Gut Microbial and Microbe-Derived Metabolomic Profiling in Patients with Peripheral Artery Disease

Sarbjeet Niraula[1], Spencer L. Stirewalt[1], Jonathan Jung[1], Erik Wu[1], Ayman Elmasri[1], James Du[1], Stefan J. Green[2], Karen J. Ho[1]

[1]Northwestern University Feinberg School of Medicine , [2]Rush University

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.

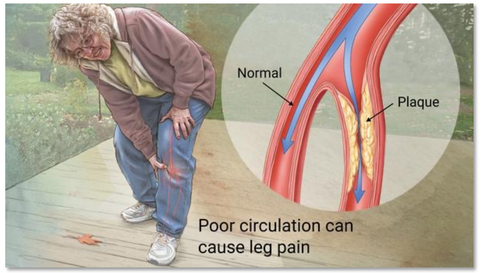

Figure 1: Peripheral artery disease (PAD) caused by atherosclerotic occlusions leads to pain and disability.

We have previously shown that the gut microbiome modulates arterial remodeling in mouse models of vascular injury. In order to identify human gut microbe-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

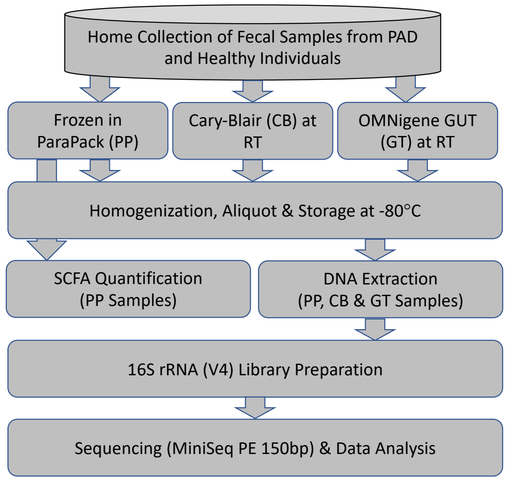

Figure 2: Schematic of overall workflow

Results

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

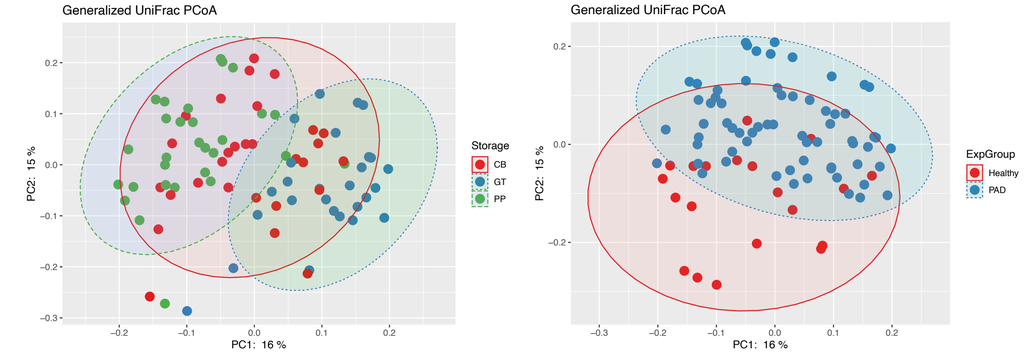

Figure 3. Beta diversity of using Generalized UniFrac (GUniFrac) matrix. Each dot represents an individual.

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

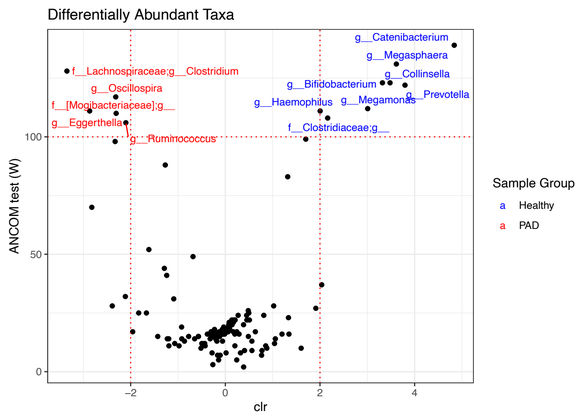

Figure 4. Differentially abundant taxa at genus level between PAD and non-PAD individuals using Analysis of Composition of Microbiome (ANCOM) test. Each black circle represents an individual.

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

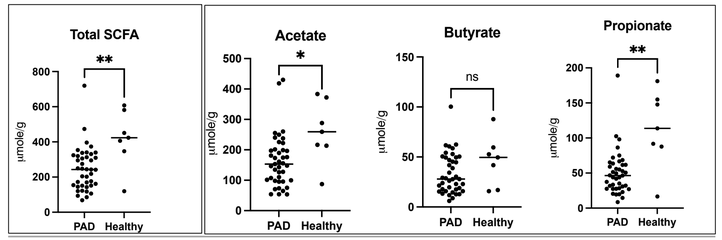

Figure 5. Fecal short chain fatty acid concentration in patients with PAD and non-PAD controls. P-values represent significance using Mann-Whitney U test.

Conclusions

This pilot study demonstrates the feasibility of home fecal sample collection for metagenomic and metabolomic analysis of patients with PAD. 16SrRNA 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.