P 47 – No differences in gastrointestinal microbiome and urinary tract among individuals with chronic spinal cord injury: Results from an exploratory, feasibility study

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Introduction

- Alterations in microbial composition of the gut and urine are associated with many seemingly diverse disorders, affecting the immune system and correspondingly influence the composition of the microbiome (i.e. reciprocal signaling)
- Individuals with spinal cord injury (SCI) are prone to infections and this could be reflected by changes in the microbiome
- Given the paucity in the current literature, there is a need to known more about the microbiota in individuals with chronic SCI

Objective

To compare human gastrointestinal (GI) and urinary tract (UT) microbiota from chronic SCI individuals with chronic / recurrent infections (YES, Y) versus without (NO, N)

Subjects and Methods

- Exploratory, feasibility (NCT02903472) was approved by the local ethics boards of all participating centers, i.e. Zurich (Switzerland), Fredericton (NB, Canada), and Manhasset (NY, USA)
- Main inclusion criterion: Individuals with an acute tetraplegic or paraplegic motor complete (American Spinal Injury Association impairment scale [AIS] A, B) or motor incomplete (AIS C, D) single non-penetrating SCI to the C2-S1 spinal cord were recruited
- Urine and stool samples were set to be obtained 1, 6, and 12 months after study begin
- DNA sequencing: 16Sv4 amplicons generated from the samples were sequenced, quality-filtered and clustered into 97% similarity operational taxonomic unit (OTUs)
- Any sample with a read count <1000 was removed the analysis
- For this preliminary analysis, we use one urine and stool sample from each participant with the highest read number, and if possible, always prior to an infection or antibiotic treatment
- OTUs were aggregated into each taxonomic rank, and plotted the relative abundance of the most abundant ones
- Alpha diversity (i.e. Shannon index) was computed and compared between both groups
- Microbiome composition similarity among samples (Beta diversity) was assessed using permutational ANOVA (PermANOVA)

Results

- **Participants:** Overall 19 individuals (5 women, 26%, median age 44 years [Q1: 36; Q3: 52] and time post injury 7 years [Q1: 2.5; Q3: 17.5]) were enrolled and provided at least one urine and stool sample (i.e., a read count >1000) for taxonomic analysis (see Figure)
- **Alpha diversity** (shown as mean [SD]): No significant differences between both groups (recurrent / chronic infections YES vs. NO) were detected for UT (1.132 [1.009] vs. 0.711 [1.018], p = 0.396) or GI microbiome (2.427 [1.355] vs. 2.545 [1.321], p = 0.854)
- **Beta diversity:** PermANOVA determined no significant differences between both groups for UT (R2=0.0408, p = 0.708) or GI (R2=0.0487, p = 0.63)
- **Differential abundance testing (DESeq2, R package)** did not identify any OTUs that were differentially abundant

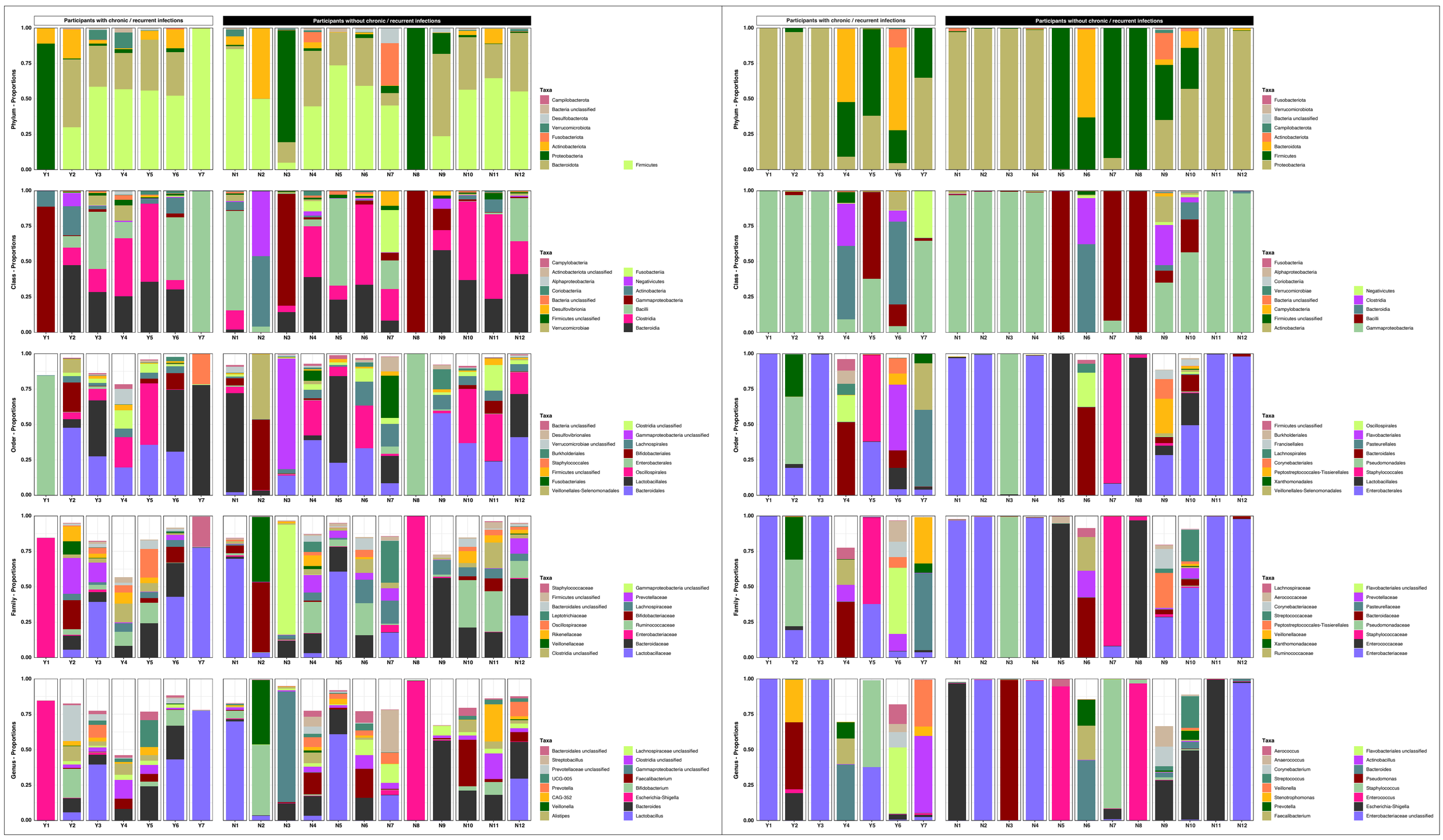

Figure: GI (left) and UT (right) taxonomic proportions (top to bottom: Pylum, Class, Order, Family and Genus) of individuals with chronic SCI (i.e. with infections [Y, n = 7] or without [N, n = 12]).

Conclusion

- **Preliminary group-level analysis revealed no significant Alpha and Beta diversity differences between chronically injured individuals with recurrent / chronic infections and those without**
- **Next, we will analyze all remaining samples as well as short-chain fatty acids (SCFA) which are known to play an important role in the maintenance of health**

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