

## The Microbiome of Inflammation and Nutrition: World Trade Center FIREHOUSE RCT

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**RATIONALE** Particulate exposure (PM) induced cardiopulmonary disease is a global health concern. Our group has investigated how a Mediterranean-type diet may improve metabolic health, lung function and mediate inflammation in World Trade Center (WTC)-PM exposed firefighters. We also know that the microbiome can play a role in mediating inflammatory responses in the lung. We studied the changes in the microbiome of WTC firefighters following 6-months(6M) of a Mediterranean diet and potential associations between certain bacterial flora and improvements in metabolic syndrome characteristics and lung function outcomes. **METHODS** A pilot and feasibility study of the gut microbiome was undertaken during our Food Intake REstriction for Health OUtcome Support and Education (FIREHOUSE) randomized clinical trial; Clinicaltrials.gov: NCT03581006. Stool was collected at the baseline and 6M timepoints using OMNIgene-GUT kits (DNA genotek). A subset of those samples was used for this pilot study, with samples from both timepoints for N=5 subjects/arm [Low Calorie Mediterranean (LoCalMed) and Usual Care (UC Stool collected. Microbiome assessed (BoosterShot Shotgun Sequencing; Diversigen). One sample failed pre-sequencing quality control, leaving N=4 paired samples in the LoCalMed arm and N=5 in UC. Microbiome profiles were generated from whole-genome shotgun (WGS) sequencing data via alignment to a custom bacterial database (Diversigen). Statistical analysis was performed in R. **RESULTS** Demographics. Mean age, exposure and years of service were similar in both arms. Subjects were predominately Caucasian. Individual microbial community diversity (Shannon diversity index) did not differ between arms at either timepoint ( $p>0.05$ ) but decreased across time for both arms ( $p=0.02$ ). Similarly, microbial community composition ( $\beta$ -diversity) did not differ between arms at either timepoint or between timepoints (PERMANOVA,  $p>0.05$ ). However, the abundance of specific microbial taxa did differ between timepoints. For example, *Bifidobacterium wadsworthia* had a higher relative abundance at the 6M timepoint compared to baseline in the UC arm only. An increase in this bacterium is usually associated with high fat diets and increased inflammation. When incorporating health measures with microbiome analysis, a reduction in BMI was associated with an increase in the abundance of *Bacteroides ovatus* in combined arm data ( $p=0.06$ ). **CONCLUSIONS** This pilot shows that improvements in health metrics are associated with changes in the microbiome. For example, increases in *Bacteroides ovatus* are associated with a reduction in BMI. Future studies will include an assessment of all samples obtained in our RCT and microbial association with clinical outcomes.

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