

# Effects of FUdR on gene expression in the *C. elegans* bacterial diet OP50

**Grace McIntyre**

Marian University

**Justin Wright**

Juniata College

**Hoi Tong Wong**

Juniata College

**Regina Lamendella**

Juniata College

**Jason P Chan** (✉ [jchan@marian.edu](mailto:jchan@marian.edu))

Marian University <https://orcid.org/0000-0001-8123-536X>

---

## Research note

**Keywords:** *C. elegans*, *E. coli*, FUdR, aging, bacterial transcriptomics

**Posted Date:** March 18th, 2021

**DOI:** <https://doi.org/10.21203/rs.3.rs-322316/v1>

**License:**   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

---

## Abstract

Objective: Many *C. elegans* aging studies use the compound, 5-fluoro-2'-deoxyuridine (FUdR), to produce a synchronous population of worms in aging studies. However, it is not fully clear what effects FUdR have on the bacterial gene expression in the *E. coli* strain OP50, the primary laboratory *C. elegans* food source. This is particularly relevant as studies indicate that intestinal microbes can affect *C. elegans* physiology. Here, we examine how exposure to FUdR can affect gene expression changes in OP50 *E. coli*.

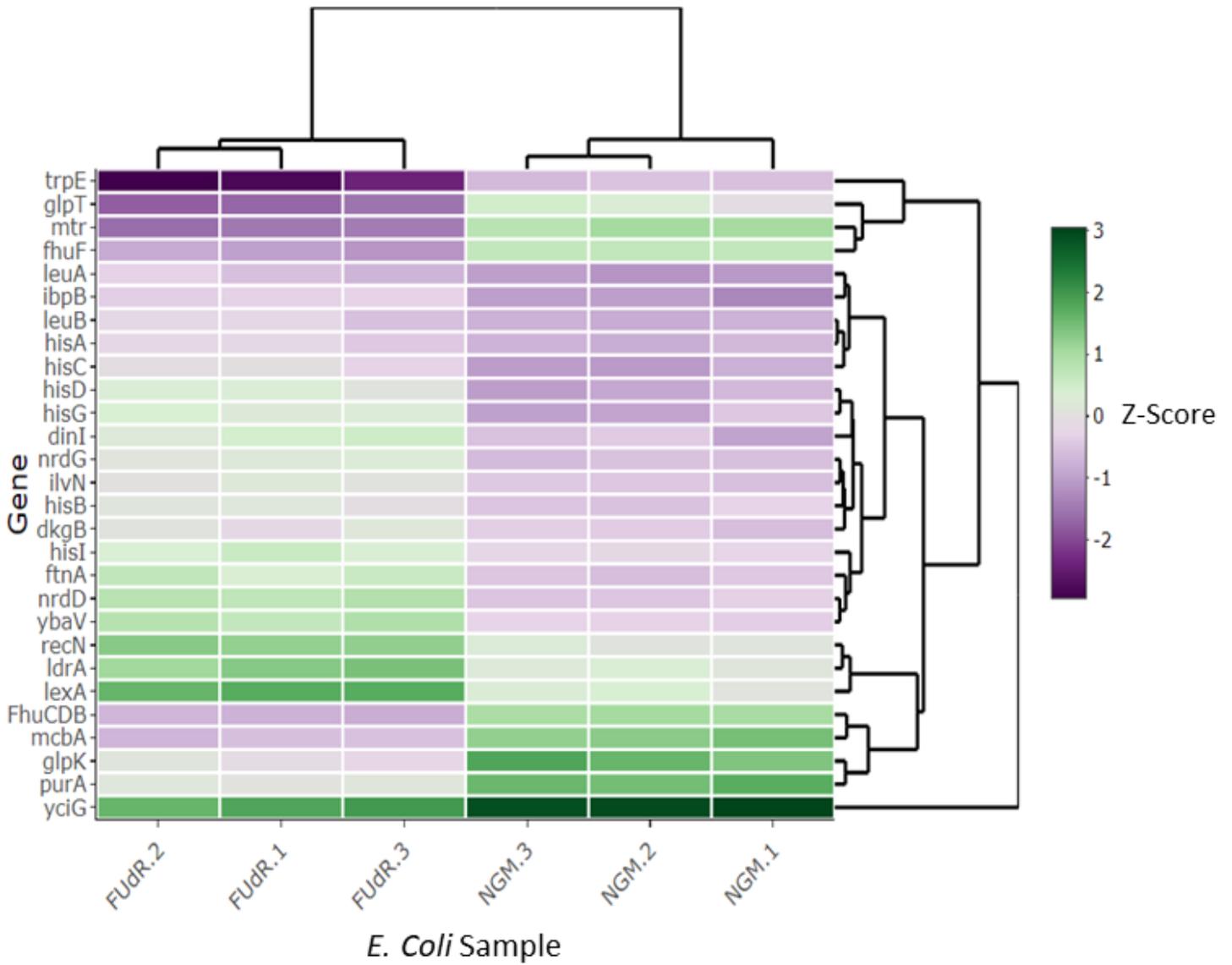
Results: RNAseq datasets were used to compare the expression patterns of *E. coli* genes in the strain OP50 seeded on either nematode growth media (NGM) plates or on FUdR (50 $\mu$ M) supplemented NGM plates. Analysis showed differential expression of genes involved in general transport, amino acid biosynthesis, transcription, iron transport, and antibiotic resistance. We specifically highlight metabolic enzymes in the L-histidine biosynthesis pathway may be regulated by FUdR exposed OP50. We conclude that OP50 exposed to FUdR results in many differentially expressed genes, including those in amino acid biosynthetic pathways.

## Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

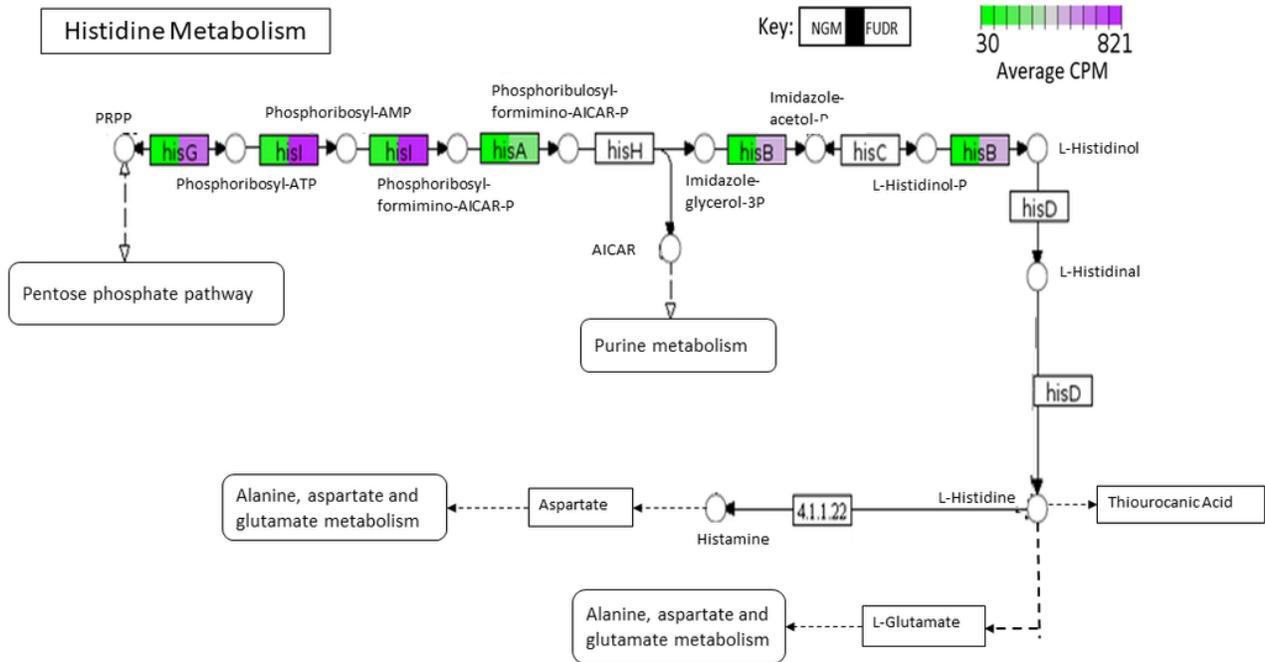
## Figures

# Differential *E. coli* Genes Expressed When Exposed to FUdR



**Figure 1**

Differentially expressed OP50 *E. coli* genes in response to FUdR. Heatmap demonstrating the top 28 differentially expressed genes in *E. coli* (in triplicate) grown on either NGM only (NGM.1-3) or NGM plates supplemented with 50 $\mu$ M FUdR (FUdR.1-3).



**Figure 2**

Gene expression differences in the bacterial L-histidine biosynthetic pathway. Pathview plots show differences in the average expression counts of functional enzymes in the L-histidine metabolism pathway between *E. coli* grown on NGM or NGM+FUDR plates. The color in the rectangles indicates the average CPM expression of *E. coli* on NGM only (left) compared to *E. coli* exposed to FUDR (right). We observed that several enzymes in the L-histidine biosynthesis pathway are upregulated in OP50 *E. coli* when exposed FUDR.

## Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [McIntyreSupplementalTable.csv](#)