The Microbiota and Individual Community Members in Colorectal Cancer: Is There a Common Theme?

Marc A Sze[1] and Patrick D Schloss[1†]

† To whom correspondence should be addressed: pschloss@umich.edu

1 Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI

Co-author e-mails:

- marcsze@med.umich.edu

Abstract

Background.

Results.

Conclusions.

Keywords

Results

Fecal Diversity is Lower in Those with Carcinoma and Increases Relative Risk:
Using power transformed and Z-score normalized alpha diversity metrics both evenness
and the Shannon diversity metrics in feces are lower in those with carcinoma then in
controls but not for tissue samples [Figure 1]. Using linear mixed-effects to control for study
and variable region there was a significant decrease from control to adenoma to carcinoma
for both evenness (P-value = 0.025) and Shannon diversity (P-value = 0.043). This effect
was not observed in tissue when additionally controlling for whether the sample came from
the same individual (P-value > 0.05). For fecal samples a decrease in Shannon diversity
and evenness resulted in a significantly increased relative risk for carcinoma (P-value =
0.01 and P-value = 0.0011, respectively) [Figure 2]. Although these values were significant
the effect size was relatively small for both metrics (Shannon RR = 1.31 and evenness RR
= 1.34) [Figure 2]. There was no increased relative risk for these metrics for adenoma or
for tissue in general [Figure S1-3].

Using the Bray-Curtis distance metric, the fecal microbiota did not have a different
community diversity between adenoma and control but did for carcinoma across studies
[Table S1 & S2]. The majority of unmatched tissue samples had a significant difference for
both adenoma and carcinoma versus controls [Table S3 & S4]. All matched tissue samples
accross studies had no difference between any of the compared groups [Table S3 & S4].

*Genera Previously Associated with Carcinoma Increases Relative Risk More than
Alpha Diversity:* Both fecal and tissue samples had a significantly increased RR for
carcinoma but not for adenoma [Figure 3] which was greater than either evenness or
Shannon diversity [Figure 2 & 3]. The relative risk did not increase when considering the
total abundance or increasing number of carcinoma associated genera [Figure 3]. The RR
effect size was greater for stool (RR range = 1.78 - 2.64) then for tissue (RR range = 1.33 -

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33 1.53) . This decrease may be explained by the fact that tissue samples include matched

34 samples.

35 ***Using the Whole Community Increases Model AUC:*** For both fecal and tissue samples

36 (matched and unmatched) there was a decrease in AUC when only OTUs from the CRC

37 associated genera are used [Figure 4 & 5]. This decrease is observed in both adenoma

38 and carcinoma groups [Figure 4 & 5]. The genus models generally had similar trends

39 as observed for the OTU based models with the full genera models performing better

40 then the CRC associated genera models [Figure S4-S5]. Both genus models perform

41 similarily in their ability to be able to predict lesion (adenoma or carcinoma) with carcinoma

42 having a higher AUC then adenoma [Figure S6-S8]. Matched tissue samples for those

43 with carcinoma had an AUC that was more similar to the adenoma models [Figure S6A,

44 S7B, & S8] then carcinoma models [Figure S6B & S7A].

45 ***Majority of Studies are Underpowered for Detecting Small Effect Size Differences:***

46 When assessing the power of each study at different effect sizes the majority of studies for

47 both adenoma and carcinoma have an 80% power to detect a 30% difference [Figure 6A &

48 B]. No single study that was analyzed had the standard 80% power to detect a difference

49 that was eqaul to or below 10% [Figure 6A & B]. In order to achieve adequate power for

50 small effect sizes it would be necessary to recruit over 1000 individuals for each arm of the

51 study [Figure 6C].

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52 **Discussion**

53 **Conclusion**

Methods

Obtaining Data Sets: Studies used for this meta-analysis were identified through the review articles written by Keku, et al. and Vogtmann, et al. [1,2]. All studies were included that used tissue or feces as their sample source for 16S rRNA gene sequencing analysis. Studies using either 454 or Illumina sequencing technology were included. Only data sets that had the raw sequences available for analysis were included. Some studies did not have publically available raw sequences or did not have meta data in which the authors were able to share. After this filtering step the following studies remained: Ahn [3], Baxter [4], Brim [5], Burns [6], Chen [7], Dejea [8], Flemer [9], Geng [10], Hale [11], Kostic [12], Lu [13], Sanapareddy [14], Wang [15], Weir [16], and Zeller [17]. The Zackular [18] study was not included becasue the 90 individuals analyzed within the study are contained within the larger Baxter study. The Kostic study was not used since after sequence processing all the case samples did not have more than 100 sequences remaining. This left a total of 13 studies in which complete analysis could be completed.

Data Set Breakdown: In total there were 7 studies with only fecal samples (Ahn, Baxter, Brim, Hale, Wang, Weir, and Zeller), 5 studies with only tissue samples (Burns, Dejea, Geng, Lu, Sanapareddy), and 2 studies with both fecal and tissue samples (Chen and Flemer). The total number of individuals initially run through the sequence processing for the fecal samples was 1899 and for the tissue samples was 462.

Sequence Processing: For the majority of studies raw sequences were downloaded from the SRA (ftp://ftp-trace.ncbi.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/) and metadata was obtained from the following website: http://www.ncbi.nlm.nih.gov/Traces/study/ by searching the respective accession number of the study. Of the studies that did not have sequences and meta data on the SRA one study had the data stored on DBGap [3] and four studies the data was obtained directly from the authors [9,11,14,16]. Each

study was processed using the mothur (v1.39.3) software program [19]. Where possible quality filtering utilized the default methods used in mothur for either 454 or Illumina based sequencing. If it was not possible to use these defaults the author stated quality cut-offs were used instead. Chimeras were identifed and removed using the VSEARCH [20] program and *de novo* OTU clustering at 97% similarity using the OptiClust algorithm [21] was utilized.

Statistical Analysis: All statistical analysis after sequence processing utilized the R software package (v3.4.2). For the alpha diversity analysis values were power transformed using the rcompanion (v1.10.1) package and then Z-score normalized using the car (v2.1.5) package. Testing for alpha diversity differences utilized linear mixed-effect models created using the lme4 (v1.1.14) package to correct for both study and variable region effect in the diversity measures when analyzing colorectal cancer groups. Relative Risk was analyzed using both the epiR (v0.9.87) and metafor (v2.0.0) packages. Relative risk significance testing utilized the chi-squred test. Beta-diversity differences utilized a Bray-Curtis distance matrix and PERMANOVA executed with the vegan (v2.4.4) package. Random Forest models were built using both the caret (v6.0.77) and randomForest (v4.6.12) packages. Random Forest testing of the obtained AUC versus a random model AUC utilized T-tests. Power analysis and estimations were made using the pwr (v1.2.1) and statmod (v1.4.30) packages. All figures were created using both ggplot2 (v2.2.1) and gridExtra (v2.3) packages.

Study Analysis Overview: Alpha diversity was first assessed for differences between controls and adenoma versus cancer and controls versus adenoma. We analyzed the data using linear mixed-effect models, and relative risk. Beta-diversity was then assessed for each inidividual study. Next, four specific CRC-associated genera (*Fusobacterium*, *Parvimonas*, *Peptostreptococcus*, and *Porphyromonas*) were assessed for differences in relative risk. We then built Random Forest models based on all genera or the select

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CRC-associated genera. The models were trained on one study then tested on the remaining studies for every study. The data was split between feces and tissue samples. Within the tissue groups the data was further divided between matched and unmatched tissue samples. Both prediction for adenoma and carcinoma were tested. This same approach was then applied at the OTU level with the exception that instead of testing on the other studies a 10-fold cross validation was utilized and 100 different models were created based on random 80/20 splitting of the data to generate a range of expected AUCs. For OTU based models the CRC Associated Genera included all OTUs that had a taxonomic classification to *Fusobacterium*, *Parvimonas*, *Peptostreptococcus*, or *Porphyromonas*. The power of each study was assessed for and effect size ranging from 1% to 30%. An estimated sample n for these effect sizes was also generated based on 80% power.

Reproducible Methods: The code and analysis can be found here https://github.com/ SchlossLab/Sze_CRCMetaAnalysis_Microbiome_2017. Unless mentioned otherwise the accession number for the raw sequences for the studies used in this analysis can be found directly in the respective batch file, on the GitHub repository or in the original manuscript.

Declarations

Ethics approval and consent to participate

Ethics approval and informed consent for each of the studies used is mentioned in the respective manuscript used in this meta-analysis.

Consent for publication

Not applicable.

Availability of data and material

A detailed and reporducible description of how the data were processed and analyzed for each study can be found at https://github.com/SchlossLab/Sze_CRCMetaAnalysis_Microbiome_2017. Raw sequences can be downloaded from the SRA in most cases and can be found in the respective studies batch file in the GitHub repo or within the original publication. When sequences were not publicly available contacting the corresponding author for raw sequences needs to be undertaken.

Competing Interests

All authors declare that they do not have any relevant competing interests to report.

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Authors' contributions

All authors helped to design and conceptualize the study. MAS identified and analyzed the data. MAS and PDS interpreted the data. MAS wrote the first draft of the manuscript and both he and PDS reviewed and revised updated versions. All authors approved the final manuscript.

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209 **Table 1:**

210 **Figure 1:**

211 **Figure 2:**

212 **Figure 3:**

213 **Figure 4:**

214 **Figure 5:**

215 **Figure 6:**

216 **Figure S1:**

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