

Multi-omic vaginal microbiome profiling reveals bacterial vaginosis subtypes

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Abstract

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Introduction

One major challenge of microbial investigation is to determine the role of the microbiome in the environment . We can divide microbiome analyses into categories of increasing resolution that correspond to the question answered: ‘who is there’ can be addressed by 16S rRNA gene sequencing (or other target gene sequencing method); ‘what is the capacity of the microbiome’ can be addressed by full metageomic sequencing or by an extrapolation method; ‘what have they produced’ can be addressed by small molecule profiling (metabolomics); and ‘what are they doing now’

can be addressed by transcriptome profiling. The vast majority of microbiome analyses are designed to address the first question, and more recently methods have been developed to estimate the second question from target gene sequencing profiles. It is widely recognized that these two approaches are largely descriptive. However, the ability to address the latter two questions is less widespread because of their high complexity in both sample collection and in the analysis.

Amy - an introductory paragraph on metabolome

There are several barriers to collecting and analyzing whole microbial community transcriptomes (meta-transcriptomes). First, RNA is a much less stable molecule than DNA, and a significant fraction of microbial genes have a half-life under two minutes, and almost all have a half-life less than 10 minutes [1, 2]. Thus, careful sample collection and storage is extremely important to preserve the integrity of the sample. Second, unlike DNA abundance, RNA abundances are not necessarily tied to organism abundance because RNA production is induced or repressed in response to environmental cues. Thus, any method that discriminates based on the abundance of an RNA molecule will be at risk of confounding the effect of organism abundance with the abundance of the RNA species. The wide dynamic range of RNA abundances also makes assembly of the sequencing output problematic since many assembly algorithms assume a somewhat constant read coverage. Third, many RNA-seq experiments have a very high background of reads that do not map or assemble into sensible contigs: the origin of these phantom reads is unknown, but they greatly reduce the amount of information available on a meta-transcriptome at all sequencing depths. These constraints mean that many meta-transcriptome experiments yield less information than expected, and in some cases.

A final issue is that high-throughput sequencing data are compositional: that is, they are constrained to an arbitrary constant sum [3–5]. Compositional data have the property of linked correlations. This means that as one feature (gene or organism) becomes more abundant, one or more others *must* become relatively less abundant. This can be seen easily in the trivial example of a two part component $x = [1, 9]$ that originally has 10 parts and the two parts are partitioned such that $x_1=10\%$ and $x_2=90\%$. If, for example, the first part increases, $x_1 \rightarrow 9$, and the second part remains unchanged then the two parts are now partitioned such that $x_1=50\%$ and $x_2=50\%$. Note that it appears that x_2 has become less abundant, when in fact it has remained unchanged.

The problem of compositional data analysis is general no matter the number of features (genes or organisms), and results in the problem of spurious correlation: where changing the membership of a composition by adding or removing one or more features, changes the correlation structure in unpredictable ways [6]. In many cases, the sign of correlation between features can change from strongly positive to strongly negative [3, 5]. This means that the observed correlations depend on group membership and not on any intrinsic correlation. There is not a current consensus on how to deal with this problem, and groups have attempted to minimize the problem [3, 7] or to approach the problem analytically [5]. Spurious correlation is very problematic because many multivariate tools such as ordination, principle component analysis and clustering are dependent upon it.

The problem of spurious correlation was recognized very early by Pearson [8], yet a general solution was not elaborated until Aitchison suggested a log-ratio approach [6]. The approach advocated by Aitchison was to convert the data into ratios between the features and then to take the logarithm to make the data symmetrical such that the choice of numerator or denominator would change only the sign, and not the absolute value of the result. Since then, much work has been done to place this approach onto a firm theoretical and practical foundation (e.g.. [9–12]), although these methods have

only recently begun to be noticed and used by biologists [3–5, 7, 13, 14].

A final complication is that the measurement error of compositional data is different than that expected for non-compositional data being non-linearly related to the read depth [4]. In fact, the measurement error is inversely and

It has been argued that that microbial communities are best thought of as ensembles of genes since the genetic makeup of individual bacterial genomes is rather fluid.

Materials and Methods

Ethics.

Collection.

Metabolome determination.

RNA isolation and sequencing.

Data analysis.

Read Mapping. XX genomes comprising the set of species observed in the human vagina from 16S rRNA gene sequencing (REFS), culture studies (REFS) and additional genomes from organisms suspected to occur were downloaded from Genbank on ?????. Open reading frames from these genomes were clustered using ?? with the following criteria (length, PID, etc) and a representative sequence was chosen to be the centroid using the following rule: ????. Centroid sequences were annotated by BLAST to SEED and KEGG databases and the best hit supplying the annotation. The taxonomy of the centroid sequences was taken to represent the taxonomy of the cluster. We will refer to the centroid sequence as the ‘transcript’. Supplementary Table S1 contains the list of accession numbers. Supplementary Table S2 contains the set of centroid sequences and their inferred annotation.

Reads in fastq format were mapped to the library of centroid sequences using bowtie2 [16] and unmapped reads were assembled with ????. The assembled fragments were annotated as above, and added to the master table of counts per sequence feature in each sample. In the end there were an average of XXX million reads mapped to each sample, and Table S3 contains the pertinent information. Reads were further grouped by KEGG function or SEED level 4 subsystem to produce two tables of functions, these will be referred to as ‘functions’.

Statistical Model for RNA-seq. The table of counts mapped to reference sequences, and aggregated to either the SEED subsystem or KEGG KO level, appears on the surface to be a table of counts. Common practice is to normalize the reads per feature such that the ‘sequencing effort’ is a constant or each sample [17]. However, we have found this approach fails in meta-RNA sequencing because of the interplay between the organism and transcript abundance [4, 5, 18]. Thus, it much more informative to model the observed count for a feature in a sample as a distribution of probabilities that the count was observed given the total number of sequence reads obtained per sample [4]. Such a model falls into the count compositional data analysis paradigm [6] where only the relative differences between abundances in a sample are informative [9, 19]. Upon reflection, this approach makes intrinsic sense because the number of reads obtained in any high throughput sequencing experiment is constrained by the capacity of the instrument. We know intuitively that the same library will give a more accurate depiction of reality with the ~ 200 million reads obtained from a HiSeq lane than with the ~ 20 million reads obtained from a MiSeq.

Compositional data has substantially different properties than do unconstrained data. The most important being that compositional data exhibits ‘spurious correlation’ between features because the possible values for the features are constrained by the constant sum [9,19]. Correlations are also unreliable because they change in unpredictable ways when a subset of the parts are examined. Thus, traditional correlation metrics are unsuitable when examining these data [5]. Note that all RNA-seq datasets are subcompositions unless ribosomal RNA, tRNA, etc are not depleted and are included in the analysis [9,19].

Some of these problems can be ameliorated by log-ratio transformations such as the centered log-ratio transformation (clr). Given a vector of numbers that contains D features, $x = [x_1, x_2, \dots, x_D]$, x can be converted to a vector of clr values, z , as follows:

$$\text{clr}(x) = \left(\ln \frac{x_1}{g_x}, \ln \frac{x_2}{g_x}, \dots, \ln \frac{x_D}{g_x} \right) = (z_1, z_2, \dots, z_n) . \quad (1)$$

Where g_x is the geometric mean of vector x .

One complication is that the geometric mean cannot be computed when the x contains a value of 0. Thus two approaches were taken. First, when a point estimate was required the ‘count zero multiplicative’ zero replacement method from the zCompositions R package [20] was used to adjust 0 values for the likelihood that the 0 represents a non-detect event in the sample. Second, when conducting quantitative analyses, the joint probability distributions for all features in a sample were generated by Dirichlet multinomial sampling within the ALDEx2 Bioconductor R package [4] using a uniform adjustment of Jeffrey’s Prior. This returns a distribution of possible values for the probability of the feature given the feature count and the total count for the sample [4,21]. We have shown previously that the relative error in these probability distributions is largest for features with 0 counts and smallest for those with the largest number of counts in both real and simulated data [4]. The distributions were subsequently transformed using the centre log-ratio transformation prior to further analysis.

Exploratory data analysis was performed as point estimates with compositional biplots [22] following clr transformation of the data. These show both the distances between samples and the variances of the transcripts.

The expected value of ϕ [5] from the clr distribution was used to determine compositionally-linked transcripts or functions, since it has been shown that traditional correlation metrics give unpredictable results [9,19]. The expected value of Kendall’s Tau (b) was used when reporting the correlation between transcript abundance and metabolite abundance since it is not expected that the metabolome and meta-transcriptome tables share even passingly similar units or scaling. We used an effect size cutoff of 2 when evaluating differential abundance between conditions, a cutoff that was used in our previous investigations [13].

Sample preparation GC-MS. Samples were collected from the mid-vaginal wall using the Cytobrush vaginal brush and sterile forceps and stored at -80°C until analysis. Vaginal brushes were pre-cut into 1.5 mL tubes and weighed prior to and after sample collection to determine the mass of vaginal fluid collected. After thawing, brushes were eluted in methanol-water (1:1) to a final concentration of 0.05 g/mL. This corresponded to a volume of 200-1500 μL , depending on the mass of vaginal fluid collected. Four control swabs were included which consisted of blank swabs eluted in 200, 400, 800, or 1500 μL of methanol-water. Samples and controls were vortexed for 10 sec to extract metabolites, centrifuged for 5 min at 10 000 rpm, vortexed again for 10 sec after which time the brushes were removed from tubes. Samples were centrifuged a final time to pellet cells and 150 μL of supernatant transferred to

GC-MS vials. Remaining supernatant was transferred to a new 1.5 mL tube, frozen at -80°C and shipped to the University of Reading for NMR analysis. Next, 25 µL of 0.2 mg/ml ribitol standard was added to each GC-MS vial. Samples were then dried to completeness using a SpeedVac. After drying 100 µL of 2% methoxyamine-HCl in pyridine (MOX) was added to each sample for derivatization and samples were incubated at 500°C for 90 min. 100 µL N-Methyl-N-(trimethylsilyl) trifluoroacetamide (MSTFA) was then added to each vial and incubated at 500°C for 30 min. After derivitization, an equal aliquot of each sample was combined to make the quality control (QC). Samples were then transferred to micro inserts before analysis by GC-MS (Agilent 7890A GC, 5975 inert MSD with triple axis detector). One µL of sample was injected using pulsed splitless mode into a 30 m DB5-MS column with 10 m duraguard, diameter 0.35mm, thickness 0.25 µm (JNW Scientific). Helium was used as the carrier gas at a constant flow rate of 1 mL/min. Oven temperature was held at 70°C for 5 min then increased at a rate of 5°C/min to 300°C and held for 10 min. Solvent delay was set to 13 min to avoid solvent and a large lactate peak, and total run time was 61 min. Masses between 25 m/z and 600 m/z were selected by the detector. All samples were run in random order and the QC was run multiple times throughout the run to ensure machine consistency.

Data analysis GC-MS. Chromatogram files were de-convoluted and converted to ELU format using the AMDIS Mass Spectrometry software [23] with the sensitivity set to medium. Chromatograms were then aligned and integrated using Spectconnect [24] software with the Support Threshold set to low. All metabolites found in the blank swab, or believed to have originated from derivatization reagents were removed from analysis at this time. After removal of swab metabolites, the IS matrix from Spectconnect was transformed using the additive log ratio transformation (alr) and ribitol as a normalizing agent, $\log_2(x)/\log_2(\text{ribitol})$. Zeros were replaced with two thirds the minimum detected value on a per metabolite basis prior to transformation. All further metabolite analysis was performed using these alr transformed values.

A total of 90 metabolites were detected by GC-MS. Upon inspection it was determine that 50 of these metabolites were either redundant, background noise or present in controls and were removed from analysis. For redundant peaks, the sum of each peak was combined resulting in a single value for each metabolite. Metabolites were initially identified by comparison to the NIST 11 standard reference database (<http://www.nist.gov/srd/nist1a.cfm>). Identities of metabolites of interest were then confirmed by authentic standards if available.

Independent Wilcox tests with a Benjamini-Hochberg correction to account for multiple testing were used to determine metabolites that differed significantly between healthy and BV ($p < 0.10$). Groups were defined as healthy or BV using a percentage *Lactobacillus* cutoff of 75%

Sample preparation NMR. Samples were dried to completeness and resuspended in phosphate buffer saline (pH 7) containing sodium azide and the internal standard Trimethylsilyl propanoic acid (TSP). Samples were run on a Bruker 700 MHz cryoprobe spectrometer. A standard one-dimensional NMR spectrum was acquired for each sample with water peak suppression using a standard pulse sequence (recycle delay (RD)-90 -t1-90 -tm-90 -acquire free induction decay(FID)). The RD was set at 2 s and the mixing time (tm)100 ms. The pulse length was approximately 12 µs and t1 was set to 3 µs. For each sample, 8 dummy scans were followed by 64 scans and collected in 64 K data points using a spectral width of 20 ppm and an acquisition time per scan of 2.73 s.

Data analysis NMR. Spectra were processed according to the methods of Swann et al 2011 [25] with the following modifications. ¹H NMR spectra were manually corrected for phase and baseline distortions and then referenced to the TSP resonance at $\delta 0.0$. Spectra were digitized using an in-house MATLAB (version R2009b, The Mathworks, Inc.; Natick, MA) script. To prevent baseline effects that arise from imperfect water saturation the region containing the water resonance was excised. An in-house peak alignment algorithm was then performed on each spectrum in MATLAB to adjust for shifts in peak position due to small pH differences between samples and then each spectrum was normalized using a sum normalization approach. Principal components analysis (PCA) using pareto scaling was applied in SIMCA (Umetrics, Umea). Orthogonal projection to latent structure discriminant analysis (OPLS-DA) models were constructed using unit variance scaling to aid the interpretation of the model and distinguish the metabolites that differed between the groups. Here, ¹H NMR spectroscopic data were used as the descriptor matrix and class information (N or BV) as the response variable. The contribution of each variable (metabolite) to sample classification was visualized by back-scaling transformation, generating a correlation coefficient plot. These coefficient plots are colored according to the significance of correlation to “class” (e.g. N or BV), with red indicating high significance and blue indicating low significance. The direction and degree of the signals relate to covariation of the metabolites with the classes in the model. For all models, one orthogonal component was used to remove systematic variation unrelated to class. Predictive performance was assessed using the Q^2 parameter.

Reproducibility. All R code needed to reproduce this analysis from the count tables can be accessed at: [github...](#)

Results and Discussion

High throughput sequencing experiments generate datasets where the total number of reads per sample are irrelevant, thus these data are compositional and contain only relative information about abundances [18]. Such data can be examined in a rigorous manner by examining the variation in ratios between all pairs of transcripts [6,9,19]. However, this can be dramatically simplified using the centre log-ratio transformation, which reduces each count value to a ratio of that count to the geometric mean count within each sample. The logarithm of the ratio makes any change in relative abundance symmetrical. The clr transformation is functionally equivalent to a matrix of all vs all ratios, and compensates for differences in read abundance, thus eliminates the need for count normalization [5]. We and others have shown that clr-transforming the data constitutes the first step towards a compositional data analysis approach that is generally useful to characterize HTS [3–5,18]. All data analysis is thus done in a compositional analysis framework with clr-transformed data as outlined in the Materials and Methods.

0.1 Exploratory analysis

We collected NN samples for RNA-seq and metabolomic analysis, and MM were sequenced on the Illumina HiSeq platform at The Centre for Applied Genomics in Toronto. We also included in the RNA-seq results four samples sequenced using the ABI SoLiD platform and reported previously [13]. We examined these samples using taxonomic abundance profiles determined both from 16S rRNA gene sequencing and from the reference sequence abundance; using compositional biplots and unsupervised clustering on clr-transformed data; and by correlating the samples with the clinical

phenotype. In the end, we excluded six samples (Supplemental Text) since they had either a very distinctive taxonomic abundance profile or had a microbiome profile did not match the clinical phenotype. This left 22 samples for RNA-seq analysis composed of three samples sequenced by ABI-SoLid and 19 sequenced by Illumina HiSeq. The table of counts for the twenty-two samples were filtered to remove all transcripts with an average of 2 or fewer reads across all 22 samples, this simplified the dataset from 48000 transcripts to 10052 transcripts.

Figure ?? shows ...

A compositional biplot of this dataset is shown in Fig. 1A. Compositional biplots summarize in one plot both the relationships between the samples and the contributions of the variables to those relationships [22]. In this plot, the distance of a transcript from the origin is related to the standard deviation of the clr value of the transcript in the samples: it is *not* directly related to the absolute abundance of the transcript. The direction of the transcript relative to the samples shows the sample group with the greatest abundance of the transcript. Our ability to interpret the distance and direction information is only as good as the projection of the PCR, which is determined by the proportion of variance explained on the plot. The biplot in Figure 1 explains 47.7% of the variance on PC1 and 11.2% of the variance on PC2. We conclude that this representation is a good one since these two principle components explain nearly 60% of the variance in such a large dataset.

There are several features of the data that can be gleaned. First, we can see that the samples partition nicely into two groups, healthy on the left and BV on the right. This separation is driven by several taxa known to be associated with health (*Lactobacillus* species) on the left and of BV furthest to the right (non-lactobacillus anaerobes). Interestingly, transcripts annotated as belonging to *Lactobacillus iners* are near the middle of PC1, indicating that transcripts associated with this organism contribute little to the health-BV separation. Within BV, we observe that *Megasphaera* and *Prevotella* species form two distinct foci suggesting the presence of distinctive species or strains of these organisms in BV. Interestingly, for *Megasphaera* one of these foci is very close to the origin on PC1, suggesting that this strain or species is contributing little to the overall BV phenotype. Finally, several de-novo assembled transcripts appear to be major contributors to the BV phenotype.

We next observe that there are potential groups of healthy and of BV samples that separate along PC2. The first healthy group, H1, is composed of samples 30S, 4S, 1B, 9B, and 10B. The second healthy group, H2, is composed of samples 2B, 4B, 0B, 1A and 6B. The first BV group, BV1, is composed of samples 16B, 27S, 14B, 13A, 8A, 17B, 18B, 12B, and the second, BV2, is composed of samples 9A, 6A, 10A and 12A. The reason for these groupings is obvious when we examine the taxonomic origin of each transcript. Here we must recall that there is *no information* regarding absolute abundance for a transcript and that two transcripts with widely varying absolute abundances but similar ratio abundances will have similar locations on the biplot. Inspection of the location of the transcripts in the biplot indicates that they are largely separable by taxonomy. Transcripts mapping to *Lactobacillus crispatus* furthest to the left and near the bottom correspond to the H1 group. Transcripts derived to the remaining lactobacilli are more closely associated with the H2 group. Such a split has been observed before, and group H1 corresponds to vaginal community state type 1 [26]. The samples in H2 are much less homogenous than those in H1, and correspond to a mixture of community state types two through 4.

The BV1 group is associated with an increased ratio abundance of *Leptotrichia* sp., one *Megasphaera* and one *Prevotella* species and the unmapped assembled transcripts. The BV2 group is more associated with *L. iners*, *Gardnerella vaginalis* and the other strain or species of *Prevotella* sp. and *Megasphaera* sp.

We note that the major lactobacillus groups separate much more strongly on PC2 than do the taxa associated with BV. This could indicate that healthy microbiotas colonized by a near monoculture of one or the other lactobacillus species have distinct ways of being healthy, or it could be an artefact of the non-overlapping gene content of these organisms. The partitioning of different lactobacillus dominated healthy microbiota types is well documented in the literature [26–28] and we did not examine this further. However, it is rarely observed that the microbiota of the BV condition partitions in a meaningful way, and we examine the causes of this in a later section.

Figure 1. Exploratory analysis of the reference sequence transcripts.

Compositional biplots of the reference sequence transcripts filtered to include transcripts present at an average count of more than 2 reads per sample. Compositional biplots are Principle Component (PC) Plots generated from the singular value decomposition of the centre log-ratio transformed dataset [22]. The bottom and left axes show the unit scaled measures for PC1 and 2, and the top and right axes show unit scaled variances for the transcripts. These plots thus show the relationship between sample distance along with the contribution of the transcripts to that distance. In this plot component 1 and 2 explain over 58% of the variance in the dataset, which is exceptional for a dataset of this complexity. Sample names are shown in black text. The location of each transcript is shown as a coloured point, with the colors corresponding to the taxonomic assignment of the centroid sequence. The second panel shows a blow-up of the area of the biplot on the right side. Taxa are labeled with the color corresponding to the points and the following legend: Lc-*L. crispatus*, Li-*L. iners*, Lje-*L. jensenii*, Ljg-*L. johnsonii* or *L. gasseri*, Gv-*G. vaginalis*, Me-*Megasphaera* sp., Pr-*Prevotella* sp., AS- assembled transcripts.

Not surprisingly, the reference sequence-based biplot shows that taxonomic abundance is the major driver of the variation of transcript abundance between samples. We were interested to determine if the different states had different underlying functions regardless of the taxonomic composition. Thus the reads were grouped by SEED subsystem 4 function or by KEGG function and Fig. ?? shows the result. Here we can see that the functions partition more strongly along the major axis of variance with 56.2% of the variance explained on PC1, and 8.5% on PC2 when aggregated by SEED subsystem and 57.3% and 8.6% when aggregated by KEGG function. Thus the first two components explain at least 64% of the variance regardless of the functional classification used. We observe that in both cases the samples group into the same four groups as observed for the non-aggregated data. This indicates that the observed splits are robust to aggregation of the data, and are not simply driven by changes in taxonomic abundance. Samples composing the healthy group on the left side of the biplot are associated with a relatively small set of functions that are proportionally increased in these samples, and the samples composing the BV group are associated with a large set of functions that are proportionally increased in the BV samples. The large number of functions with small variance indicates the presence of a core set of functions that are required regardless of condition. The health and BV samples also partition along PC2 similarly to the partitioning seen in Panel A.

We note that that the majority of functions are at or near the origin with the greatest density being near -5 on PC1. A limitation of the a centered log-ratio approach, or indeed of any ratio-based approach is that the geometric mean of a sample depends on the density of 0 values in the sample. Samples will have a high density of 0 values in the group that has fewer expressed genes. The H1 and H2 group samples, composed of *Lactobacillus* species will have a much smaller set of functions than will the BV1 and BV2 groups that comprise a mixed bag of organisms, and which generally include at least some functions found only in *Lactobacillus*. Thus the

geometric mean for the H groups will be closer to 0 than will the geometric mean for the BV group samples, and the resulting ratio values will be higher.

0.2 Exploring differential abundance

Traditional statistical approaches, while widely used, are inappropriate when examining compositional abundances using the ϕ metric that assesses the stability of the abundance ratios across samples for all possible pairs of transcripts [5]. Samples that have stable ratios are said to be compositionally associated and have a value of ϕ near 0.

As with any compositional data analysis approach, values of 0 are not compatible with the transformation required. In the original paper, the authors removed from analysis all genes that had a 0 count in any sample and then calculated the clr and ϕ as point estimates. We took a different approach and estimated the distribution of values that 0 could reasonably assume and then clr-transformed the data using the `aldex.clr` function from the ALDEx2 Bioconductor package [4, 18]. The ϕ measure was then calculated for each independent element of the distribution and the expected value of ϕ was reported. This approach allowed us to determine reasonable estimates for compositional association values even for functions with a dichotomous distribution, while still maintaining a low false positive background.

Figure 2 shows a graphical depiction of ϕ groupings determined for the SEED subsystem 4 functional grouping and the KEGG functional grouping. In both approaches, there were four major clusters that partitioned on PC1, and Supplementary Tables 3 and 4 contain the clusters of SEED subsystem 4 and KO annotations. The first group, composed of XX members was the small group of functions that were much more relatively abundant in the healthy than in the BV group. Inspection of these functions shows that they are belong to ????. These same functions were generally observed to be differentially abundant in our previous analysis (REF). The second group which is nearer the origin was also relatively more abundant in health than in BV, and were found to correspond largely to replication and gene expression housekeeping genes. This confirms our previous observation that these abundant housekeeping genes are slightly increased relative to the remainder in the healthy microbiome. The third major group had a much greater relative abundance in BV than in health. These functions are largely functions that are absent in lactobacilli and correspond to functions involved in the greater biosynthetic and respiratory capacities of the majority of the BV-associated organisms (REF). In addition to the three major groups, there were a number of smaller clusters. These were generally found to correspond to functions in the same pathway or in many cases to co-expressed subunits. A full list of functions and their associated group is found in tabular format in the supplement.

Figure 2. Compositional association of microbial functions. Panel A shows a compositional biplot of the SEED subsystem 4 aggregated data with different groups of compositionally associated transcripts coloured by group membership. Panel B shows the same for data aggregated and analyzed by KEGG annotation. In both cases we determined the expected value of ϕ with a cutoff of 0.03.

Acknowledgments

The VOGUE Research Group is Deborah Money, Alan Bocking, Sean Hemmingsen, Janet Hill, Gregor Reid, Tim Dumonceaux, Gregory Gloor, Matthew Links, Kieran

Figure 3. Correlation between metabolite abundance and microbial function. Correlations between metabolite abundance and position of each sample on a compositional biplot built from SEED subsystem 4 aggregated data were calculated using the kendall method. These correlations were then scaled according to the first and second component of this biplot and plotted according to their scaled position. A. Metabolites detected by GC-MS. B. Metabolites detected by NMR. Only metabolites which differed significantly between BV and health are shown. GHB: gamma-hydroxybutyrate, 2HG: 2-hydroxyglutarate, 5AV: 5-aminovalerate, 2HIC: 2-hydroxyisocaproate, Tyr: tyramine, Cad: cadaverine, Pip: pipercolate, Gluc: glucose, Malt: maltose, Fruc: fructose, TMA: trimethylamine, Lact: lactate, Acet: acetate, Form: formate, 2HV: 2-hydroxyisovalerate, Chol: choline, Succ: succinate.

Table 1. Table caption Nulla mi mi, venenatis sed ipsum varius, volutpat euismod diam.

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cell1row2	cell2 row 2	cell3 row 2	cell4 row 2	cell5 row 2	cell6 row 2	cell7 row 2	cell8 row 2
cell1row3	cell2 row 3	cell3 row 3	cell4 row 3	cell5 row 3	cell6 row 3	cell7 row 3	cell8 row 3

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O'Doherty, Patrick Tang, Julianne Van Schalkwyk and Mark Yudin. We thank Jennifer Reid, Shinthujah Arulanantham and Yohanna Emun for assistance with data compilation.

Funding Statement Financial support for this study was provided by a joint Canadian Institutes of Health Research (CIHR) Emerging Team Grant and a Genome British Columbia (GBC) grant awarded to DM, SMH, GR and JEH (grant reference #108030). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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