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Introduction

- Porphyromonas gingivalis* is a keystone pathogen found in patients with periodontitis and produces toxic proteases called gingipains.¹
- This bacterium has also been found in the brains of patients with Alzheimer's disease.¹
- In mouse models, inhibiting gingipain (Kgp) decreased the colonization of *P. gingivalis* in the brain.¹
- Kgp inhibitors also block the acquisition of host heme by *P. gingivalis* – a process mediated by *hmuY*, a unique hemophore.²
- The nitrate-nitrite-nitric oxide pathway relies on bacteria within the oral microbiome to convert nitrate to nitrite, and this pathway may be important in overall health.³
- Supplementing the diet with nitrate could alter the oral microbial community composition and reduce *P. gingivalis* abundance.

Previous Work

- Ten healthy participants were recruited to participate in the study.
- A 10-day nitrate supplement was administered to assess changes in vascular health and the oral microbiome.
- Oral microbiome composition and the abundance of *P. gingivalis* were evaluated using 16S rRNA gene sequencing.

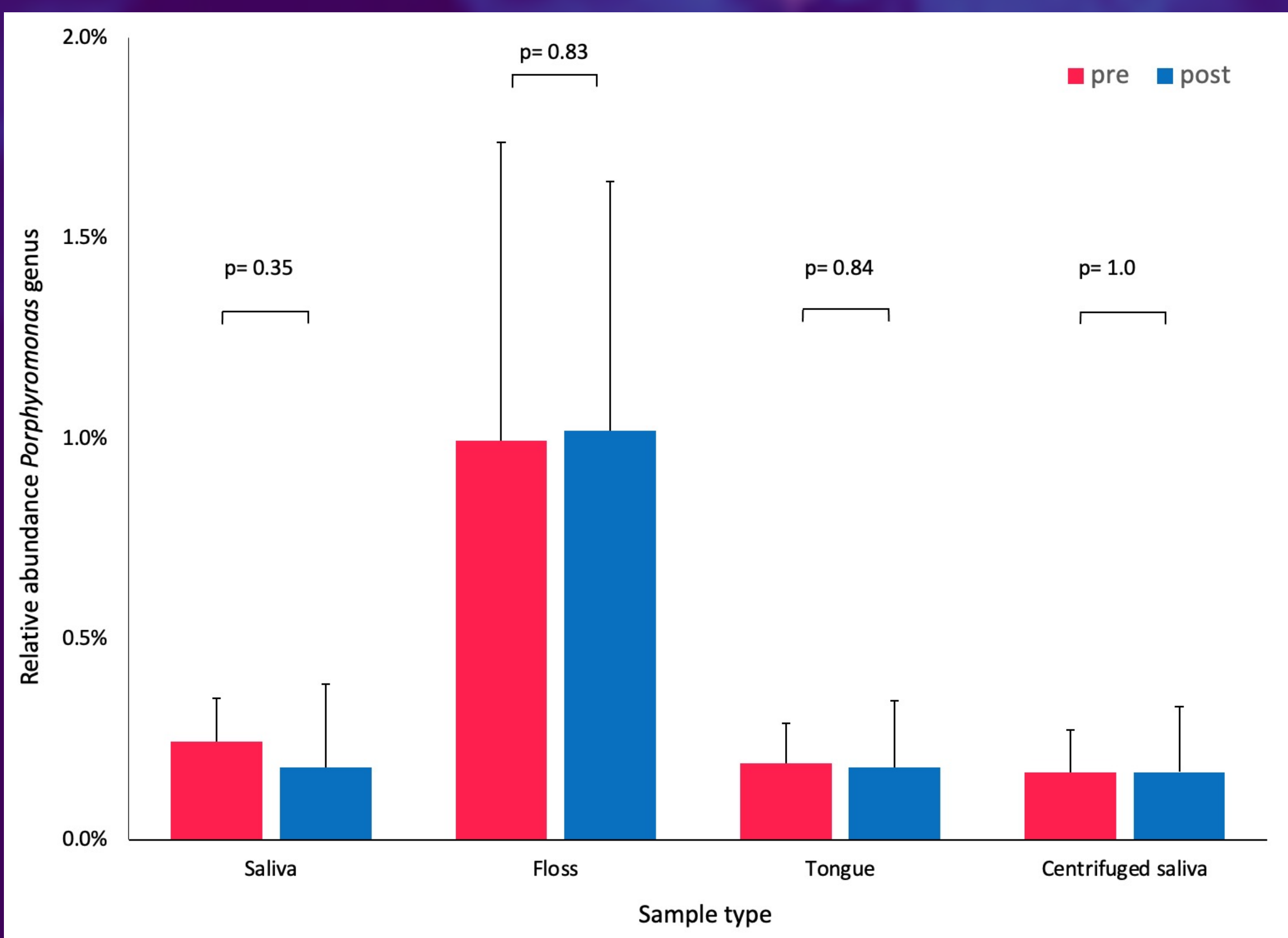


Figure 1. Mean relative abundance of *Porphyromonas* both pre and post nitrate supplementation as detected in four different sample types (n=8). There were no differences found between pre and post conditions in any sample type (p>0.05).

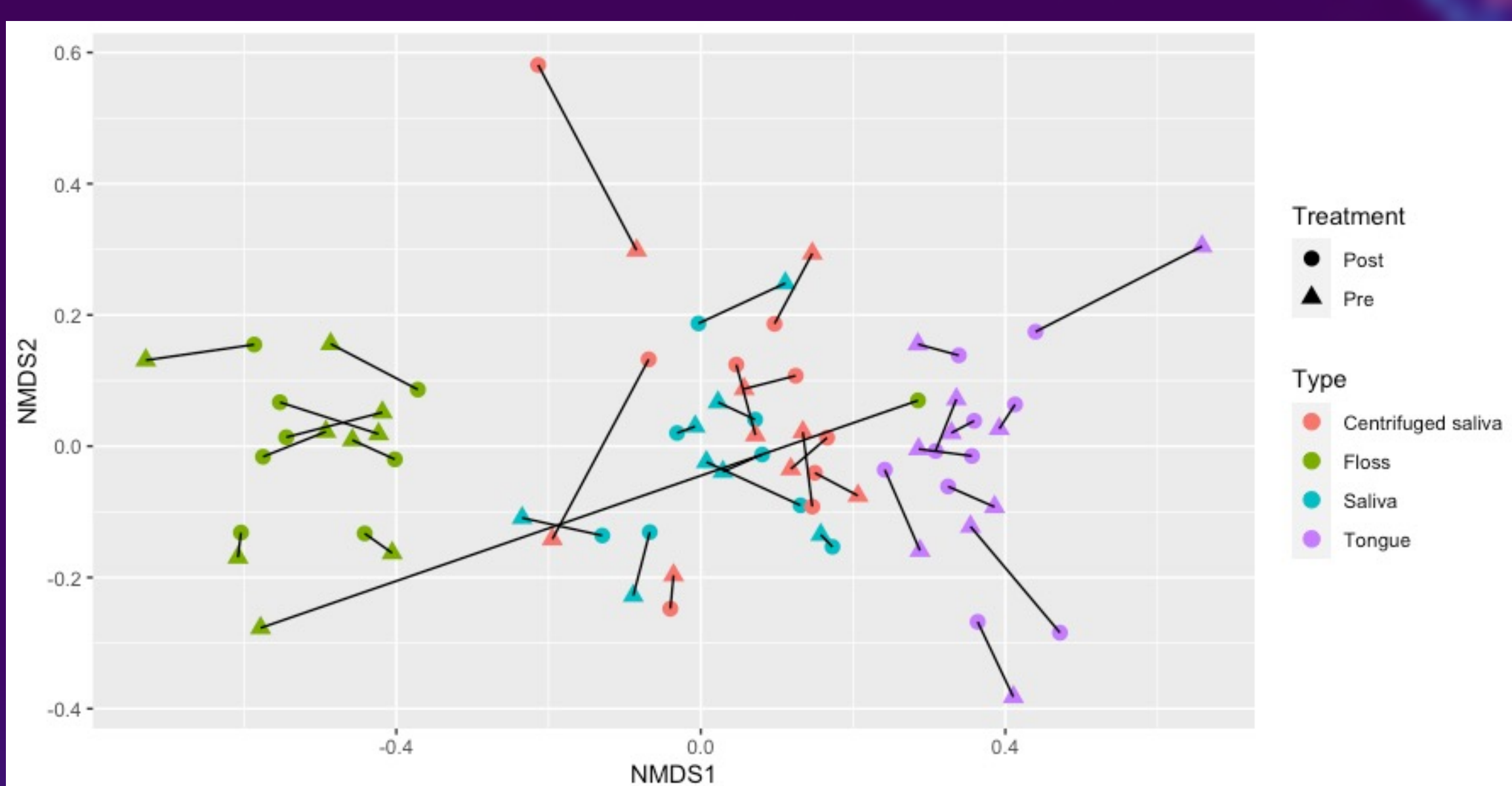


Figure 2. Multidimensional scaling (MDS) plot reflecting similarities in oral microbiome composition between samples. Plot shows comparisons between pre and post nitrate conditions and sample types. Lines between points show individual responses (n=8).

- Endothelial function was assessed using B-mode ultrasound and a flow mediated dilation (FMD) test following occlusion downstream of the brachial artery.

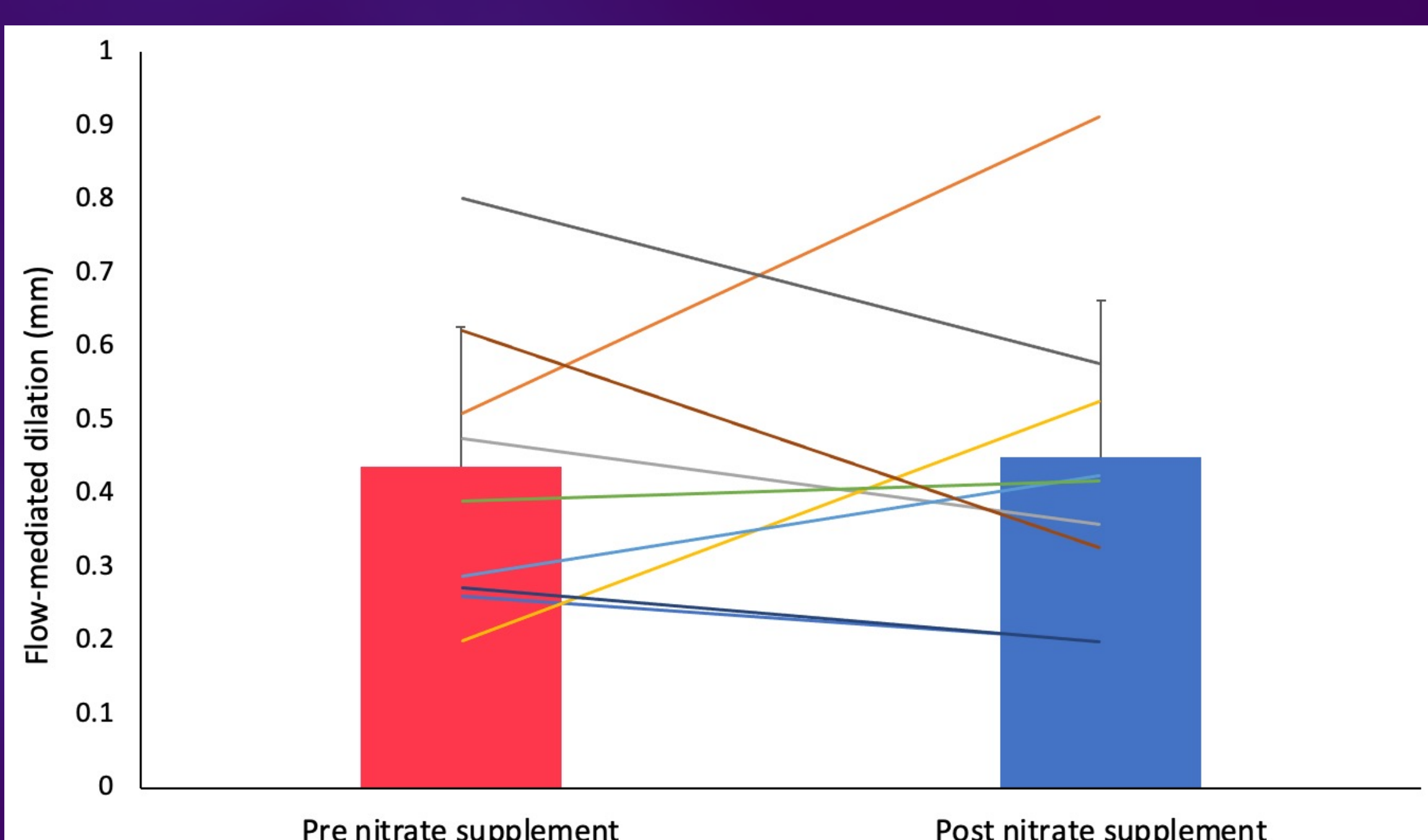


Figure 3. Mean absolute change in brachial artery FMD from pre to post nitrate conditions. Lines show individual responses (n=9). There were no differences between conditions (p>0.05).

Current Work

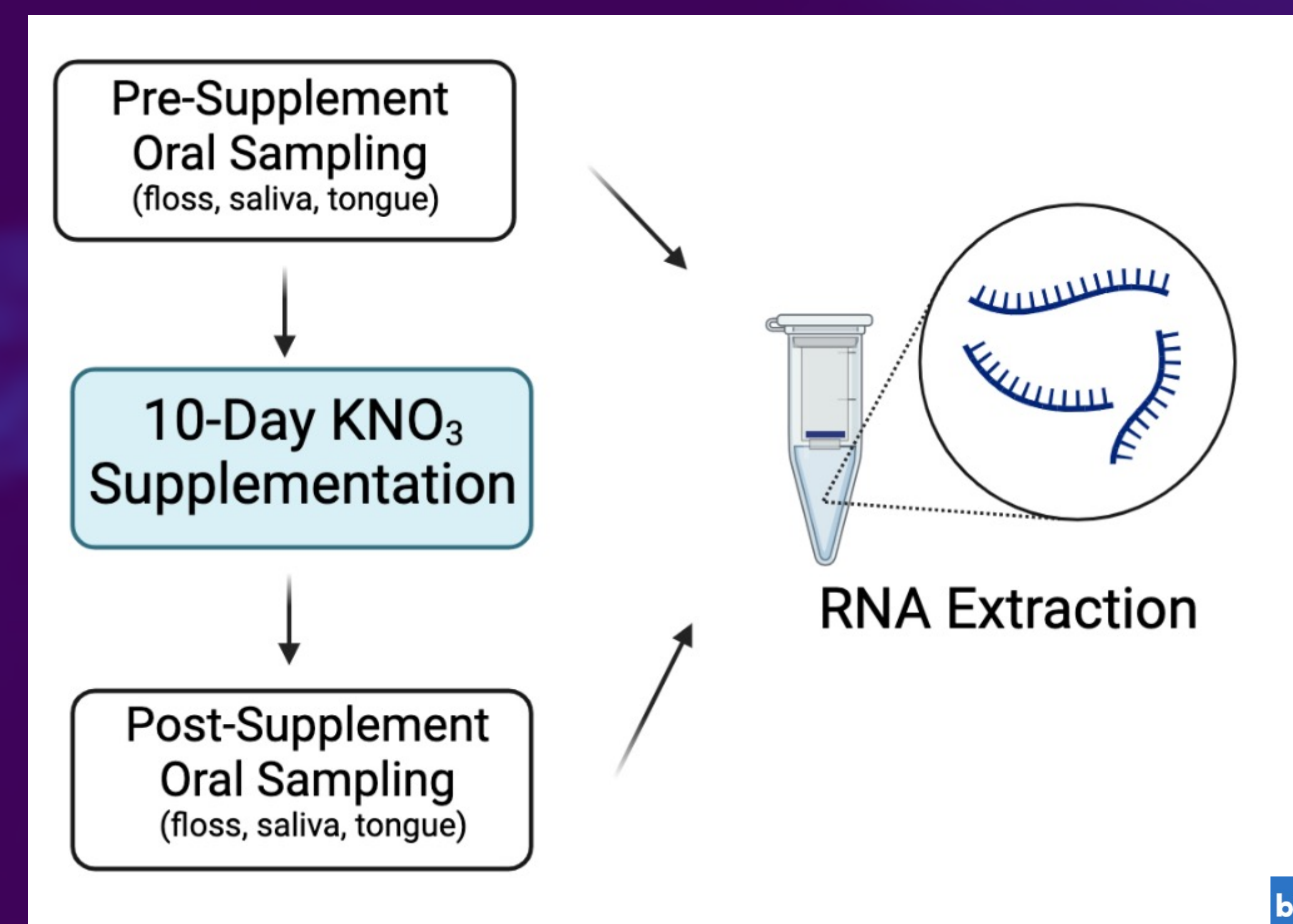


Figure 4. Oral microbiome sampling design for subsequent RNA extraction.

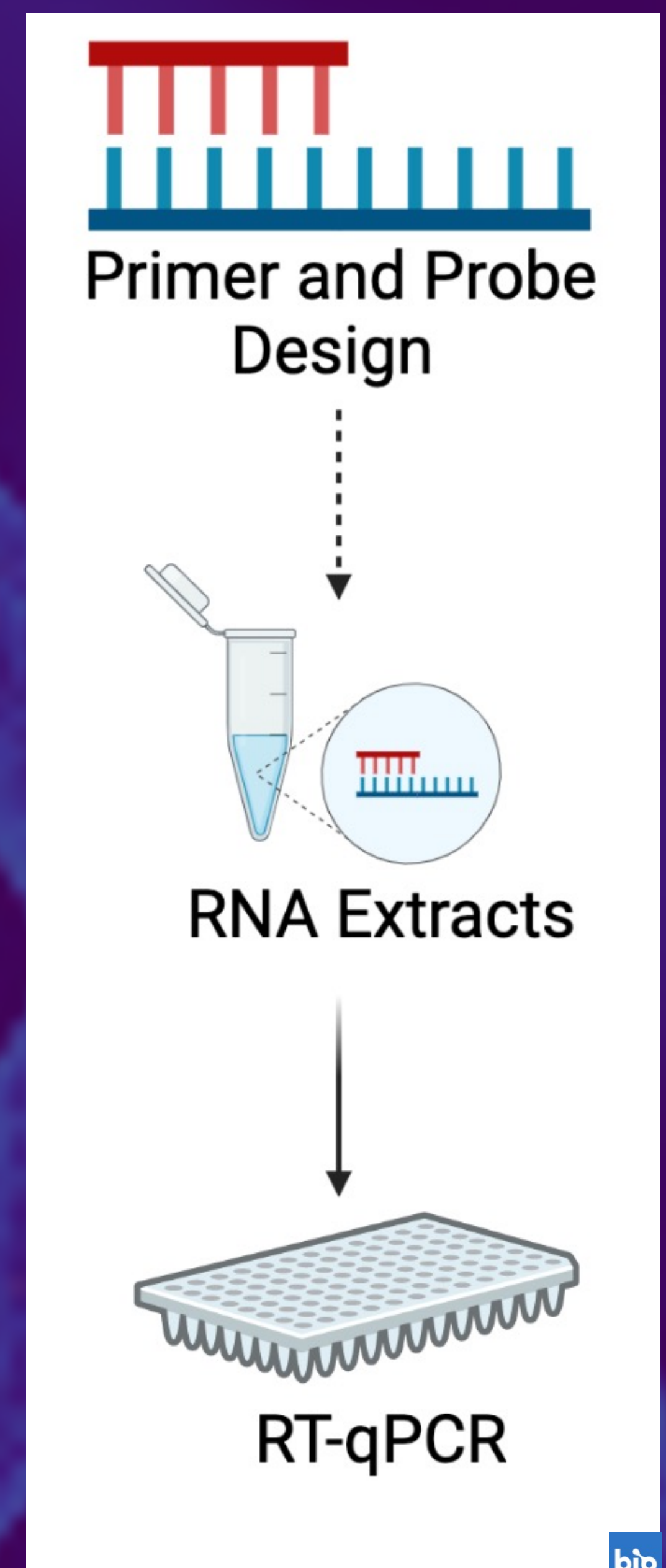


Figure 5. Method for the study presented here.

- Oral samples were subjected to an RNA extraction protocol to obtain material for RT-qPCR analysis.
- Primers and probes will be designed for RT-qPCR to target 16SrRNA, *hmuY*, *kgp*, and nitrate reductase genes.

Future Analysis

- Results will be compared pre- and post-nitrate supplementation using paired t-tests to see if there are significant differences in gene expression levels, and in absolute abundance of *P. gingivalis*.
- Linear regression will be used to assess shifts in microbial communities compared to shifts in physiological outcomes including blood pressure and FMD.

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