HUMAN GUT MICROBIOME MODULATION AFTER A DIETARY CLEANSING AND DETOXIFICATION SUPPLEMENT REGIMEN IN HEALTHY SUBJECTS: AN EXPLORATORY STUDY

David Vollmer, Brent Vaughan, Tory Parker, Paula Brock, and Barbara Olsen, 4Life Research, Sandy, UT

ABSTRACT

OBJECTIVE The purpose of this exploratory study was to measure the gut microbiome impact after a dietary cleansing and detoxification supplement regimen.

METHODS Twenty healthy adult subjects were selected to undergo a 25-day dietary cleansing and detoxification supplement regimen, which included digestive enzymes, fiber and diuretic herbs, prebiotics, probiotics, and other ingredients that support immune and liver function. The study was comprised of four visits: a screening visit, a pre-regimen visit, a post-cleanse visit, and a post- regimen visit.

Stool microbiome samples were self-collected on or around the visits using commercially available sampling kits and were processed by uBiome. Self-assessments of well-being were collected at each visit, along with Bristol stool consistency, hydration status, dietary intake and body composition.

RESULTS Weight-influencing, sleep and anti-inflammatory microbes changed during different portions of the study. Hydration status was shown to steadily improve throughout the course of the regimen. Measures of well-being that met statistical significance were improvement of gastrointestinal distress, decrease in cravings and compulsive eating, fatigue, apathy, restless, sleep, concentration, and decision making. No changes were observed with stool consistency, microbial diversity, phylum composition or body measurements.

CONCLUSION Microbial variability limited the conclusions regarding the impact of the supplement regimen on the gut microbiome. In general, the regimen was well-tolerated with subtle changes in several microbes, and certain measures of well-being such as sleep. Larger studies including a control group are recommended.

BACKGROUND

Cleanse and detox regimens are generally short-term dietary supplement interventions designed to eliminate toxins from the body, promote health and assist in weight management. Their programs can range from severe caloric restriction to dietary modification. Often times, these approaches involve the use of laxatives, diuretics, vitamins, minerals and other nutrients such as probiotics.

While these widely popular regimens are marketed and used for the reasons described above, most, if not all, of them have also been shown to be a major disruptor of many body systems, including the digestive system. Interestingly and to the best of our knowledge, there have been no studies that have measured the impact of these regimens on the gut microbiome. To date, there have been a few studies that have demonstrated significant changes in the stability of the gut microbiome within the context of bowel preparations [1].

4Life Research has had a dedicated interest in immune health from the beginnings of the company over 20 years ago. Recently, we have focused on the interplay between immune health and digestive health, which has led to the development of a regimen that includes cleanse and detoxification steps, as well a complement of products (including prebiotics and probiotics) that “replenish” the digestive system.

[1] Jalanka, J. *et al. Effects of bowel cleansing on the intestinal microbiota*. Gut 64, 1562–1568, (2015).

REGIMEN PRODUCT INGREDIENTS

Step 1 Cleanse & Prep

- Fibre System Plus
  - –Psyllium husk, slippery elm inner bark, marshmallow root, black walnut hull, cascara sagrada bark
- Digestive Enzymes
  - –Amylase, protease, galactosidase, glucanase and other proteases, lipases, and carbohydrases

Step 2 Detox

- Super Detox
  - –Red clover flower tops, milk thistle fruit extract, calcium d-glucarate, and bupleurum root

Step 3 Replenish

- Aloe Vera
  - –Aloe barbadensis
- Pre/o Biotics
  - –Filtered bovine colostrum, chicken egg yolk concentrate, GOS, XOS, FOS, *B. Longum, B. Lactis, B. Infantis, L. rhamnosus, L. acidophilus*
- Transfer Factor
  - –Filtered bovine colostrum, chicken egg yolk concentrate

EXPERIMENTAL METHODS

STUDY PARTICIPANTS Twenty healthy participants were selected from a pool of forty-two candidates based on their dietary and lifestyle habits and willingness to comply with all study requirements. By the end of the study, stool samples from three participants did not meet uBiome’s quality control threshold, leaving results from seventeen participants to be used in the data analysis.

INTERVENTION The intervention included a 25-day regimen comprised of three stages: (1) cleanse and preparatory – Day 1 to Day 11, (2) detoxification – Day 11 to Day 25 , and (3) replenishment – Day 11 to Day 25, using the six products described earlier. Participants were instructed to minimize any changes to diet and exercise habits, to mitigate their impact during the dietary supplement regimen.

DATA COLLECTION AND ANALYSIS Data was collected from gut microbiome analysis, an abbreviated metabolic screening questionnaire, Bristol stool consistency, hydration status, dietary intake and body composition. This data was collected across three visits: (1) a baseline visit - Day 0 - to assess the participants gut microbiome prior to starting the regimen, (2) an interim visit - Day 11 - to measure the effect of the cleanse and preparatory portion of the system, and (3) a post-regimen visit - Day 25 - to understand the impact of the detoxification and replenishment segments of the system. These visits were also used to monitor product consumption, to ensure the participants were compliant with the regimen, and dietary or exercise habits were consistent across the entire study.

Gut microbiome composition of the self-collected stool samples was determined using commercially available kits from uBiome, Inc. Briefly, stool samples were stored in vials with lysis and stabilization buffers, shipped to uBiome facilities, where DNA was extracted and then analyzed using PCR-amplification of the 16s rRNA genes [2]. Gut microbiome results for participants were determined relative to a healthy cohort of 897 individuals using the uBiome Explorer report [2].

The abbreviated metabolic screening questionnaire was based on a five-point scale, self-assessment of different categories of health, including digestive, energy/activity, sleep, cognitive, and weight [2]. Changes in intestinal function and hydration status were self-assessed using a Bristol Stool chart and a urine color chart, respectively. Body weight and composition was determined using a body composition analyzer, Tanita Model BC-418.

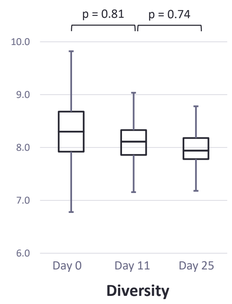
Treatment effects and interactions were determined by t-test and ANOVA.

[1] Apte, Z. *et al. 16S rRNA gene sequencing and healthy reference ranges for 28 clinically relevant microbial taxa from the human gut microbiome*, PLoS One. 2017 May 3;12(5).

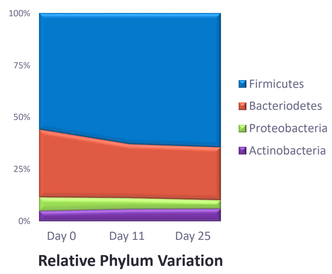
[2] Bland JS, Bralley JA. *Nutritional upregulation of hepatic detoxification enzymes*. J Appl Nutr. 2-15, 44 (3,4) 1992.

RESULTS AND DISCUSSION

MICROBIAL COMPOSITION The microbial diversity showed a general trend downwards, though not significant, indicative of a decrease in the number of bacterial families and evenness. These changes were also reflected in the relative variation at the phylum level.



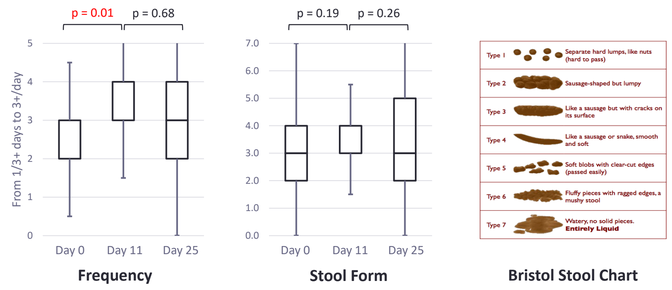
Diversity



Relative Phylum Variation

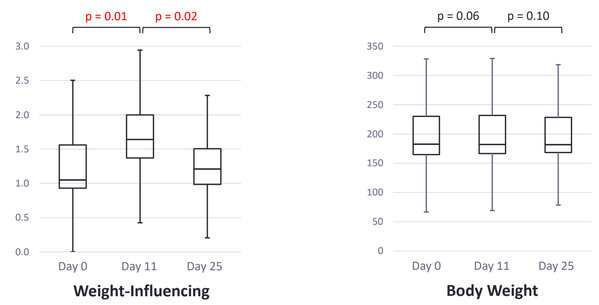
RESULTS AND DISCUSSION

BOWEL FREQUENCY AND FORM As expected, an increase in self-reported bowel movements were observed from Day 0 to Day 11, with an effective return to baseline at Day 25. Overall changes in form, as assessed by the Bristol stool chart, remained consistent, indicating that intestinal transit times were unchanged.



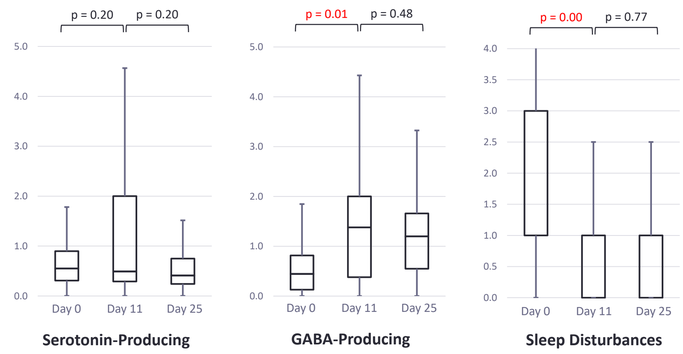
Frequency | Stool Form | Bristol Stool Chart

WEIGHT Weight-influencing microbes demonstrated an increase from Day 0 to Day 11, with an effective return to baseline at Day 25. Body weight and composition did not change over the course of the study, though self-reported cravings and compulsive eating did show a decreasing trend (data not shown).



Weight-Influencing | Body Weight

SLEEP Sleep-influencing microbes that help produce the neurotransmitters serotonin and GABA generally did not show any changes over the course of the study. Interestingly, GABA-producing microbes did see an increase from Day 0 to Day 11, which corresponded to a decrease in self-reported sleep disturbances.



Serotonin-Producing | GABA-Producing | Sleep Disturbances

ADDITIONAL Other microbes associated with nutrient metabolism and inflammation did not change over the course of the study, with the minor exception of an increase of butyrate-producing microbes from Day 0 to Day 11. Hydration status was observed to improve over the course of the study.

CONCLUSIONS

Microbial variability limited the conclusions regarding the impact of the supplement regimen on the gut microbiome. In general, the regimen was well-tolerated with subtle changes in several microbes associated with weight and sleep, and certain measures of well-being such as eating habits, sleep and hydration. Larger studies including a control group are recommended.