

The Influence of the Gut Microbiome on Physiological Function: A Focus on Microorganisms and Their Role in Human Metabolism



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Abstract

- The bacterial organisms within the gut microbiome have complex interactions between the bacterial species that reside within the organism and the overall health of the host. The bacterial organisms influence various physiological traits of the host by impacting genetic expression, signaling pathways, and metabolism. In this study, we measured changes in *C.elegans* metabolism when colonized with various microbiome strains and compared the effects they produce on *C.elegans* physiology. Colonization by various microbiome strains resulted in measurable changes in body size, and lipid quantification. Triglyceride concentration was used to study the physiological impact of the host, utilizing oil-red and triglyceride assay techniques. The results of this study suggest that it is possible the microbiome can influence metabolic changes within the host organism, as seen in physiological changes.

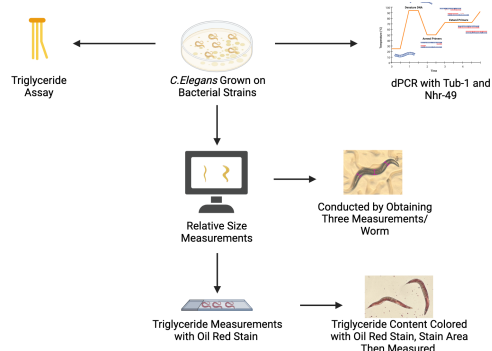
Introduction

- The obesity epidemic is on the rise around the world, causing a multitude of health problems.
- Triglyceride levels can act as a sensitive meter for metabolic health.
- Different Microbiomes may lead to changes in triglyceride levels, impacting metabolism. Metabolites produced by intestinal bacteria may impact the host's overall health.
- C. elegans* is an ideal model organism for studying human metabolism and disease.

Research Questions

- How does the microbiome influence nematode energy metabolism through triglyceride storage?
- How does the categorization of bacterial species that are within the microbiome reflect changes in triglyceride content and body size characteristics?

Research Methods



Research method to observe the influence of the gut microbiome on physiological function.

To distinguish the impact that the bacterial organisms have on the host, the body size was measured using Image J. In addition to this, the triglyceride content of the *C.elegans* was studied using oil red and a triglyceride assay. PCR was conducted to observe gene expression.

Does the microbiome impact body size?

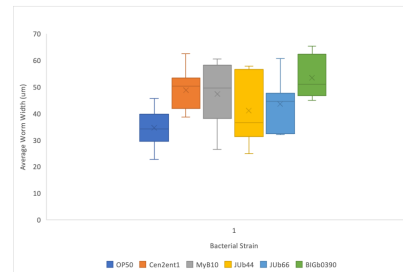


Figure 3. Body size measurements of *C.elegans* fed on different microbiome strains. Nematodes three days post-hatch on OP50 seeded NGM plates were transferred to microbiome strains via worm picking, followed by photographing 72 hours post-transfer and analyzing relative size using Image J software, revealing statistical significance ($P = .0167$) through one-way ANOVA in Excel for comparison between bacterial strains.

Does the microbiome impact triglyceride deposits?

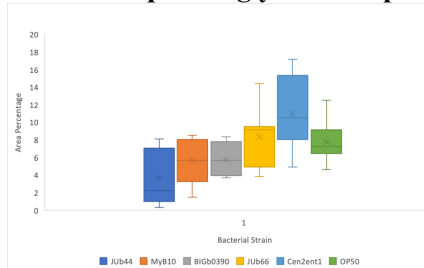


Figure 4. Triglyceride accumulation in *C. elegans* fed various microbiome strains. Nematodes fed different bacterial strains were stained with Oil Red to visualize triglyceride levels, using a stock solution of Oil Red O dissolved in 2-propanol. The stained worms were photographed and analyzed with Image J software to measure lipid droplet area percentage. Statistical analysis via one-way ANOVA in Excel revealed significant differences ($P = .000613$) among bacterial strains.

Does the microbiome impact triglyceride quantification?

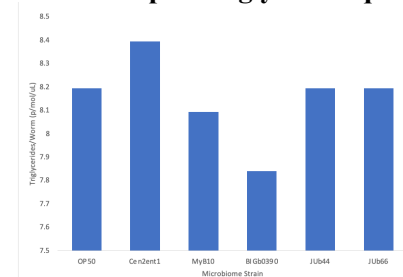


Figure 5. Quantified triglyceride accumulation in *C. elegans* when fed various microbiome strains. After 72 hours on their respective bacterial strains, 45 nematodes from each strain were individually placed in microcentrifuge tubes and underwent lysis to quantify stored triglycerides, with statistical analysis via one-way ANOVA in Excel showing no significant differences ($P = .436$) among bacterial strains.

Greater Connections

- Both *Cent2ent* and *BIG0393* exhibited the highest body size and triglyceride percentage (Figures 4, and 5), while *JUB44* showed the lowest (Figures 3 and 5).
 - JUB44 (Flavobacterium):** Connected to maintaining appropriate fat storage, found to slow down larval stage progression (Dirksen et al. 2020, Berg et al. 2016).
 - Enterobacteriaceae:** Lipopolysaccharides interact with immune cell receptors to trigger inflammation (Baldelli et al. 2021).
 - Cent2ent (Enterobacteriaceae)** has been connected to obesity by disturbing the gut barrier, suggesting that the decrease in protection from the intestinal tract induced an alteration in the nematode's metabolism.

Potential Connection of Gram-Negative Bacterial Structural Components and Inflammatory Pathways

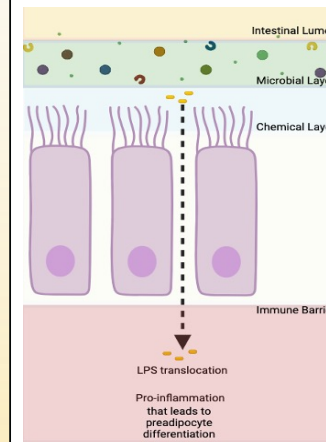


Figure 6. Gut microbiota metabolites modulate the intestinal barrier (Mohammad and Thiemermann 2021). The intestinal barrier consists of microbial, chemical, and immune components. Short-chain fatty acids (SCFAs), bile acids, and indole metabolites enhance barrier integrity by upregulating tight junction proteins. Disruption of this barrier can lead to translocation of lipopolysaccharides (LPS) and other molecules, activating immune cells and promoting pro-inflammatory cytokine production, ultimately fostering preadipocyte differentiation into adipocytes.

Future Work

- Aim to categorize additional bacterial families, distinguish them into beneficial or negative categories.
- Mirror the human microbiome closely, studying the strains in combinations that reflect the human intestinal tract.

References

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