Introduction

The human gut microbiome is linked to many cardiovascular diseases. Among patients with peripheral artery disease (PAD), surgical treatment is an option. However, the risk of restenosis is high and clinical outcomes have high inter-individual variability.

We have previously shown that the gut microbiome modulates arterial remodeling in mouse models of vascular injury. In order to identify human gut microbiome-associated biomarkers of disease, we are conducting multi-omics profiling of patients with PAD and non-PAD controls.

We hypothesize that there are gut microbial features that correlate with clinical features of PAD and outcomes after vascular surgery.

Objectives

- To evaluate feasibility of home fecal sample collection using different storage media
- To identify microbial community features associated with PAD and clinical outcomes

Methods

1. Microbial communities differ by storage conditions and patients with PAD and non-PAD controls.

2. There are differentially abundant genera between patients with PAD and non-PAD controls.

Results

1. Microbial communities differ by storage conditions and patients with PAD and non-PAD controls.

2. There are differentially abundant genera between patients with PAD and non-PAD controls.

3. Short chain fatty acid levels are reduced in PAD.

Conclusions

This pilot study demonstrates the feasibility of home fecal sample collection for metagenomic and metabolomic analysis of patients with PAD. 16S rRNA and SCFA findings suggest shifts in structural and functional activities of gut microbial communities associated with PAD. Reduced prevalence of SCFA producers such as Collinsella, Bifidobacterium, Megamonas, Megasphaera, and Prevotella indicates their association with PAD.