Impact of a Whole Foods Based High Fiber Diet on Gut Microbiome in Melanoma Survivors

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Introduction

The development and approval of checkpoint inhibitor immunotherapy (ICI) has revolutionized the treatment of many cancers. However, patient responses are mixed. Recent evidence has demonstrated that the gut microbiome influences response to ICI(1).

Observational data in melanoma supports that a habitual high-fiber diet is associated with a pro-response microbiome and improved response to ICI; further, in mouse models, fiber manipulation can improve response to ICI(2).

Additionally, fiber consumption can shape microbiome metabolic output (3) and, in turn, host metabolism (4).

Towards testing our hypothesis that a whole foods, plant-based, fiber-rich diet can favorably modulate the microbiome, we first conducted a pilot feasibility study of a high-fiber dietary intervention (HFDI) in melanoma survivors and conducted exploratory profiling of the gut microbiome.

Methods

Study design. Six melanoma survivors were enrolled in a 4-week high-fiber diet intervention (HFDI) study. As a controlled feeding study, participants were provided with all meals from our Biostatistics Research Core for the duration of the six-week study. The provided diet was individually tailored to energy needs and targeted 50g of dietary fiber, derived from whole fruits, vegetables, legumes, and whole grains.

Diet metrics were obtained to assess usual dietary intake, throughout HFDI to measure adherence. Diet records were obtained at baseline to assess usual diet, throughout HFDI to measure diet.

Statistical analysis: Analysis is only shown for 5 of the 9 patients as blood and stool analysis of the 4 other patients is not yet completed. Alpha diversity (Inverse Simpson) were compared across different timepoints. Beta diversity among individuals was ordinated using a distance metric and visualized using a heat map. Due to the exploratory nature of this study, adjustment of significance levels was not employed. The mean difference between baseline was calculated for each taxon. All statistical analyses were performed using R (version 3.5.1). p values less than 0.05 were considered statistically significant.

Results

A HFDI was well-tolerated and feasible in a melanoma population.

Baseline microbiome taxonomic composition for each patient. Overall Relative Abundance of Presel ected Carbohydrate and Amino Acid Metabolism Pathways remained stable across the HFDI.

Our data suggested that fiber may induce a promotion of fiber-related carbohydrate-processing pathways in specific genera, not the entire gut microbiome. Further studies are needed to link these genera/pathways to host immunity, as well as look specifically at genes for Carbohydrate-Active Enzymes involved in individual pathways that make up larger carbohydrate-processing pathways.

References


Figure 1: Participant baseline characteristics. A. Average daily fiber intake per participant. B. Average weekly compliance with consuming provided diet.