Characterization of the Duodenal Microbiome in Children with and without Crohn’s Disease

Kenneth Schmidt, MD
Primary Mentor: Valentina Shakhnovich, MD
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Disclosures

- No disclosures or conflicts of interest
- First time presentation
Background

- Inflammatory bowel disease (IBD) is a chronic condition of the GI tract that is multifactorial in etiology
- Known contributing factors to IBD development include dysregulation of the host immune system and dysbiosis of the GI microbiome
The exact interplay between the microbiome and host immune system in IBD pathogenesis remains poorly understood.

Which specific members of the GI microbiome contribute to IBD pathogenesis also remains unknown.

Differing composition of the microbiome throughout the GI tract adds to this knowledge gap.
Aim(s)

- Describe the bacterial species of the duodenal microbiome in children
- Compare the duodenal microbiome composition between healthy children and those with IBD (Crohn’s disease)
Hypothesis

Crohn’s disease alters the duodenal microbiome, resulting in a different composition of bacterial species compared to healthy controls.
Methods

- Retrospective case/control study of treatment naïve patients undergoing endoscopy from 2014-2019
- Eligibility criteria included any consenting child undergoing EGD/colonoscopy for suspected IBD, or those with IBD who had not received treatment with immunomodulators
Methods (cont.d)

- Fresh-frozen duodenal and TI mucosal biopsies collected at endoscopy were sent for rRNA sequencing via Illumina 250 base-pair sequencing platform (Novogene)

- Relative bacterial abundance, alpha and beta composition, and diversity were compared using Unifraq dissimilarity coefficients and LEfSe analysis
Results

- 73 total children ages 2-18, 35 diagnosed with Crohn’s disease and 38 healthy controls
- 118 total fresh frozen biopsies, 49 from duodenum and 69 from terminal ileum
Results (cont.d)

- Significant difference in bacterial abundance between duodenal and TI microbiome based on linear discriminant analysis (p<0.03)
- Significant difference remained despite disease status (control vs CD-active vs CD-inactive)
Results (cont.d)
In duodenum, significant increase in *Pseudomonodales* abundance in controls, while *Prevotellaceae* abundance increased in CD.
Results (cont.d)
Results (cont.d)
Conclusions

- This is the first study to characterize the duodenal microbiome in children
- Our results confirm the previously established model of inflammatory bowel disease significantly altering the GI microbiome
Future Directions

- Larger sample size in further studies could increase power in further statistical analysis
- Expanding study to include other pathology known to affect duodenum (such as Celiac disease)
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