The Inner-Colonic Bacterial Communities of the Human Gut Are Unique and Profoundly Different than those of Stool Samples

Orly Levitan, PhD\(^1\), Dawn B. Burleson, RN, MBA, CRA\(^1\), David A. Johnson, MD MACG\(^2\)

\(^1\)Hygieacare Inc., Norfolk, VA, USA, \(^2\)Eastern VA Medical School, Norfolk VA, USA

Introduction:
- The gut microbiota is a major factor in managing health and disease.
- There are numerous studies discussing the gut microbiome; however, they are mainly based on stool samples.
- Here we compare the microbial diversity of stool samples versus inner-colonic effluent samples collected prospectively during high-volume colon irrigation.

Methods:
- Samples were collected from 11 participants (mean age: 66, min–41, max–78) during an IRB-approved clinical trial. All patients underwent high-volume colon irrigation before screening colonoscopy.
- The inner-colonic samples (n=35) were collected three times during the prep as changes were noted in effluent appearance, to represent the left, transverse, and right colon. Stool samples were collected by patients in their home (n=11) using standard collection kit.
- Samples were immediately stabilized and stored following standard procedures and analyzed by PCR amplicon for bacterial rRNA, 16S V4.

Results:
- Bacterial communities detected in inner-colonic samples were significantly different that those of stool samples.
- Of all bacterial strains detected, a third of the strains (n=344) were unique to the inner-colonic samples, with a unique contribution from the different colon biogeographic locations.
- There are numerous studies discussing the gut microbiome, however, the phylogeny of the microbiota community in all stool samples was relatively similar regardless of the patient.

Discussion:
- There are distinctive and large differences between stool and inner-colonic samples.
- For most patients there is a detectable phylogenetic progression with a predictable, yet personal, trajectory.
- The phylogenetic spread in the multivariate space of the weighted analysis explains approximately 50% of the population diversity of the inner-colonic samples diversity (n=35) and is much wider than the phylogenetic difference of the stool samples.
- The patented process of collection of microbial samples using a high-volume colon irrigation is currently the only way of obtaining microbiome information from within the colon, non-invasively, and without the effects of oral prep purgatives.
- Obtaining information from inner-colonic microbiome communities can be imperative for developing personalized medicine.