Caenorhabditis elegans (C. elegans) Laboratory

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In order to understand the mechanism of gut microbiota-induced microbial translocation and inflammation, and the role of FMT to reverse the microbial translocation, it is imperative to develop an appropriate animal model. *C. elegans* is an important animal model system that has been the platform for many discoveries in biology, including key findings in the fields of neurobiology, development and small RNAs (Fire et al., 1998;). *C. elegans* lives in temperate soil environments. It is commonly found in rotting fruits and stems and appears to feed on a variety of different microbes, which can be nutritious or pathogenic. *C. elegans* has a simple transparent body plan, which has facilitated many studies in the worm.

C. elegans feeds on microbes and its intestine is comprised of 20 epithelial cells that are mostly in pairs of cells that form a tube that runs the length of the animal (McGhee, 2007). *C. elegans* intestinal cells share many morphological similarities with human intestinal epithelial cells, including actin-rich microvilli on the apical side of cells that absorb nutrients from the lumen.



C. elegans will serve as a model for studying the interaction between faecal Gut microbiota and host epithelial cells. We hypothesize that Gut microbiota derived from Inflammatory Bowel Diseases (IBD) patients will cause increased microbial translocation in *C. elegans* compared to those from healthy subjects.

The gut epithelial cells of *C. elegans* show significant similarity with that of human. Therefore, this may serve as a model for GI study in humans. *C. elegans* has previously been used to examine host microbiome interaction in the intestine at the apical surface of the epithelial cells. This unique feature could be exploited to study the interaction of Gut microbiota and host epithelial cells

To develop *C. elegans* as a model to study the interaction between gut microbiota and host epithelial cells. *C. elegans* is cultured on Nematode Growth Medium. To assess the effect of gut microbiota on gut epithelial cells