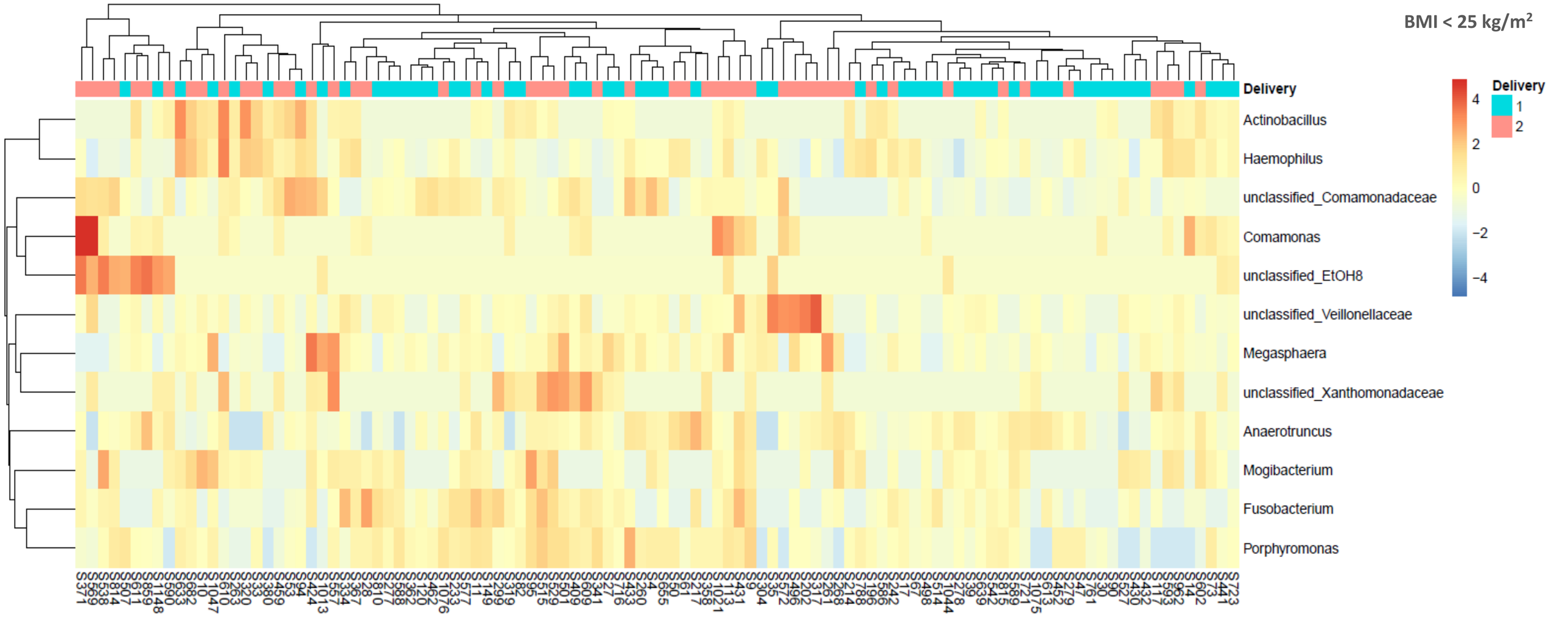
Exemplos?

- 150 pacientes
  - Parto normal Vs. Cesária
  - Estratificado por BMI >= 25

	Normal BMI			Elevated BMI		
	Vaginal delivery	Cesarean delivery	p-value	Vaginal delivery	Cesarean delivery	p-value
	n = 55	n = 52		n = 22	n = 21	
Age (years)	25.0 (5.5)	22.8 (4.3)	0.021	28.6 (7.4)	2.,0 (6.2)	0.224
Waist circumference (cm)	72.5 (5.8)	71.3 (4.4)	0.230	93.5 (11.4)	89.8 (11.2)	0.288
Systolic BP (mmHg)	10.6 (11)	107 (12)	0.717	116 (13)	113 (12)	0.198
Diastolic BP (mmHg)	71.1 (8.3)	70.7 (8.6)	0.831	75.5 (10.5)	73.0 (7.3)	0.374
Plasma glucose (mg/dL)	80.1 (9.0)	81.4 (7.7)	0.453	86.4 (11.3)	81.7 (9.1)	0.138
HOMA-IR #	1.8 (0.8)	1.9 (0.9)	0.770	2.0 (1.0)	2.1 (1.0)	0.883
Non-HDL chol (mg/dL)	116 (27)	115 (28)	0.900	119 (46)	123 (32)	0.748
LDL-chol (mg/dL)	99 (26)	99 (27)	0.860	94 (44)	105 (29)	0.351
C-reactive protein (mg/dL)	2.9 (1.3)	3.0 (0.8)	0.160	2.4 (1.2)	2.7 (1.1)	0.513
LPS (pg/mL)	9.6 (3.2)	11.9 (8.3)	0.105	10.7 (4.1)	9.0 (4.2)	0.087


BMI < 25 kg/m²
Delivery
Actinobacillus
Haemophilus
unclassified_Comamonadaceae
Comamonas
unclassified_EtOH8
unclassified_Veillonellaceae
Megasphaera
unclassified_Xanthomonadaceae
Anaerotruncus
Mogibacterium
Fusobacterium
Porphyromonas
Delivery
1
2
4
2
0
−2
−4

Cell. 2013 Mar 28;153(1):240-52. doi: 10.1016/j.cell.2013.02.049.

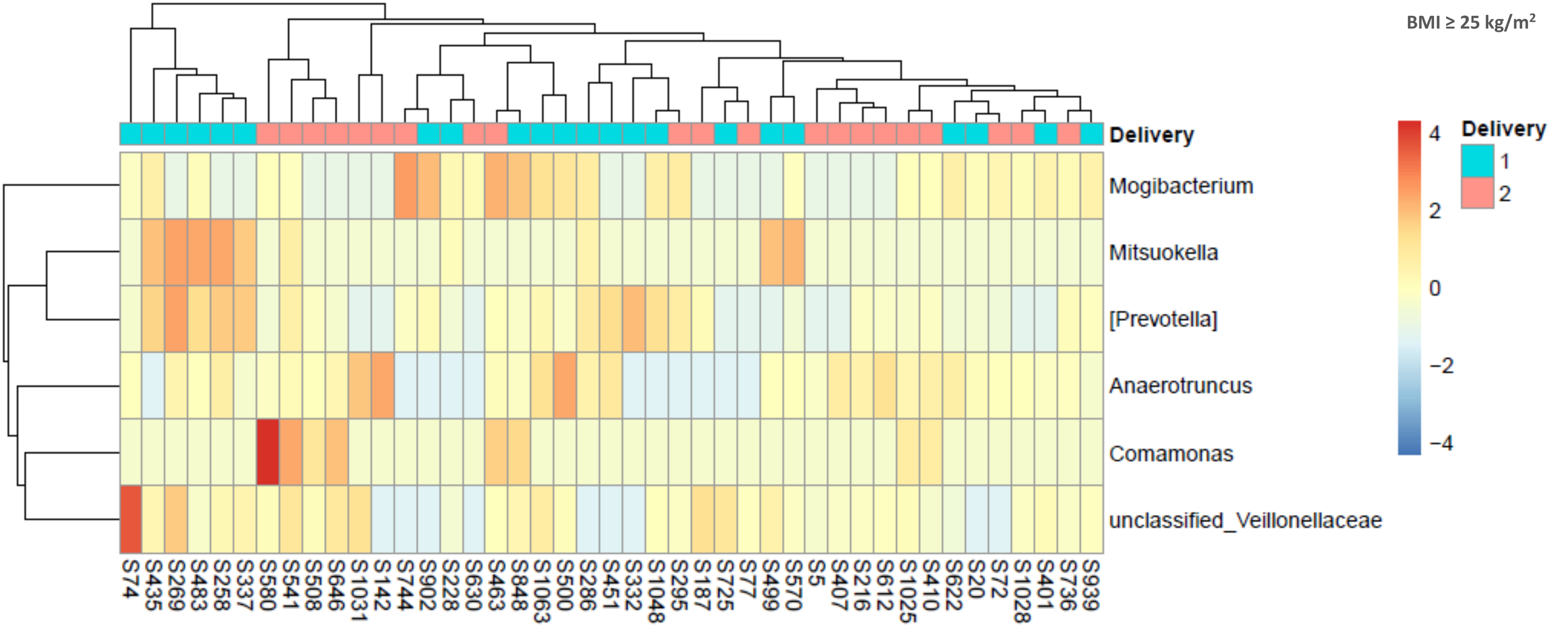
Diet-induced developmental acceleration independent of TOR and insulin in C. elegans.

MacNeil LT[1], Watson E, Arda HE, Zhu LJ, Walhout AJ.

Author information

Abstract

Dietary composition has major effects on physiology. Here, we show that developmental rate, reproduction, and lifespan are altered in C. elegans fed Comamonas DA1877 relative to those fed a standard E. coli OP50 diet. We identify a set of genes that change in expression in response to this diet and use the promoter of one of these (acdh-1) as a dietary sensor. Remarkably, the effects on transcription and development occur even when Comamonas DA1877 is diluted with another diet, suggesting that Comamonas DA1877 generates a signal that is sensed by the nematode. Surprisingly, the developmental effect is independent from TOR and insulin signaling. Rather, Comamonas DA1877 affects cyclic gene expression during molting, likely through the nuclear hormone receptor NHR-23. Altogether, our findings indicate that different bacteria elicit various responses via distinct mechanisms, which has implications for diseases such as obesity and the interactions between the human microbiome and intestinal cells.


BMI ≥ 25 kg/m²
Delivery
Mogibacterium
Mitsuokella
[Prevotella]
Anaerotruncus
Comamonas
unclassified_Veillonellaceae
4
2
0
−2
−4
Delivery
1
2
S74
S435
S269
S483
S258
S337
S580
S541
S508
S646
S1031
S142
S744
S902
S228
S630
S463
S848
S1063
S500
S286
S451
S332
S1048
S295
S187
S725
S77
S499
S570
S5
S407
S216
S612
S1025
S410
S622
S20
S72
S1028
S401
S736
S939

Benef Microbes. 2015 Mar;6(1):97-111. doi: 10.3920/BM2013.0097.

Shifts in microbiota species and fermentation products in a dietary model enriched in fat and sucrose.

Etxeberria U[1], Arias N[2], Boqué N[3], Macarulla MT[4], Portillo MP[4], Milagro FI[5], Martinez JA[5].

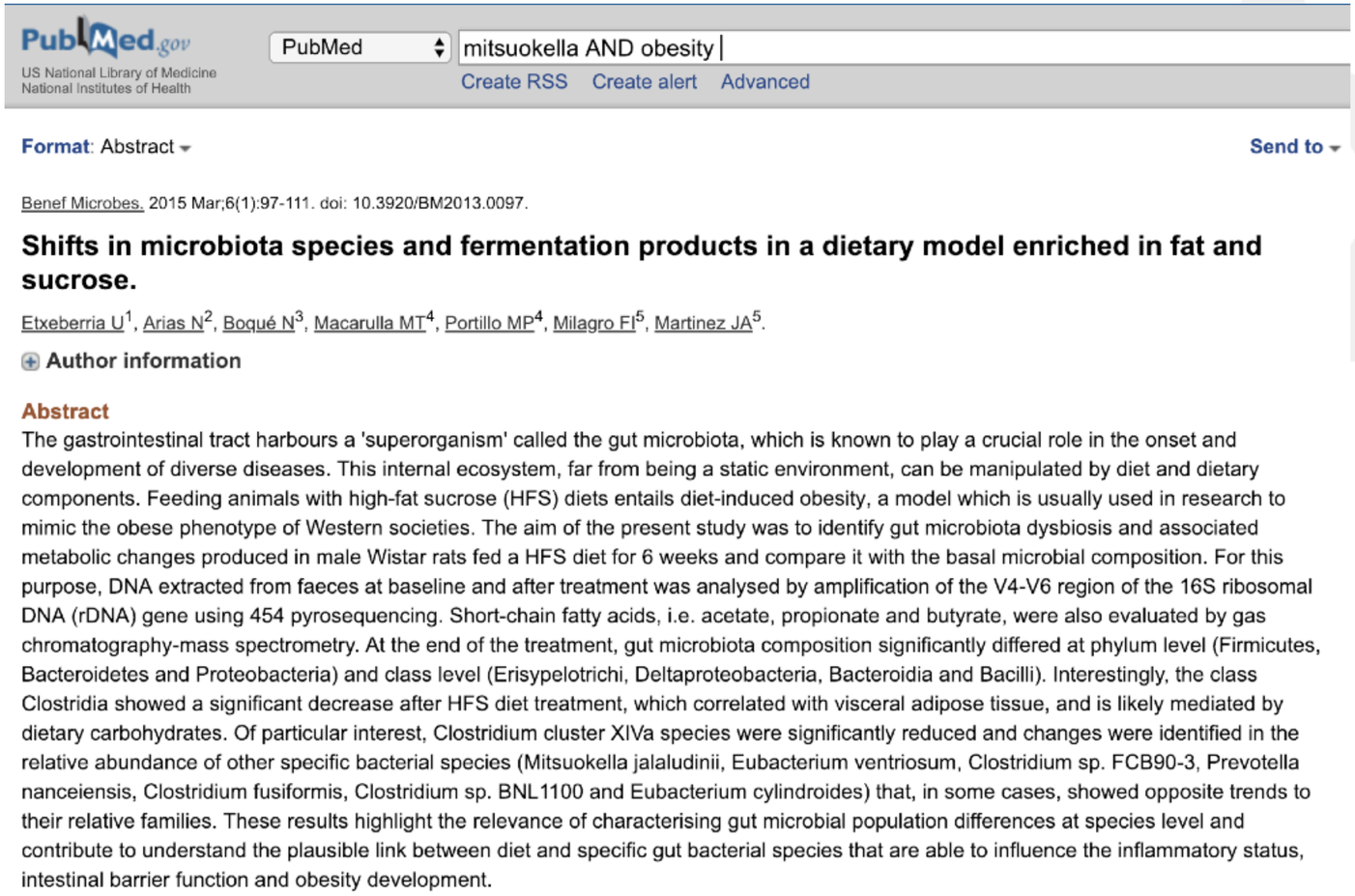
Author information

Abstract

The gastrointestinal tract harbours a 'superorganism' called the gut microbiota, which is known to play a crucial role in the onset and development of diverse diseases. This internal ecosystem, far from being a static environment, can be manipulated by diet and dietary components. Feeding animals with high-fat sucrose (HFS) diets entails diet-induced obesity, a model which is usually used in research to mimic the obese phenotype of Western societies. The aim of the present study was to identify gut microbiota dysbiosis and associated metabolic changes produced in male Wistar rats fed a HFS diet for 6 weeks and compare it with the basal microbial composition. For this purpose, DNA extracted from faeces at baseline and after treatment was analysed by amplification of the V4-V6 region of the 16S ribosomal DNA (rDNA) gene using 454 pyrosequencing. Short-chain fatty acids, i.e. acetate, propionate and butyrate, were also evaluated by gas chromatography-mass spectrometry. At the end of the treatment, gut microbiota composition significantly differed at phylum level (Firmicutes, Bacteroidetes and Proteobacteria) and class level (Erisypelotrichi, Deltaproteobacteria, Bacteroidia and Bacilli). Interestingly, the class Clostridia showed a significant decrease after HFS diet treatment, which correlated with visceral adipose tissue, and is likely mediated by dietary carbohydrates. Of particular interest, Clostridium cluster XIVa species were significantly reduced and changes were identified in the relative abundance of other specific bacterial species (Mitsuokella jalaludinii, Eubacterium ventriosum, Clostridium sp. FCB90-3, Prevotella nanceiensis, Clostridium fusiformis, Clostridium sp. BNL1100 and Eubacterium cylindroides) that, in some cases, showed opposite trends to their relative families. These results highlight the relevance of characterising gut microbial population differences at species level and contribute to understand the plausible link between diet and specific gut bacterial species that are able to influence the inflammatory status, intestinal barrier function and obesity development.

Exemplos?

- 150 pacientes
  - Parto normal Vs. Cesária
  - Estratificado por BMI >= 25



PubMed.gov
US National Library of Medicine
National Institutes of Health

PubMed | mitsuokella AND obesity

Create RSS Create alert Advanced

Format: Abstract Send to

Benef Microbes. 2015 Mar;6(1):97-111. doi: 10.3920/BM2013.0097.

Shifts in microbiota species and fermentation products in a dietary model enriched in fat and sucrose.

Etxeberria U[1], Arias N[2], Boqué N[3], Macarulla MT[4], Portillo MP[4], Milagro FI[5], Martinez JA[5].

Author information

Abstract

The gastrointestinal tract harbours a 'superorganism' called the gut microbiota, which is known to play a crucial role in the onset and development of diverse diseases. This internal ecosystem, far from being a static environment, can be manipulated by diet and dietary components. Feeding animals with high-fat sucrose (HFS) diets entails diet-induced obesity, a model which is usually used in research to mimic the obese phenotype of Western societies. The aim of the present study was to identify gut microbiota dysbiosis and associated metabolic changes produced in male Wistar rats fed a HFS diet for 6 weeks and compare it with the basal microbial composition. For this purpose, DNA extracted from faeces at baseline and after treatment was analysed by amplification of the V4-V6 region of the 16S ribosomal DNA (rDNA) gene using 454 pyrosequencing. Short-chain fatty acids, i.e. acetate, propionate and butyrate, were also evaluated by gas chromatography-mass spectrometry. At the end of the treatment, gut microbiota composition significantly differed at phylum level (Firmicutes, Bacteroidetes and Proteobacteria) and class level (Erisypelotrichi, Deltaproteobacteria, Bacteroidia and Bacilli). Interestingly, the class Clostridia showed a significant decrease after HFS diet treatment, which correlated with visceral adipose tissue, and is likely mediated by dietary carbohydrates. Of particular interest, Clostridium cluster XIVa species were significantly reduced and changes were identified in the relative abundance of other specific bacterial species (Mitsuokella jalaludinii, Eubacterium ventriosum, Clostridium sp. FCB90-3, Prevotella nanceiensis, Clostridium fusiformis, Clostridium sp. BNL1100 and Eubacterium cylindroides) that, in some cases, showed opposite trends to their relative families. These results highlight the relevance of characterising gut microbial population differences at species level and contribute to understand the plausible link between diet and specific gut bacterial species that are able to influence the inflammatory status, intestinal barrier function and obesity development.

Jarking

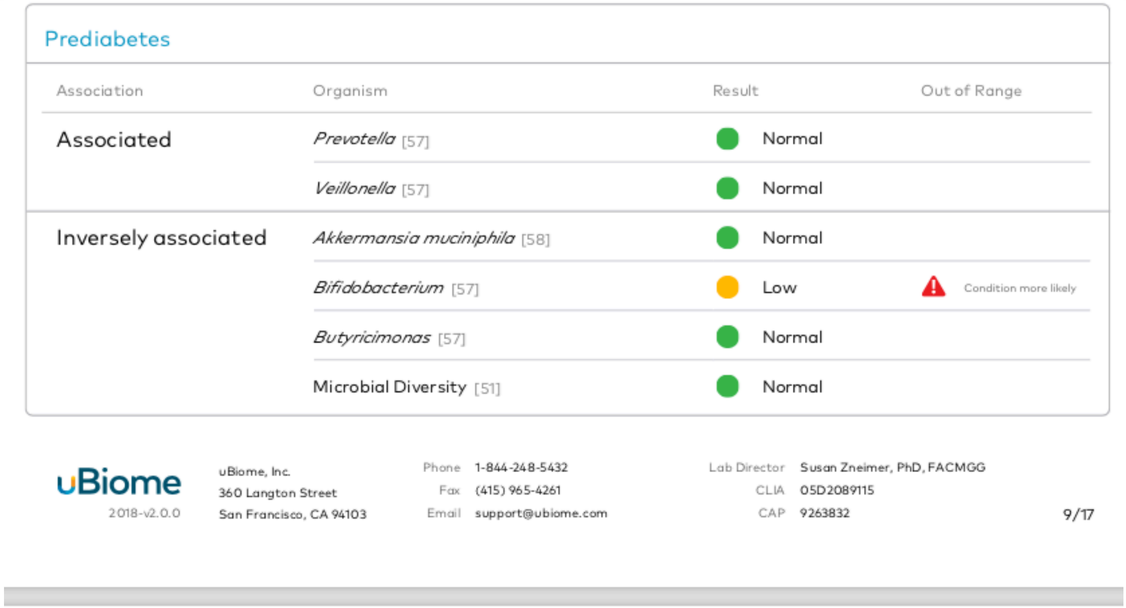
- JARK effect
  - Justify After Results are Known
- Qualquer resultado pode ser publicado
  - Vai achar referências que suportem seu desenho experimental errado.

Too many journals? Towards a theory of repeated rejections and ultimate acceptance

Jan Oosterhaven

- Muitos trabalhos de microbioma (Science, Nature, PNAS…) não são reprodutíveis.
  - Clustering method
  - Classification method
  - Assembly method

Instituto René Rachou FIOCRUZ MINAS



Prediabetes

Association	Organism	Result	Out of Range
Associated	*Prevotella* [57]	Normal	
	Veillonella [57]	Normal	
Inversely associated	*Akkermansia muciniphila* [58]	Normal	
	Bifidobacterium [57]	Low	Condition more likely
	Butyricimonas [57]	Normal	
	Microbial Diversity [51]	Normal	

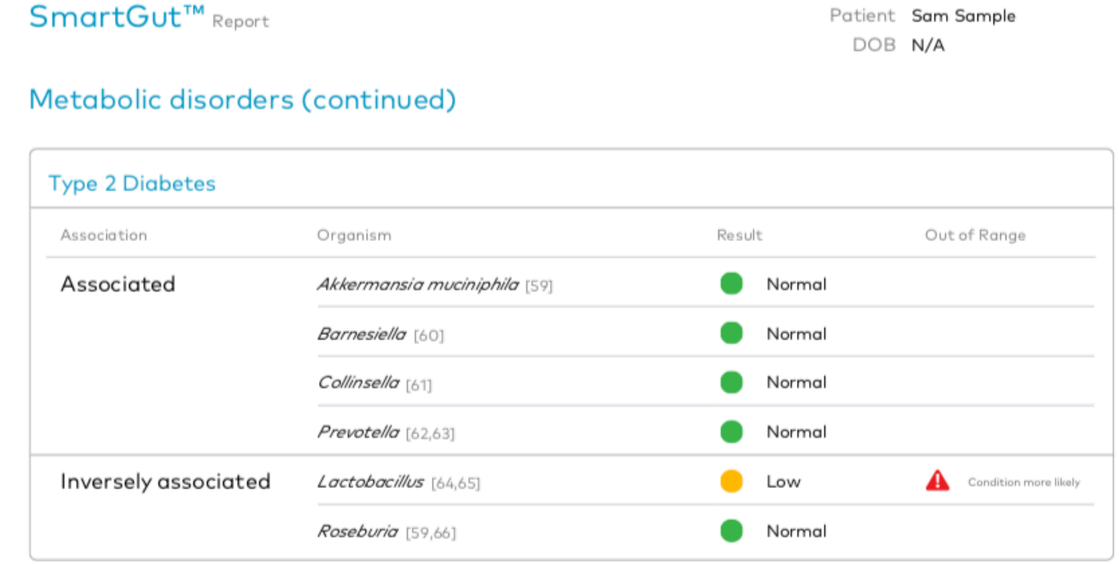
uBiome 2018-v2.0.0

uBiome, Inc.
360 Langton Street
San Francisco, CA 94103

Phone 1-844-248-5432
Fax (415) 965-4261
Email support@ubiome.com

Lab Director Susan Zneimer, PhD, FACMGG
CLIA 05D2089115
CAP 9263832

9/17



SmartGut™ Report

Patient Sam Sample
DOB N/A

Metabolic disorders (continued)

Type 2 Diabetes

Association	Organism	Result	Out of Range
Associated	*Akkermansia muciniphila* [59]	Normal	
	Barnesiella [60]	Normal	
	Collinsella [61]	Normal	
	Prevotella [62,63]	Normal	
Inversely associated	*Lactobacillus* [64,65]	Low	Condition more likely
	Roseburia [59,66]	Normal	