Revisiting the Relationship between Short-Chain Fatty Acids, the Microbiota, and Colorectal Tumors

Running title: SCFAs and colorectal tumors

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Abstract

Background. Colorectal cancer (CRC) is a growing health concern with the majority of the risk for developing disease being due to environmental factors. The microbiota is one of these environmental factors with certain bacterial community members being associated with CRC, while other taxa are associated to colons without tumors. Some of the taxa associated to colons without tumors can use fiber to produce short-chain fatty acids (SCFAs) that can inhibit tumor growth in model systems. However, the data supporting the importance of SCFAs in human CRC is less certain. Here, we test the hypothesis that SCFA concentrations are different in individuals with colorectal tumors.

Methods. We analyzed a cross-sectional (n=490) and longitudinal pre- and post-treatment (n=67) group for their concentrations of acetate, butyrate, and propionate. Analysis also included tumor classification models using Random Forest, imputed gene relative abundance with PICRUSt, and metagenomic sequencing on a subset (n=85) of the total cross-sectional group.

Results. No difference in SCFA concentrations were found between individuals without tumors and patients with adenomas or carcinomas (P-value > 0.15). There was no difference in classification models with or without SCFAs in their ability to predict patients with adenomas or carcinomas versus individuals without tumors (P-value > 0.05). Using metagenomic sequencing, there was also no difference in genes involved with SCFA synthesis between individuals without tumors and patients with adenomas or carcinomas (P-value > 0.70).

Conclusions. Although our data does not support the hypothesis that SCFAs are different in individuals that have colorectal tumors, there may be context specific scenarios where SCFAs may still be beneficial for treatment of CRC. Alternatively, there may be other mechanisms that have not been thoroughly investigated that are more important to the development of human CRC.

Introduction

Colorectal cancer (CRC) is currently the third highest cancer-related cause of death within the US (1, 2). Although there is a genetic component to the disease, the environment is attributed to being a larger risk factor for CRC (3). These environmental risk factors include but are not limited to smoking cigarettes, diet, and the microbiota (4–6). Many of these environmental risk factors are capable of being modified, and this has lead to the investigation of how the microbiota may exacerbate or cause tumorigensis (7–9) and whether the bacterial community is altered (10, 11). Multiple reports in case/control studies have identified bacterial taxa commonly associated with individuals without tumors to be decreased in patients with carcinoma tumors (11–13). Many of these taxa within individuals wihtout tumors actively produce short-chain fatty acids (SCFAs) from fiber that are a part of our general diet (14). The most extensively studied of these SCFAs are acetate, butyrate, and propionate (15). Overall, the specific bacterial taxa of the microbiota that create SCFAs are an attractive target to modulate the risk of CRC.

Specific SCFAs, like butyrate, have shown positive results for CRC treatment within model systems (16). Butyrate has been shown to inhibit cancer cell growth in *in vitro* systems (17). Additionally, supplementation with food sources that bacteria use to create these SCFAs may also be able to confer beneficial effects. For example, fiber supplementation in mouse models of CRC caused an overall reduction in tumor burden while also increasing SCFA concentrations (18). Although these model systems provide important preliminary evidence towards the ability of SCFAs to reduce and treat tumors, the studies reporting benefit in humans has been less convincing.

There is a lack of evidence on the benefit of increasing SCFA concentrations to protect against CRC in human populations. The initial case/control studies that investigated SCFA concentrations in CRC found that patients with carcinomas had lower concentrations of acetate, butyrate, and propionate versus either patients with adenomas or individuals without colon tumors (19). Although this would argue that increasing SCFA concentrations could be protective against tumorigenesis, fiber supplementation in randomized controlled trials have consistently failed to protect against tumor recurrence (20). These findings would argue against the utility of treatments that aim to use SCFAs to reduce or protect against tumorigenesis. Given the lack of clear evidence in human

studies of the benefit of SCFAs in CRC, there is a need for more investigation into this area.

Our study fills some of the current gaps in the literature that relate to the study of SCFAs and CRC in human populations. Specifically, it tests previous case/control findings on SCFA concentrations in individuals with and without tumors. We also test previous suggestions that there is a continuous reduction in SCFA concentrations as tumor severity increases by increasing the number of patients with adenomas in our study. Additionally, we build upon these observations and assesses the utility of using SCFAs and Operational Taxonomic Units (OTUs) as a risk stratification tool of colorectal tumors (adenoma or carcinoma). Collectively, this study provides important information on the replicability of previous findings in humans by extensively studying how SCFAs are associated with colorectal tumors.

To accomplish this task we directly measured the concentration of acetate, butyrate, and propionate within fecal samples for two different groups. The first group had a sample obtained at a single cross sectional point in time while the second group had samples obtained before (pre-) and after (post-)treatment for colorectal tumors. Additionally, we (i) assessed the affect adding SCFA concentrations to OTU data had on classification of patients with adenoma or carcinoma using the Random Forest algorithm (21), (ii) used PICRUSt (22) and metagenomic sequencing to assess the presence of genes involved in SCFA synthesis, and (iii) analyzed how well 16S rRNA gene sequencing predicts SCFA concentrations. This investigation provides additional information as to whether SCFAs are decreased in patients with colorectal tumors and provides context as to whether targeting taxa to increase SCFA concentrations is a viable option to protect against colon tumorigenesis.

Results

Decreased SCFA concentrations are not associated with tumors. We used high-performance liquid chromatography (HPLC) to measure acetate, butyrate, and propionate concentrations of frozen fecal samples from 490 individuals at a cross-sectional point in time. There was no difference between individuals without colon tumors (n=172) and patients with either an adenoma (n=198) or carcinoma (n=120) for any of the SCFAs measured after multiple comparison correction (P-value > 0.15) [Figure 1A - 1C]. We next measured the concentration of SCFAs in 67 patients with an adenoma (n=41) or carcinoma (n=26) in which we had pre- and post-treatment fecal samples. Although there was a general trend for increasing acetate, butyrate, and propionate concentrations after treatment for tumors, there was no significant difference pre- and post-treatment for patients with adenoma (P-value > 0.20) or carcinoma (P-value > 0.80) [Figure 1D - 1F]. Even though there was no difference in SCFA concentrations between individuals with normal colons and those with tumors, this information could still be important to help classify disease.

Random Forest models with SCFA concentrations do not classify tumors better. SCFA concentrations could improve prediction of tumors based on specific bacterial community structures. Our OTU data can be used in combination with SCFAs to assess whether there is a community dependent context to SCFA classification of tumors. Using the Random Forest algorithm we built models with OTU abundance data only or OTU abundances and SCFA concentrations to classify normal versus adenoma and normal versus carcinoma fecal samples. For adenoma and carcinoma models, there was no difference between the median AUC of models with or without SCFA concentrations (P-value > 0.05) [Figure 2]. Although including SCFA concentrations did not improve classification of colorectal tumors using Random Forest models, it is possible that the genes for enzymes involved in SCFA synthesis may vary based on the type of colorectal tumor. This would be consistent with previous 16S rRNA gene sequencing results where many taxa associated with SCFA production are decreased (10, 11).

Changes in genes for enzymes involved in SCFA synthesis are not associated with tumors. Using a list of specific genes that are important for the synthesis of SCFAs [Table S1], we looked for differences in gene abundance between individuals without colon tumors and patients with

adenomas or carcinomas. First, using imputed gene relative abundance based on 16S rRNA gene sequencing we found no difference in any of the genes involved with acetate, butyrate, or propionate synthesis (P-value > 0.90) [Table S2]. This similarity between groups is highlighted by visualizing genes important in butyrate synthesis [Figure 3A]. Using a paired Wilcoxon rank-sum test, there also was no difference in imputed gene relative abundance between pre- and post-treatment samples for any genes involved with SCFA synthesis (P-value > 0.70) [Table S3]. Next, we took a subset of these 490 fecal samples (n=85) and used metagenomic sequencing to confirm these results. Like the imputed gene results, metagenomic analysis found that there was no difference in any of the genes involved in SCFA synthesis between individuals without colon tumors (n=29) and patients with adenoma (n=28) or carcinoma (n=28) (P-value > 0.70) [Table S4]. This lack of difference is highlighted when we visualize the results for butyrate kinase [Figure 3B]. These observations provide evidence that gene prevalence does not change due to colorectal tumors.

Expected taxa are associated with higher SCFA concentrations regardless of tumor status. Using OTU data we built Random Forest models to classify higher than median and lower than median SCFA concentrations. Overall, OTU data had a reasonable ability to classify high and low SCFA concentrations [Figure S1A]. However, these models tended to be over fit, suggesting that rarer taxa may be important for this classification [Figure S1A]. The most important OTUs to these models (assessed with mean decrease in accuracy (MDA)) were taxa that are normally associated with SCFA production [Figure S1B]. These results highlight that within our data, SCFA concentrations are associated with taxa known to produce acetate, butyrate, and propionate. Additionally, OTUs associated with these taxa are the most important to models that can classify high and low SCFA concentrations. Overall, our results are robust and do not support the hypothesis that differences in SCFA concentrations are associated with colorectal tumors.

Discussion

The observations from this study do not support the hypothesis that SCFA concentrations are different in individuals with tumors. Whether we directly measured the SCFA concentration or investigated genes associated with their production, no difference could be identified [Figure 1 & 3]. There is an intriguing reason why taxa associated with SCFA production are decreased in CRC but the genes involoved with its' production are not. Mouth-associated microbes such as *Fusobacterium nucleatum* and *Porphyromonas asaccharolytica* have been found to be increased in patients with carcinomas versus individuals without tumors (10, 11, 23). Both of these bacterial species are known to have strains that can produce SCFAs such as butyrate (24). Thus the reason we may be observing no change in genes involved with SCFA synthesis, as well as no change to SCFAs themselves, is because the production is being supported by more inflammatory microbes associated with CRC. Additionally, our observations that no benefit could be found in using the concentrations to help classify individuals with and without tumors would be consistent with this reason [Figure 2]. However, our observations are in stark contrast to some of the previous literature.

Much of the previous research on SCFA benefit to human CRC has been illustrated in model systems (16). Many SCFAs are produced through the breakdown of fiber (14) and a recent study in mice found that fiber supplementation increased SCFA concentrations and decreased tumor burden (18). Additionally, SCFAs such as butyrate can inhibit tumor growth in *in vitro* experiments (17). Yet, observations in humans has been mixed. Previous case/control studies found associations with lower SCFA concentrations in individuals with carcinoma tumors (19). However, individual randomized controlled trials and a recent meta-analysis on fiber supplementation to prevent tumor recurrence has found no benefit (20, 25). Our results align with what has been reported in randomized-controlled trials, that SCFAs do not provide general protection against colorectal tumors. It is possible though that there are specific instances where SCFAs may be beneficial.

One limitation of current research into the effect of SCFAs in CRC has been that all tumors are treated as the same type. However, there are known differences in the types of mutations that occur (26) and treating all tumors as equal may actually hide any benefit that could be found in specific subsets of individuals. Similar to the idea of specific immunotherapy for specific tumors

(27), SCFAs may have beneficial effects for specific types of colorectal tumors. Future research will need to test if this is a valid hypothesis. Another limitation is that a fecal sample may not be an ideal type of biospecimen and that the effect SCFAs have on tumorigenesis is only detected in the colon. However, most *in vivo* studies as well as human studies have used fecal material in their analysis (18, 19). Additionally, studies that measure SCFA changes after fiber supplementation use fecal material to track these responses (28). Although there are limitations with the current research on SCFAs and colorectal tumors, our observations along with the randomized controlled trials on fiber supplementation in tumor recurrence (20) provide evidence that these specific metabolites may not be protective. Yet, taxa that are associated with SCFA production are consistently higher in indivdiuals without colon tumors than patients with carcinomas (10, 11, 23).

The potential protection against colorectal cancers may not be from SCFAs even though taxa associated with their production are higher in individuals without tumors versus patients with carcinomas (10, 11, 23). Protection could be via a different pathway and by extension other metabolites that have not been extensively studied. Alternatively, protection may not occur via a metabolite but instead through niche exclusion of mouth-associated microbes (e.g. *Fusobacterium*, *Porphyromonas*, *Parvimonas*, *Peptostreptococcus* (6, 12, 13)). The idea of niche exclusion is similar to how the community protects against *Clostridium difficile* infection (29) with chronic inflammation replacing the role of antibiotics. Although we did not find lower concentrations of SCFAs associated with colorectal tumors, we think that there are many exciting new avenues to explore because of these results.

Conclusions

Our observations found no difference in SCFA concentration, their utility as a classification tool, or for genes of enzymes involved in SCFA synthesis between individuals without colon tumors and patients with either adenoma or carcinoma tumors. Although these results are different than other reports in the literature, they do align with the randomized controlled trials that have tested fiber use in preventing colorectal tumor recurrence. Overall, these results suggest that the SCFAs typically produced by resident microbes do not protect against tumor. By focusing on other types mechanisms, the identification of more promising therapeutic options for use in treating colorectal cancer may be found.

Materials and Methods

Study design and sampling. The overall protocol has been described in detail previously (30, 31). In brief, this study used fecal samples obtained at either a single cross-sectional time point (n=490) or from before (pre-) and after (post-) treatment of a patient's tumor (n=67). For patients undergoing treatment for their tumor the length of time between their initial and follow up sample ranged from 188 - 546 days. Our use of treatment has been previously defined as encompassing removal of a tumor with or without chemotherapy and radiation (30). Diagnosis of tumor was made by colonoscopic examination and histopathological review of biopsies obtained (30, 31). The University of Michigan Institutional Review Board approved the study and informed consent was obtained from all participants in accordance to the guidelines set out by the Helsinki Declaration.

Measuring specific SCFAs. Our protocol for the measurement of acetate, butyrate, and propionate followed a previously published protocol that used a High-Performance Liquid Chromatography (HPLC) machine (28). The following changes to this protocol included the use of frozen fecal samples suspended in 1ml of PBS instead of fecal suspensions in DNA Genotek OmniGut tubes, and the use of the actual weight of fecal samples instead of the average weight for SCFA concentration normalizations. These methodological changes did not affect the overall median concentrations of these SCFAs between the two studies (see Table 1 (28) and Figure 1 here).

16s rRNA gene sequencing. The workflow and processing have been previously described (30, 32, 33). The major differences from these previous reports include: the use of version 1.39.5 of the mothur software package and clustering Operational Taxonomic Units (OTUs) at 97% similarity using the OptClust algorithm (34).

Generating imputed metagenomes. The use of PICRUSt version 1.1.2 with the recommended standard operating protocol (22) was used. Briefly, the mothur shared file and metadata was converted into a biom formatted table using the biom convert function, the subsequent biom file was processed with the 'normalize_by_copy_number.py' function, and subsequent imputed metagenomes created using the 'predict_metagenomes.py' function.

Obtaining Operational Protein Families from metagenomes. A subset of the cross-sectional

group (n=490) containing a total of 85 individuals (normal n=29, adenoma n=28, and carcinoma n=28) was shotgun sequenced on an Illumina HiSeq using 125 bp paired end reads and a previously described method (35). Briefly, the sequences were quality filtered and sequences aligning to the human genome were removed prior to contig assembly with MEGAHIT (36). Open Reading Frames (ORFs) were identified using Prodigal (37), counts generated using Diamond (38), subsequent clustering into Operational Protein Families (OPFs) used mmseq2 (39), and OPF alignment used the KEGG database (40).

Pulling genes involved with SCFA synthesis. Specific genes located near the end of the pathways involved in the synthesis of acetate, butyrate, and propionate were analyzed for any differences between individuals with normal colons and those with tumors. These genes were based on pathways from KEGG as well as previous research (40, 41) and a list can be found in the supplemental material [Table S1].

Random Forest models. The model was first trained on 80% of the data and then tested on the held out 20% (80/20 split) using the Random Forest algorithm for classification models (21). This was repeated on 100 different 80/20 splits of the data to generate a reasonable range for the AUC of the model. The reported AUCs, unless otherwise specified, are for the test sets. The classification models were built to group normal versus adenoma, normal versus carcinoma, and high versus low SCFA concentrations.

Statistical analysis workflow. All analysis was performed using the statistical language R (42). Generally, a Kruskal-Walis rank sum test with a Dunn's post-hoc test was used to assess differences between the groups used. Where appropriate Benjamini-Hochberg was used to correct for multiple comparisons (43). First, we assessed differences in SCFA concentrations measured by HPLC between individuals with normal colons and patients with tumors (adenoma or carcinoma). We then analyzed whether SCFA concentrations changed in patients with an adenoma or carcinoma pre- versus post-treatment. Next, we assessed whether OTUs alone or OTUs and SCFAs were better able to classify individuals with and without tumor using Random Forest models. Next, the imputed gene counts of important mediators of SCFA synthesis was tested. Additionally, the counts generated for OPFs that matched important genes involved with SCFA creation were analyzed.

Finally, models to classify high or low SCFA concentration based on the median of each SCFA and 16S rRNA gene sequencing data was created using the Random Forest algorithm.

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Figure 1. No change in SCFA measurements was observed between normal, adenoma, and carcinoma individuals using HPLC. Acetate concentrations in fecal samples of individuals without colon tumors, adenomas, and carcinomas (A). Butyrate concentrations in fecal samples of individuals without colon tumors, adenomas, and carcinomas (B). Propionate concentrations in fecal samples of individuals without colon tumors, adenomas, and carcinomas (C). The black lines indicate the median SCFA concentration. Acetate concentrations in fecal samples before and after treatment for adenoma (yellow) and carcinoma (red) (D). Butyrate concentrations in fecal samples before and after treatment for adenoma (yellow) and carcinoma (red) (E). Propionate concentrations in fecal samples before and after treatment for adenoma (yellow) and carcinoma (red) (F). The black dots and lines represent the median change in SCFA concentration.

Figure 2. SCFAs do not improve OTU-based Random Forest models. The area under the curve of 100 different 80/20 split OTU-based normal versus adenoma 10-fold CV models with and without SCFAs (A). The area under the curve of 100 different 80/20 OTU-based normal versus carcinoma 10-fold CV models with and without SCFAs (B). The black line represents the median AUC. The dotted line highlights an AUC of 0.5.

Figure 3. No change in butyrate producing genes identified between normal, adenoma, and carcinoma individuals. Imputed gene relative abundance of important butyrate pathway genes using PICRUSt (A). Counts per million (corrected for size and number of contigs in an OPF) for the Butyrate Kinase gene (B). The other butyrate pathway genes from the PICRUSt analysis did not align to any of the OPFs in the metagenome analysis.

Figure S1. OTU-based Random Forest models of SCFA concentrations. The train and test results of 100 different 80/20 OTU-based models with 10-fold CV based on higher or lower than the median SCFA concentration using classification Random Forest (A). The top 10 OTUs based on mean decrease in accuracy (MDA) for each model, colored by their lowest taxonomic identification (B).