal-5-Phosphate; PNP = Pyridoxine-5-Phosphate; PMP = Pyridoxamine-5-Phosphate; PL = Pyridoxal; PN = Pyridoxine; PM = Pyridoxamine; PA = Pyridoxic acid.

(B) Media supplementation with 10 μM PL rescues 5-FU efficacy on worms fed ΔpdxJ bacteria to control levels (BW + PL = 0.25 μM versus BW = 0.25 μM, p = 0.779; ΔpdxJ + PL = 0.25 μM versus ΔpdxJ = 2 μM, p < 0.001; ΔpdxJ + PL = 0.25 μM versus BW = 0.25 μM, p = 1; ΔpdxJ + PL = 0.1 μM versus BW + PL = 0.1 μM, p = 1).

(C) Inhibition of both B₆ de novo and salvage pathways using a ΔpdxJ/ΔpdxK double mutant decreases 5-FU efficacy which cannot be rescued by supplementation with 1 mM PN, PM or PL.

(D) Efficient RNAi knockdown of the worm F57C9.1 gene, an ortholog of human PDXK.

(E) Knockdown of F57C9.1 by RNAi does not alter worm responses to 5-FU upon supplementation with PL.

(F) Gene expression levels by qRT-PCR of enzymes involved in the glycine cleavage system, folate and vitamin B₆ metabolism in worms grown on ΔpdxJ bacteria. Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. For statistics, see Table S3.
**Figure S4. Bacterial Folate Metabolism Regulates 5-FU Action, Related to Figure 4**

(A) Diagram of the chorismate and PABA biosynthetic pathways.

(B) Disruption of chorismate and PABA biosynthesis impairs 5-FU action in worms.

(C) Polyglutamylation profiles of detectable folate metabolites in control, ΔgcvP and Δfau mutants. No striking changes are observed for the majority of folates.

(D) 5-FU treatment (50 μM) impairs OP50 growth, but not in the presence of metformin (50 or 100 mM).

(E) 5-FU treatment (50 μM) impairs OP50 metformin-resistant strain (OP50-MR) growth regardless of metformin effects (50 or 100 mM).

(F) Metformin effects on bacterial growth are antagonistic to 5-FU effects in OP50 but not OP50-MR.

(G) Impairment of the folate cycle (Δfau) and the glycine cleavage system (ΔgcvP) in E. coli does not modulate folate metabolism in C. elegans. Each metabolite is the ratio between the sum of the values for the different glutamate side chains (1-7) and the sum of all metabolites measured.

Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. For statistics, see Table S4.
Figure S5. Bacterial Bioconversion of Fluoropyrimidines, Related to Figure 5

(A) Disruption of nucleobases (ΔuraA) and nucleosides import (ΔnupCΔnupG) reduces 5-FU efficacy.

(B) Supplementation with 200 μM uridine impairs 5-FU effects in worms fed BW25113 by 320-fold but not the triple mutant ΔudpΔudkΔupp.

(C) Supplementation with 200 μM orotate impairs 5-FU effects in worms fed BW25113. The effect is partially rescued when worms are fed ΔpyrE but not ΔpyrD mutant bacteria.

(D) Supplementation with 200 μM thymidine improves 5-FU effects in worms fed Δtdk mutant bacteria but not control BW25113 or Δupp mutants.

(E) Pre-conversion of 5-FO by WT bacteria enhances drug effects on the host. Note that incubation of 5-FO with ΔpyrE mutant bacteria fully abolishes bacterial-mediated effects on host metabolism. Thus, de novo nucleotide metabolism is the unique pathway for the conversion of 5-FO.

(F) Vitamin B6 supplementation increases GFP expression in ndk, udk, and upp promoter reporter strains.

(G) Disruption of bacterial vitamin B6 production impairs 5-FC bioconversion.

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(H) LC-MS/MS quantification of fluoropyrimidines in *E. coli* supplemented with 50 μM 5-FU.
(I) LC-MS/MS quantification of fluoropyrimidines in *C. elegans* supplemented with 50 μM 5-FU.
(J) LC-MS/MS quantification of fluoropyrimidines in *E. coli* supplemented with 50 μM 5-FU.
(K) LC-MS/MS quantification of fluoropyrimidines in *C. elegans* supplemented with 50 μM 5-FU.
(L) Developmental response to 5-FU is uniquely mediated by bacterial genotype (BW control or triple mutant ΔudpΔudkΔupp) but not host genotype (N2 Wild-type or umps-1(zu456)).

Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. For statistics, see Table S5.
Figure S6. Bacterial Deoxynucleotide Metabolism Effects on 5-FU Efficacy, Related to Figure 6

(A) Effects of 5-FU on bacterial growth of sensitive ΔyjG, resistant Δupp and neutral Δndk or Δdcd. Drug response curves were calculated using a log(inhibitor) versus response - variable slope (four parameter) model.

(B) Supplementation with 200 μM and 2 mM uridine impairs 5-FU effects in worms fed ΔyjG and Δndk mutants in a distinctive manner.

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(C) Heatmap of metabolite profiles for bacterial nucleotide metabolism mutants. Absolute metabolite levels shown by color scale, clustering done by Euclidean distance.

(D) Difference in metabolite levels between Δndk (y axis) and ΔpyrE (x axis) mutants in comparison to BW. Color gradient shows Δndk/ΔpyrE logFC, indicating opposing/concordant effects of mutants on metabolite levels. Metabolites with significant changes in Δndk/BW and Δndk/ΔpyrE are labeled (See Table S6).

(E) 5-FU does not alter folate metabolism homeostasis in whole worms at 5 and 20 μM.

(F) LGG-1::GFP expression in embryos from DA2123 worms fed BW25113, UV-irradiated BW25113 and triple mutant ΔudpΔudkΔupp treated with 5-FU at various concentrations and supplemented with 200 μM uridine or thymidine. Uridine supplementation rescues 5-FU induction of autophagy while thymidine supplementation improves it in a bacterial dependent manner.

(G) Increased resistance to 5-FU in the mismatch repair worm mutant msh-6(pk2504) is mediated by bacteria. Resistance to 5-FU by msh-6 mutant worms is only observed when fed on HT115 but not HT115(Δndk) mutant bacteria.

(H) msh-6(pk2504) does not confer resistance to 5-FU compared to WT worms when fed BW25113 or Δndk bacteria.

(I) Efficient knockdown of ndk-1 in worms by RNAi.

Data are represented as mean ± SD. *p < 0.05; **p < 0.01; ***p < 0.001. For statistics, see Table S6.
Figure S7. 5-FU Effects on Tumor Size and Survival of the Host Are Dependent on Bacterial Genotype, Related to Figure 7

(A) Supplementation with uridine and orotate (200 µM or 2 mM) impairs 5-FU effects in worms fed diverse bacterial strains.

(B) Role of bacterial yjjG, udk, upp, and ndk in E. coli K-12 strains in the regulation of 5-FU effects on the host.

(C) Role of bacterial yjjG, udk, upp, and ndk in E. coli B strains in the regulation of 5-FU effects on the host. OP50p refers to OP50 prototroph for uracil/uridine.

(D) Representative 10x images of DAPI stained gld-1 RNAi whole worms treated for 4 days with 5-FU and fed control or Δupp mutant bacteria. Tumor retraction as measured by distance (A' to B')/(A to B).

(E) 5-FU extends the lifespan of gld-1 worms when fed on BW25113 bacteria but not HB101 or HT115.

(F and G) 5-FU extends the lifespan of gld-1 (F) and glp-1 (G) gain-of-function worms when fed on control bacteria, but not Δupp mutants. Data are represented as mean ± SD. For statistics, see Table S7.