

## A POLYPHENOL-RICH SUMAC SORGHUM CEREAL ALTERS COLON MICROBIOTA AND PLASMA METABOLITES IN HUMAN SUBJECTS

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### BACKGROUND

Diet has the potential to impact gut microbiota and metabolism, with implications for inflammation resulting from a variety of environmental stressors, including: infection, injury, and radiation. While much research is aimed at eliminating these risks altogether, diet remains one of the most prospective means for preventative care and treatment, particularly in space. Previous work by our lab has demonstrated the susceptibility of gut microbes to radiation- and microgravity-induced population shifts, which appear to mimic the dysbiosis observed during inflammation and the induction of obesity. We have also shown that polyphenol-rich sumac sorghum alters microbial populations and metabolites in a rat model. Although the astronaut population is not typically overweight, spaceflight-induced alterations in microbiota may reflect a dysbiosis that is similar to that observed in overweight individuals. The goal of this study was to determine if an analogous dietary intervention was able to mitigate the perturbations in microbiota and their metabolism that occur in individuals prone to sub-clinical inflammation induced by excess body weight.

### METHODS

Overweight subjects (n=24) were randomized in a crossover design with high (100 g/d) and low (50 g/d) intakes (4 wk) of sumac sorghum cereal incorporated in their normal diets. Subjects consumed each amount of sorghum cereal for 3 weeks with a 4 week washout period separating the treatment periods. Fecal and blood samples were taken at baseline, post-treatment 1, at the end of the washout period, and post-treatment 2. Fecal samples were used to characterize microbial composition by 454 pyrosequencing of 16S rRNA PCR amplicons and to measure short chain fatty acid concentrations by gas chromatography. Plasma was collected from whole blood and used to measure the presence of over 300 metabolites, including molecules derived from microbial metabolism.

### RESULTS

Sumac sorghum induced compositional changes in the fecal microbiota, such as an increase (q=0.076) in anti-inflammatory *Faecalibacterium prausnitzii* species. Untargeted metabolomic analysis of plasma revealed reductions in amino acid (AA) metabolites as well as increases in microbially-derived aromatic AA and polyphenol metabolites. 3-hydroxyhippurate, a product of chlorogenic acid metabolism, was increased (q=0.0145) following sumac sorghum consumption. Additionally, three of the gamma-glutamyl AAs produced by gamma-glutamyl transferase, a biomarker for metabolic syndrome and cardiovascular risk, were decreased (q<0.05) with the 100 g intake.

### CONCLUSION

These data confirm the ability of diet to modify human gut microbe composition and metabolism, and support our hypothesis that these changes can affect host metabolism. Specifically, these observations suggest sumac sorghum is able to induce putatively beneficial shifts in fecal microbiota and to modify the presence of metabolites that are known biomarkers for metabolic disorders (e.g. glucose intolerance). Furthermore, these data suggest that diets supplemented with polyphenol-rich foods may help to mitigate a potentially harmful shift in gut microbial populations during spaceflight while simultaneously providing direct effects of the bioactive compounds on host physiology. Although the subject phenotypes are unlike those of the astronaut corps, the knowledge concerning the impact of diet on host microbiota and metabolism is of critical importance for determining optimal dietary regimes for a hazardous space environment.

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