Variability in Eating Frequency is Associated with the Human Gastrointestinal Microbiota

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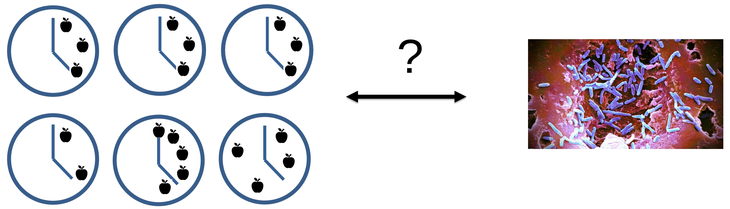
Background

- Research suggests an association between irregular meal frequency and adverse metabolic health risk factors (1).
- Findings relating the gastrointestinal microbiota to disease states may help combat this prevalent issue (2).
- Relations between meal pattern and the microbiota remain to be elucidated (3).

Objective

We aimed to assess the relationships between eating frequency variability and the composition and function of the human gastrointestinal microbiota.



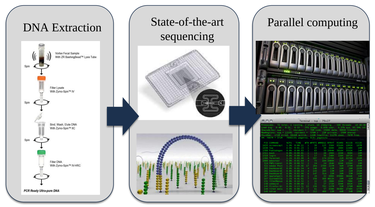
Methods

Secondary data analysis from a clinical dietary intervention study:

- 7-day dietary intake records including types, amounts, and times of food intake
- Fecal bacterial DNA
- Fecal short-chain fatty acids

Microbiota analyses:

- DNA was extracted and sequenced to determine the relative abundances of bacterial operational taxonomic units.
- Gas chromatography mass spectroscopy was utilized to quantify short-chain fatty acid concentrations.



$$\text{Variability score} = \frac{\sum_{i=1}^{7} |F_i - \bar{F}|}{7}$$

F=Number of eating occasions in one day

Dietary analyses:

- Variability in eating frequency was calculated from 7-day diet records by taking the average of the absolute difference between each participant's eating frequency per day and their average number of eating occasions.
- A higher value of variability score indicates a more irregular eating pattern.

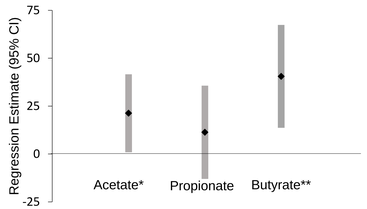
Results

Table 1. Descriptive Characteristics of Sample

Participants: n=29, females=15, samples=189

	Mean	Median	SD	Range
Age (years)	28.1	26.9	4.1	21.1 - 36.3
BMI (kg/m^2)	24.2	24.2	2.2	20.2 - 28.9
Variability score	0.82	0.83	0.32	0.28 - 1.67

Figure 1. Associations of Short-Chain Fatty Acids with Variability Score



* *P* <0.05
** *P* <0.01

Figure 2. Associations of Bacterial Operational Taxonomic Units with Variability Score

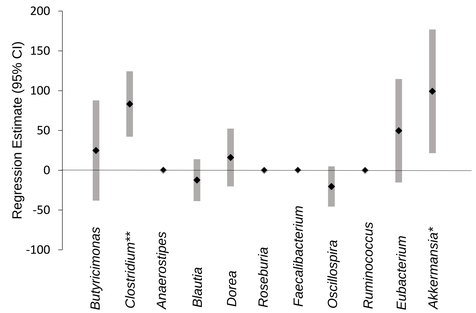


Table 2. Associations of Metabolite Concentrations and Bacterial Operational Taxonomic Unit Relative Abundances with Eating Frequency Variability

	Variability Score[1]				
	Participant N	**Sample N**	**Estimate±SEE**	**95% CI**	**P value**
Outcome					
Acetate (μmole/g)	25	155	**21.28 ± 10.38**	**0.94, 41.62**	**0.04**
Propionate (μmole/g)	25	155	11.35 ± 12.41	-12.97, 35.67	0.36
Butyrate (μmole/g)	25	155	**40.52 ± 13.7**	**13.67, 67.37**	**<0.01**
Butyricimonas (% of reads)	25	99	24.89 ± 32.12	-38.07, 87.85	0.44
***Clostridium* (% of reads)**	25	154	**83.31 ± 20.95**	**42.25, 124.37**	**<0.01**
Anaerostipes (% of reads)	25	156	0.03 ± 0.22	-0.40, 0.46	0.88
Blautia (% of reads)	25	156	-12.31 ± 13.4	-38.57, 13.95	0.36
Dorea (% of reads)	25	156	16.07 ± 18.5	-20.19, 52.33	0.39
Roseburia (% of reads)	25	156	-0.2 ± 0.23	-0.65, 0.25	0.38
Faecalibacterium (% of reads)	25	156	0.12 ± 0.13	-0.13, 0.37	0.38
Oscillospira (% of reads)	25	156	-20.35 ± 12.9	-45.63, 4.93	0.12
Ruminococcus (% of reads)	25	156	-0.2 ± 0.21	-0.61, 0.21	0.35
Eubacterium (% of reads)	25	156	49.71 ± 33.17	-15.30, 114.72	0.14
***Akkermansia* (% of reads)**	25	156	**99.23 ± 39.62**	**21.57, 176.89**	**0.01**

[1].Results of linear mixed model analysis adjusted for repeated sampling, age, BMI, sex, and normalized total fiber intake including treatment fiber. Estimate represents the percent change in the predicted value of the outcome variable for each one-unit change in variability, if all the other predictors remain constant. Variability in eating frequency was calculated from 7-day diet records by taking the average of the absolute difference between each participant's eating frequency per day and their average number of eating occasions. A higher value indicates a more irregular eating pattern.

Conclusions

- Higher relative abundances of *Clostridium* and *Akkermansia* are associated with higher variability in eating frequency.
- Higher fecal concentrations of acetate and butyrate are associated with higher variability in eating frequency.
- These results indicate that human gastrointestinal microbes and metabolites are associated with eating behaviors (1).
- These relationships, especially acetate with appetite, may be bidirectional.

Future Research

- Future research should utilize randomized, controlled trials to establish causality between the microbiota and variability in eating frequency.
- A stronger relationship between variability in eating frequency and the metabolic syndrome should be established, and mechanisms for the microbiota's role proposed.
- Eventually, individuals may be able to apply strategies of meal timing to gain health benefits.

References

1. Sierra-Johnson J, Undén A-L, Linestrand M, et al. Eating meals irregularly: a novel environmental risk factor for the metabolic syndrome. *Obesity*. 2008;16(6):1302-1307.
2. De Vos WM, De Vos EA. Role of the intestinal microbiome in health and disease: from correlation to causation. *Nutr Rev*. 2012;70(Suppl. 1):S45-S56.
3. Kaczmarek JL, Thompson SV, Holscher HD. Complex interactions of circadian rhythms, eating behaviors, and the gastrointestinal microbiota and their potential impact on health. *Nutr Rev*. 2017;75(9):673-682.

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