P 118 – Assessing longitudinal changes in urinary tract microbiome in individuals with acute SCI: 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 learn more about changes in human microbiota after acute SCI

Objective

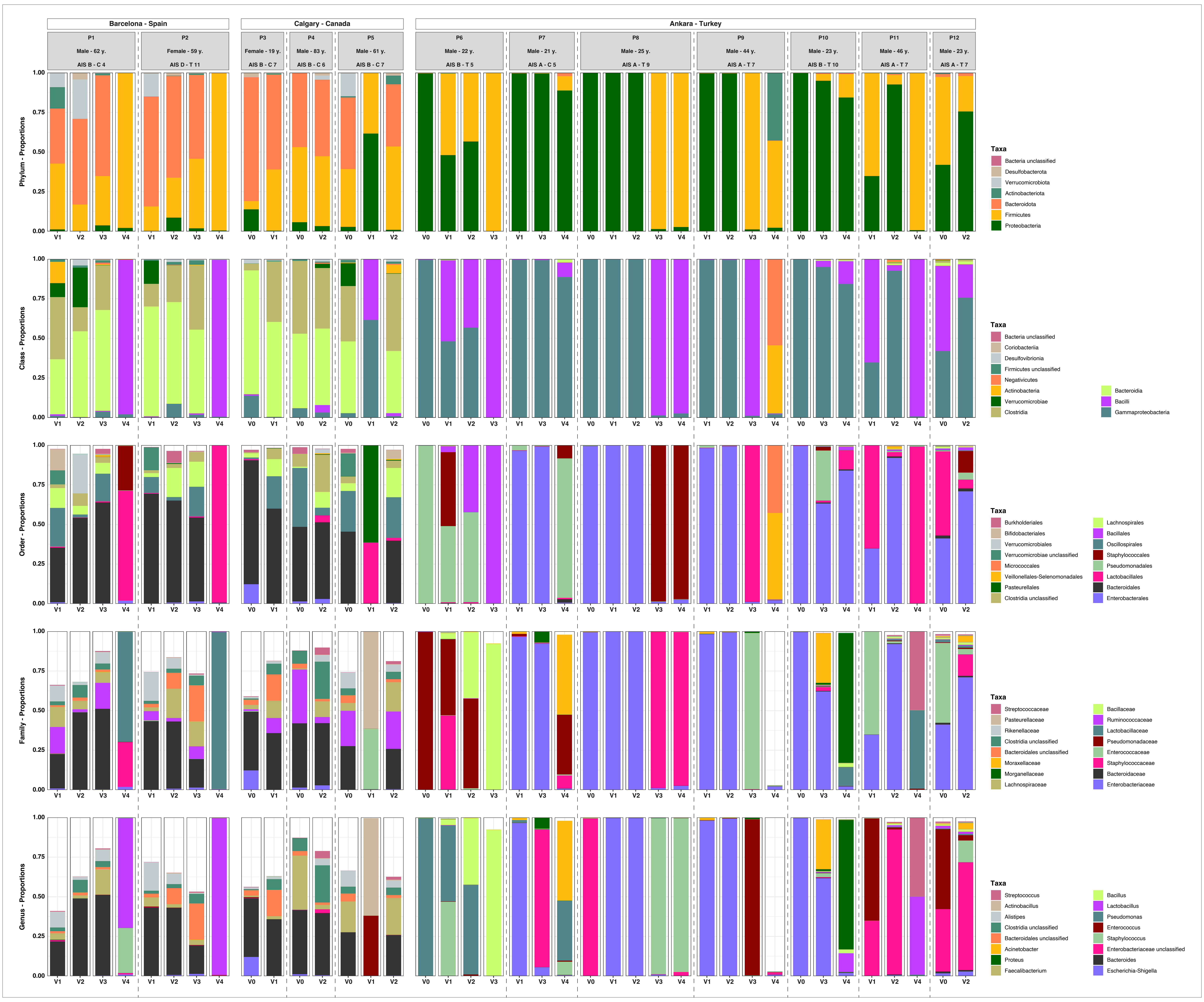
To tract changes in human urinary tract (and gastrointestinal) microbiota after acute SCI

Subjects and Methods

- Exploratory, feasibility (NCT02903472) was approved by the local ethics boards of all participating centers, i.e. Calgary (Canada), Barcelona (Spain), and Ankara (Turkey)
- 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 scheduled to be obtained at baseline (i.e. visit, V0, within the first week after SCI) and then, when available, longitudinally at approximately 1, 3, 6, and 12 months (i.e. V1 to V4) after SCI
- 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
- OTUs were aggregated into each taxonomic rank, and plotted the relative abundance of the most abundant ones

Results

Participants: Overall 24 individuals (3 women, 12.5%, median age 34 years [Q1: 24; Q3: 46]) with an acute SCI were enrolled. However, only 12 Individuals with at least one sufficient (i.e., a read count >1000) urine sample at baseline (V0) or within the first month following SCI (V1) were included for this analysis (see Figure)



Conclusion

- ➢ **Our study revealed changes in urinary tract microbiota over time as well as regional differences**
- ➢ **Despite a significant number of samples with low read count, shipping, storing and analysis of urine samples were feasible**
- ➢ **The major challenge of this study was obtaining baseline and long-term follow-up samples (i.e. 6 and 12 months)**
- ➢ **To gain more in-depth knowledge about temporal microbiome changes, we will analyze the participants' stool samples**

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