tory colitis is associated with visceral and somatic hyperalgesia, similar to that seen in IBD.

Results: The effects of BDNF mRNA and TRPV1 responses to 100 nM capsaicin were significantly increased in naïve colonic DRGs incubated with colonic supernatants obtained from ABX-treated and post-inflammatory DSS mice. Nociceptive sensitization was determined by evaluating capsaicin-induced TRPV1 responses in DRGs using calcium imaging.

Conclusion: We have demonstrated a novel link of microbiome, SOD1 aggregation, and intestinal mobility. Dysbiosis and SOD1 mutated aggregation occurred at the early stage (1 month old) of the G93A mice before observed dysfunction of enteric nervous system. Manipulating the microbiome of G93A mice with antibiotic treatment showed no significant body weight changes at 101 day-old, and a significantly longer latency to fall in the rotarod test. Butyrate treatment led to enhanced CNS function and reduced SOD1/G93A aggregation in intestine. G93A mice with antibiotic treatment showed a significantly longer latency to fall in the rotarod test. G93A mice with antibiotic treatment showed a significantly longer latency to fall in the rotarod test. G93A mice with antibiotic treatment showed a significantly longer latency to fall in the rotarod test. G93A mice with antibiotic treatment showed a significantly longer latency to fall in the rotarod test.

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**ANALYSIS OF THE SMALL INTESTINAL MICROBIOME REVEALS MARKED DIFFERENCES FROM STOOL MICROBIOME IN A LARGE SCALE HUMAN COHORT: REDEFINING THE "GUT MICROBIOME"**

Gabrela Leite, Stacy Weissman, Shreyaa Celty, Walter Morales, Kishan Sedighi, Ruchi Mahur, Gonzalo Pavón, Maria Jesus Villamaría-Millán, Ali Rezaie, Martiza Sanchez, Anasheh Enjely, Kathleen Shari Chua, Tahli Singer-Englar, Christine Chang, Mark Pimentel

The Human Microbiome Project characterized the microbial communities of healthy individuals across several sites of the human body, including the GI tract. While there are many different microenvironments within the GI tract, the “Gut microbiome” was defined solely by stool samples. No specimens from small intestine were obtained or analyzed. While sampling is difficult, the impressive potential role the small intestine and its resident microbes play in absorption, metabolism, and immunity cannot be overlooked. The lack of information on the small intestinal microbiome hinders our full understanding of microbial patterns in the GI tract. For the first time, this study aims to compare and contrast the duodenal microbiome to stool, in a large-scale human cohort.**Methods:** 153 subjects undergoing endoscopy as part of the REMAGINE study were recruited. Duodenal aspirates were collected using sterile technique. Stool samples were self-collected in a subset, using the OmniGene-GUT for Microbiome kit. DNA was isolated using the MagAtract PowerSoil DNA Kit. Microbiota was analyzed by 16S rRNA metagenomic sequencing. Operational Taxonomic Units clustering and taxonomic analysis were performed with CLC Microbial Genomics Module v. 2.5. Statistical analysis was done on GraphPad Prism 7.04. **Results:** 153 subjects had their duodenal microbiome fully sequenced, and 29 also provided stool. Among the 29 paired samples microbiome analysis revealed marked differences between the duodenum and fecal microbiome (Fig1, Fig2.A). The Bacteroidetes phylum was markedly lower in fold change (FC) when compared to stool (FC=-58.42, p=7.98E-13). The Verrucomicrobiota phylum was undetectable in the duodenum (p=0.0001) (Fig1B). The Bacteroidetes diversity profile demonstrated (Fig2C) higher levels of Prevotellia species (p=0.001) and Porphyromonas species (p=5.90E-14) in the duodenum. Conversely, Bacteroides species, the most abundant COG degraders in stool, were markedly decreased in the duodenum (and completely absent in 16 subjects) (FC=-334.3, p=0.0001) (Fig1B). Aspirates also showed increases in the phyla Firmicutes (FC=1.8, p=0.0009), Actinobacteria (FC=8.47, p=2.35E-7) and Proteobacteria (FC=3.54, p=7.98E-7) (Fig1B) compared with stool. In addition, these three phyla showed very different diversity profiles when present in the small intestine compared to feces (Fig2B, 2D and 2F respectively). **Conclusion:** In this first paired comparison of stool and duodenal microbiome analysis, there is a radically distinct microbiome in the small intestine. Based on these findings, the concept of a “gut microbiome” defined solely by fecal analysis must be questioned. Characterization of the small bowel microbiome is imperative if we are to truly understand the relationship between the human microbiome and disease.

**Sa1910**

**LIFE COURSE ANTIBIOTIC USE AND ALTERATIONS IN THE GUT MICROBIOME IN A COHORT OF OLDER MEN**


**Introduction:** Accumulating evidence suggests that exposure to antibiotics may be associated with an increased risk of illnesses including inflammatory bowel disease, celiac disease, obesity, and colorectal neoplasia. Such links may be mediated by perturbations of the gut microbiome. However, the influence of chronic antibiotic use throughout life course on the gut microbiome is not well characterized. **Methods:** We evaluated the association between life course antibiotic use among 269 healthy men (mean age of 71 years) within the Health Professionals Follow-up Study who provided up to four stool samples over a six-month period in 2012. Participants also recalled their total time using antibiotics (excluding skin creams, mouthwash or isoniazid) for the time periods during age ≤20 and every 10 year period thereafter in 2012. To reflect long-term antibiotic exposure, we derived the cumulative average of antibiotic use (continuous) up to the current age. Associations between cumulative and age period-specific (≤20, 20-39, 40-59, 60+ years old) antibiotic use and overall taxonomic profile were assessed using PERMANOVA. To examine antibiotic use and differential abundance of the 139 bacterial species that surpassed prevalence and abundance filtering, we also conducted multivariable linear modeling in MaAsLin adjusting for age and antibiotics by fecal analysis must be questioned. Characterization of the small bowel microbiome is imperative if we are to truly understand the relationship between the human microbiome and disease.

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