Introduction

- The gut microbiome impacts response to immune checkpoint blockade (ICB) treatment in melanoma patients (1).
- A habitual high-fiber diet was associated with significantly improved progression-free survival (PFS) in melanoma patients on ICB (2) and bacteria associated with response to ICB are fiber-responsive taxa (3).
- A high-fiber diet intervention (HFDI) was therefore conducted in melanoma survivors to prospectively evaluate the effect of a HFDI on the microbiome.
- To explore community dynamics and identify keystone taxa responsive to a HFDI, we conducted microbial association network analysis on baseline and end of intervention fecal microbiome WGS data.

Methods

- Ten melanoma survivors were enrolled to a 6-week HFDI, targeting 50 grams of fiber daily, derived from whole fruits, vegetables, legumes, and whole grains with all meals provided by Biostimulation Research Core.
- Metagenomic sequencing was conducted on fecal samples to extract DNA and bacteria with associated response to ICB are fiber-responsive taxa (3).
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Results

- Characterization of the changes in community structure of the gut microbiome in response to dietary intervention is possible via association network analysis.
- Our analysis indicates that increase in fiber intake prompts the gut microbiome to become a more interconnected and dynamic ecosystem.
- Networks demonstrated an overall increase in centrality in known fiber-responsive taxa.
- Despite heterogeneity across networks generated from different association statistics, analysis of consensus and differential networks consistently identified D. longicatena and R. bromii as becoming hubs taxon post-HFDI.
- This study confirms that the microbiome can be characterized via network analysis, and further studies are needed to fully understand the microbial pro-response to fiber.

References