

The effect of an abrupt change to a four-week vegan diet on the body composition, mental health and gut microbiome

A study on the effect of veganism to the body
based on five separate personal health studies

Project Ve-gang

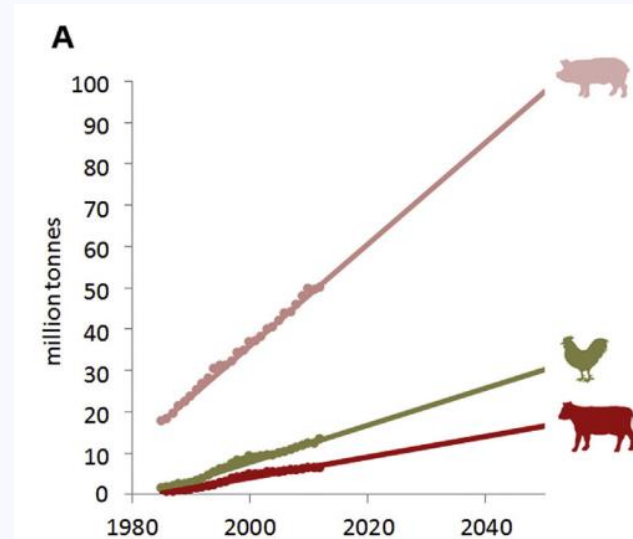
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André de la Rambelje and Henrike Vaartstra

Content

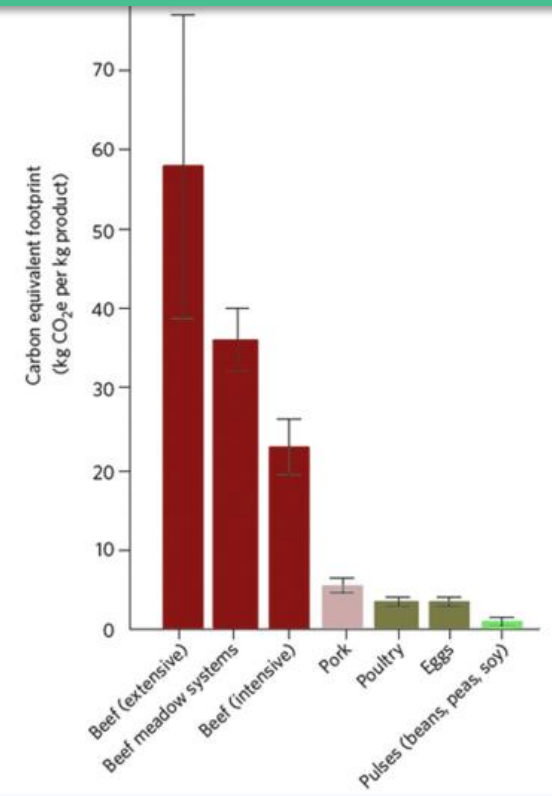
- Background
 - Veganism in health
- Goal
 - Research question
- Methods
 - Data collection, pre-processing and analysis
- Results:
 - Interactive dashboard
- Discussion
 - Food intake
 - Body composition
 - Mental state
 - Microbiota
- Conclusion
- Future work
- Questions

Background

- The production of meat
 - sixth mass extinction.^{1,2}
- Veganism
 - Health effects
 - Body composition³
 - Mental health⁴
 - Microbiome^{5,6}
- Nanopore sequencing
 - For gut microbiome analysis⁷



1



1

1. Machovina, B., Feeley, K. J., & Ripple, W. J. (2015). Biodiversity conservation: The key is reducing meat consumption. *Science of The Total Environment*, 536, 419–431. <https://doi.org/10.1016/j.scitotenv.2015.07.022>
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3. Craig, W. J. (2009). Health effects of vegan diets. *The American Journal of Clinical Nutrition*, 89(5), 1627S–1633S.
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7. Jain, M., Koren, S., Miga, K. H., Quick, J., Rand, A. C., Sasani, T. A., Tyson, J. R., Beggs, A. D., Dilthey, A. T., & Fiddes, I. T. (2018). Nanopore sequencing and assembly of a human genome with ultra-long reads. *Nature Biotechnology*, 36(4), 338–345.11.141

Goal

- Does an abrupt change to a four-week vegan diet influence the mental health, body and microbiota composition?
 - five separate personal health studies
 - two-week baseline to a four-week plant-based diet
 - Results presented in an interactive dashboard

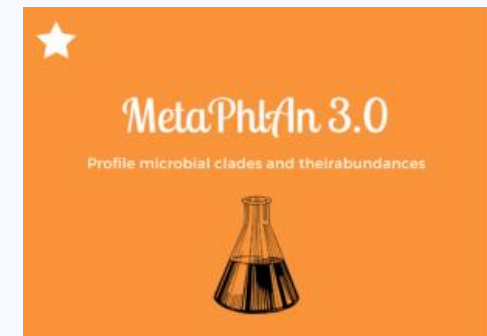
Methods

- Data collection
 - Food intake
 - Body composition
 - Mental health
 - Microbiota
 - Faecal sample collection
 - DNA extraction
 - MinION sequencing
 - Base calling



Methods

- Data pre-processing
 - Food intake
 - Mental health
- Data analysis
 - Food intake
 - Body composition
 - Mental health
 - Microbiota
 - Interactive dashboard



Results

- Shown in the interactive dashboard

Discussion

- Food intake
 - Human error
 - No exact measurements
- Body composition
 - Sensor error
 - Hydration
- Mental state
 - Exam week
 - Food satisfaction vs Hunger
 - Testing method, nature of questions asked

Discussion

Table 1. Distribution of recovered barcodes in reads.

Barcode	Subject	Sample	Number of reads	Total bp (Mbp) ^a	Average read Length (bp) ^a
Barcode01	A	Vegan	100 191	156.6	1563
Barcode02	B	Vegan	6204	13.1	2115
Barcode03	C	Vegan	2624	6.7	2546
Barcode04	D	Vegan	302 240	475.8	1574
Barcode05	E	Vegan	12 131	28.4	2344
Barcode06	A	Control	190 740	376.8	1976
Barcode07	B	Control	110 360	107.7	976
Barcode08	C	Control	12 218	18.6	1521
Barcode09	D	Control	85 015	152.2	1790
Barcode10	E	Control	136 068	162.3	1193
Unknown	Unknown	Unknown	68 366	126.3	1847

^abp = base pair, Mbp = base pair 1×10^6

Discussion

Table 2. Information about taxonomic profiles generated by MetaPhlAn per barcode. Most common species and percentage of unknown taxa are taken by the mean for the category “Pooled subjects”. Sample sizes of pooled subjects can be found under the table.

Barcode	Subject	Sample	Most common species (relative abundance)	Second most common species (relative abundance)	Third most common species (relative abundance)	Number of unique species	Percentage of unknown taxa
Barcode01	A	Vegan	<i>Prevotella copri</i> (24.74%)	<i>Alistipes putredini</i> (9.76%)	<i>Bacteroides uniformi</i> (9.76%)	55	0
Barcode02	B	Vegan	<i>Bacteroides uniformi</i> (2.51%)	<i>Alistipes putredini</i> (1.46%)		2	96
Barcode03	C	Vegan	<i>Bacteroides vulgate</i> (5.03%)			1	94
Barcode04	D	Vegan	<i>Bacteroides uniformi</i> (32.77%)	<i>Bacteroides vulgate</i> (20.75%)	<i>Bacteroides ovatu</i> (9.37%)	60	0
Barcode05	E	Vegan	<i>Bacteroides vulgate</i> (13.21%)	<i>Bacteroides stercori</i> (12.06%)	<i>Gemmata obscuriglobu</i> (6.41%)	11	45
Barcode01-Barcode05	Pooled subjects	Vegan	<i>Prevotella copri</i> (24.74%) ^a	<i>Bacteroides vulgate</i> (13.0%) ^a	<i>Bacteroides uniformi</i> (12.72%) ^a	83	47
Barcode06	A	Control	<i>Bacteroides uniformi</i> (11.07%)	<i>Bifidobacterium adolescent</i> (7.59%)	<i>Alistipes putredini</i> (6.91%)	96	0
Barcode07	B	Control	<i>Eubacterium rectale</i> (23.78%)	<i>Bacteroides plebeiu</i> (20.47%)	<i>Roseburia intestinali</i> (18.14%)	36	0
Barcode08	C	Control	<i>Alistipes sp An31A</i> (14.93%)	<i>Alistipes putredini</i> (14.58%)	<i>Bacteroides uniformi</i> (9.56%)	7	45
Barcode09	D	Control	<i>Bacteroides uniformi</i> (30.5%)	<i>Bacteroides vulgate</i> (23.59%)	<i>Bacteroides ovatu</i> (17.17%)	26	0
Barcode10	E	Control	<i>Bacteroides vulgate</i> (14.71%)	<i>Bacteroides stercori</i> (13.44%)	<i>Bacteroides uniformi</i> (11.33%)	45	6
Barcode10-Barcode11	Pooled subjects	Control	<i>Bacteroides plebeiu</i> (20.47%) ^a	<i>Roseburia intestinali</i> (18.14%) ^a	<i>Alistipes sp An31A</i> (14.93%) ^a	112	10

^aSample size (presence in number of barcoded samples) for *Prevotella copri* = 1, *Bacteroides vulgate* = 3, *Bacteroides uniformi* = 4, *Bacteroides plebeiu* = 1, *Roseburia intestinali* = 1 and *Alistipes sp An31A* = 1.

Discussion

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Barcode10-Barcode11	Pooled subjects	Control	<i>Bacteroides plebeiu</i> (20.47%) ^a	<i>Roseburia intestinali</i> (18.14%) ^a	<i>Alistipes sp An31A</i> (14.93%) ^a	112	10

^aSample size (presence in number of barcoded samples) for *Prevotella copri* = 1, *Bacteroides vulgate* = 3, *Bacteroides uniformi* = 4, *Bacteroides plebeiu* = 1, *Roseburia intestinali* = 1 and *Alistipes sp An31A* = 1.

Discussion

- Most common species taken by sum

- Control

- *Bacteroides uniformi*
 - *Bacteroides vulgate*
 - *Eubacterium rectale*

- Vegan

- *Bacteroides uniformi*
 - *Bacteroides vulgate*
 - *Prevotella copri*

Wu, G. D., Chen, J., Hoffmann, C., Bittinger, K., Chen, Y.-Y., Keilbaugh, S. A., Bewtra, M., Knights, D., Walters, W. A., & Knight, R. (2011). Linking long-term dietary patterns with gut microbial enterotypes. *Science*, 334(6052), 105–108.



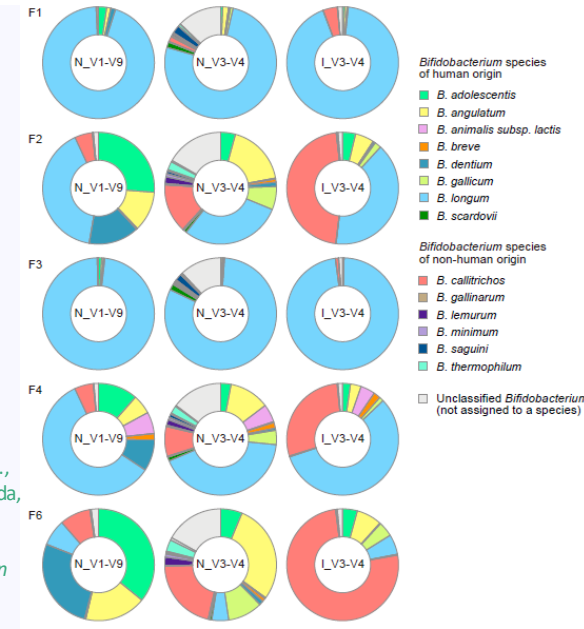
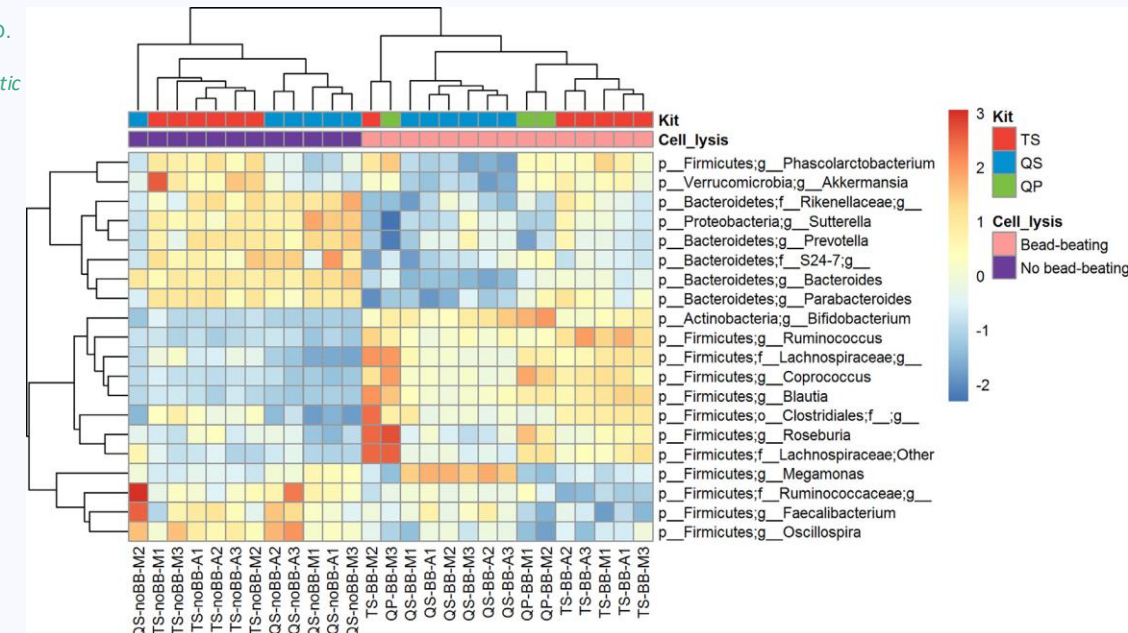
Dennis Kunkel Microscopy/science Photo Library. (2021). *Bacteroides* Sp. *Bacterium* [Image]. Retrieved from <https://fineartamerica.com/featured/2bacteroides-sp-bacterium-dennis-kunkel-microscopy-science-photo-library.html>

Discussion

• Microbiota

- Quality of sequencing
- Taxonomic analysis
 - MetaPhlAn
 - BLAST
 - Most common taxa
 - Gut Feeling Knowledge Base
 - Literature review to David et al. 2013; Zimmer et al. 2012
- Visualization of metagenomic comparisons
- Compatibility of MetaPhlAn with nanopore sequencing

Lim, M. Y., Song, E.-J., Kim, S. H., Lee, J., & Nam, Y.-D. (2018). Comparison of DNA extraction methods for human gut microbial community profiling. *Systematic and Applied Microbiology*, 41(2), 151–157. <https://doi.org/10.1016/j.syapm.2017.11.008>



Matsuo, Y., Komiya, S., Yasumizu, Y., Yasuoka, Y., Mizushima, K., Takagi, T., Kryukov, K., Fukuda, A., Morimoto, Y., Naito, Y., Okada, H., Bono, H., Nakagawa, S., & Hirota, K. (2020). Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinION™ nanopore sequencing confers species-level resolution [Preprint]. *Microbiology*. <https://doi.org/10.1101/2020.05.06.078147>

Conclusion

- No significant changes as expected
 - Food intake, body composition and mental state
 - Measured for only a short time frame
- No significant changes, not as expected
 - Microbiota
 - Low sample size
 - Quality of results may be degraded because of
 - Wet lab
 - Dry lab

Future work

- Food intake, body composition and mental state
 - Longer time frame studies
- Microbiota
 - Possible with current data
 - Metabolic analysis of taxonomic profiles
 - Alternative dry lab methods
 - Alternative visualization of metagenomic comparisons
 - New study
 - Higher sample size
 - Alternative wet lab methods

Questions

