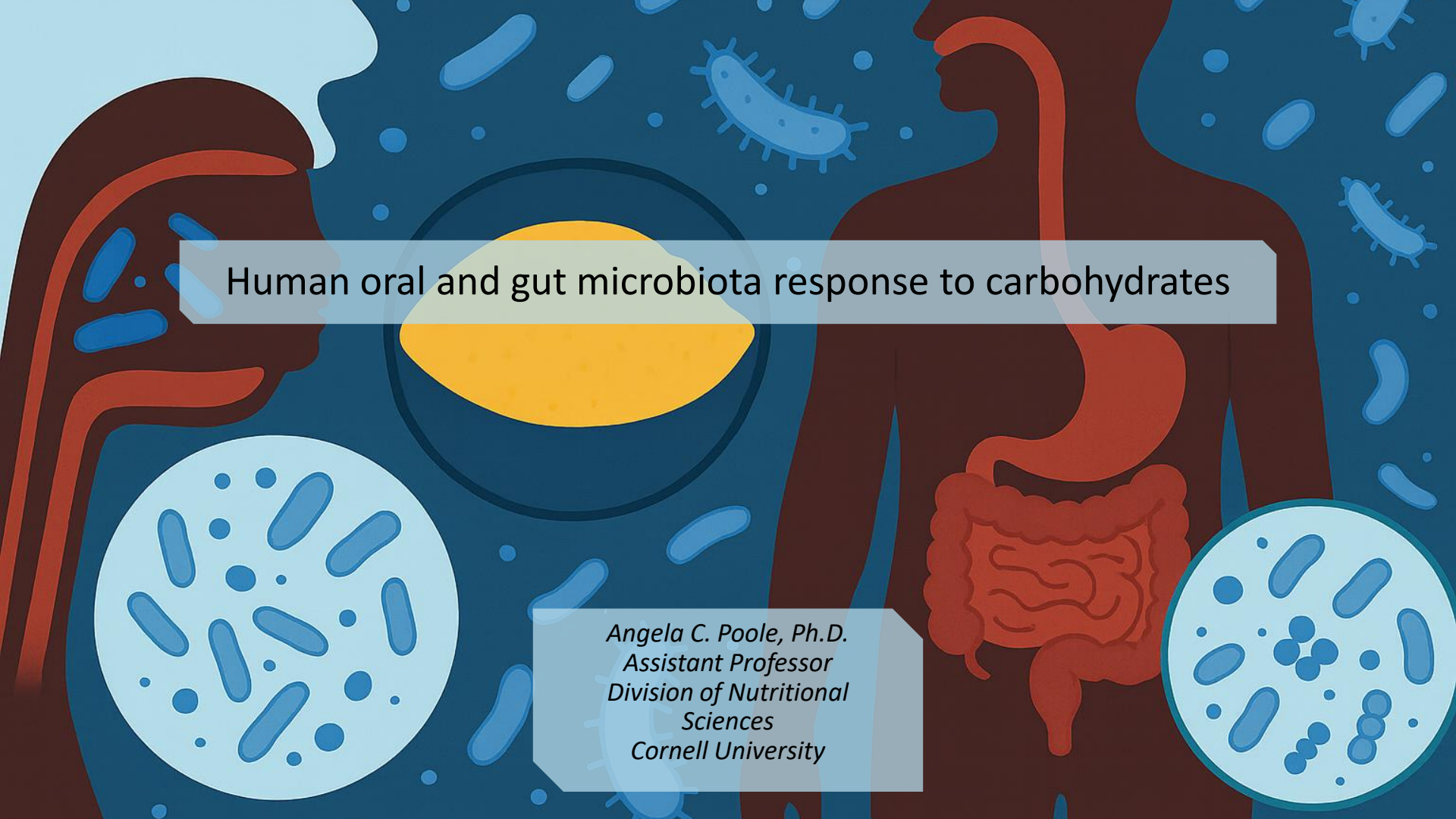
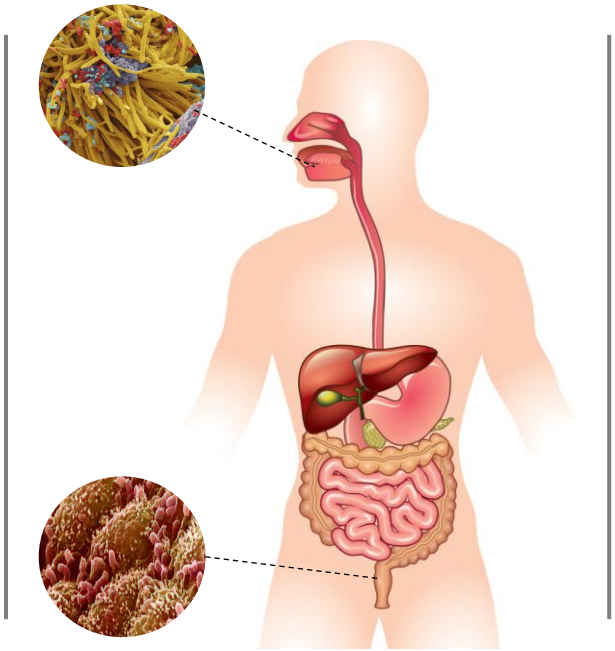
Human oral and gut microbiota response to carbohydrates

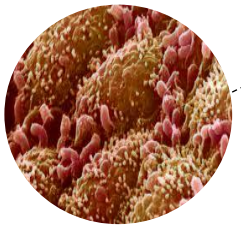


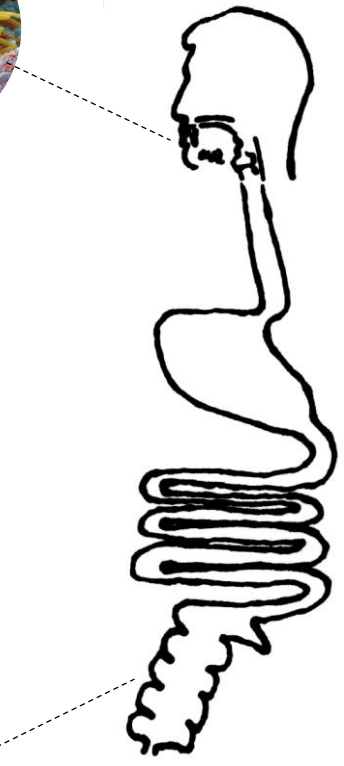
Angela C. Poole, Ph.D.
Assistant Professor
Division of Nutritional Sciences
Cornell University

POOLE RESEARCH GROUP



- Carbohydrate intake influences oral and metabolic health partly via
  - Oral microbiota
  - Gut microbiota





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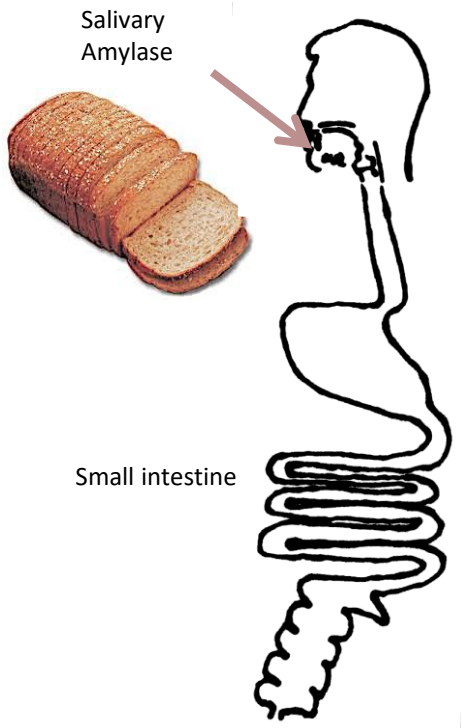
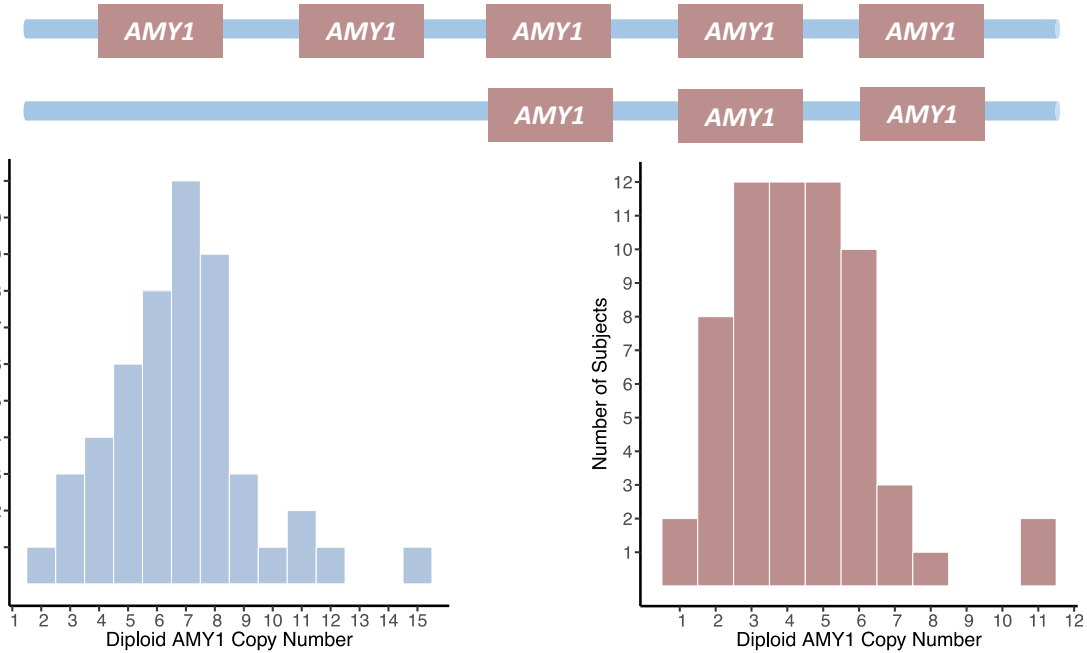
Carbohydrate digestion

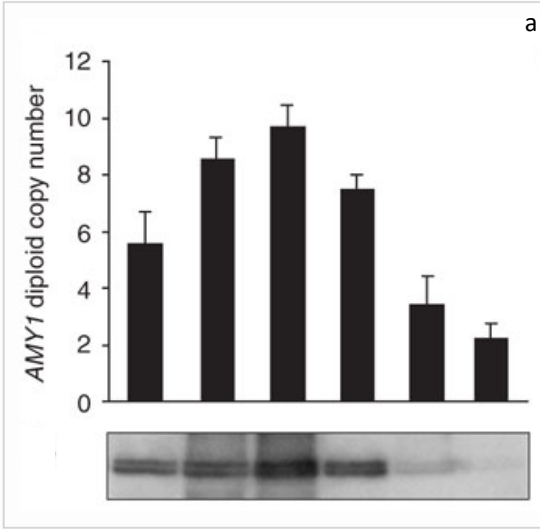


- Starch breakdown is initiated in the mouth
- Amylase (*AMY1*) breaks down starch

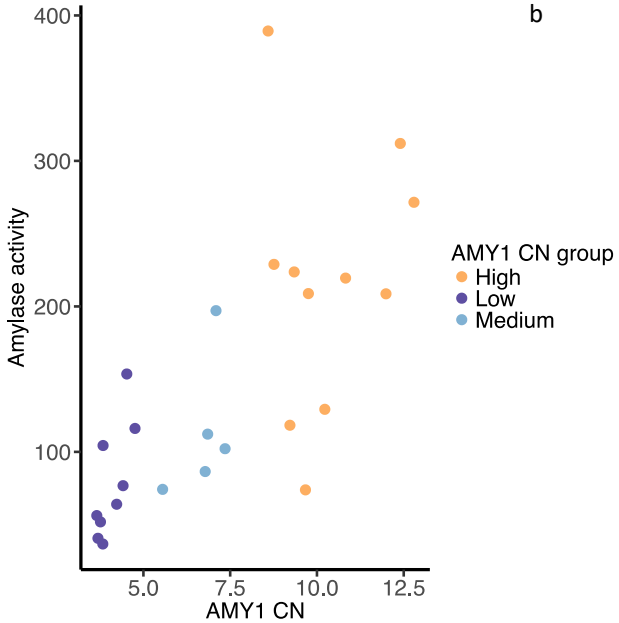


PMID: 17828263
PMID: 20967220

AMY1 CN correlates with protein and activity level

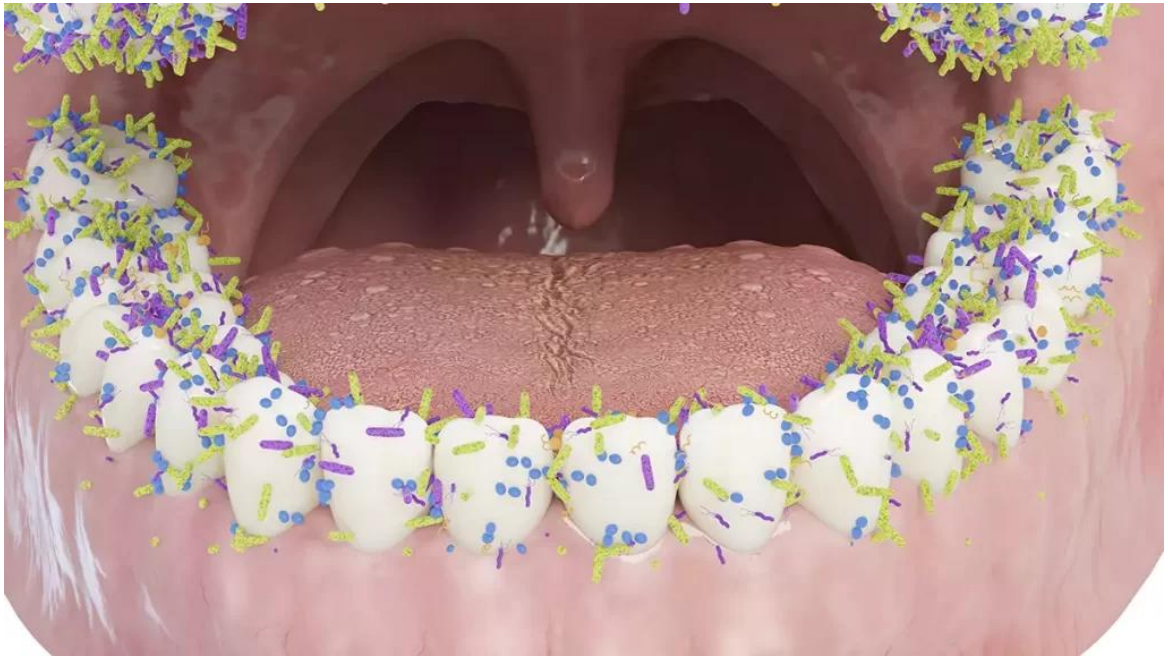


Western blot: anti-AMY1



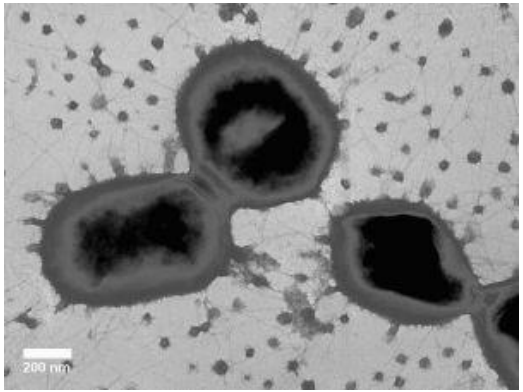
PMID: 17828263
PMID: 30974084

How does host *AMY1* CN impact oral microbiota?



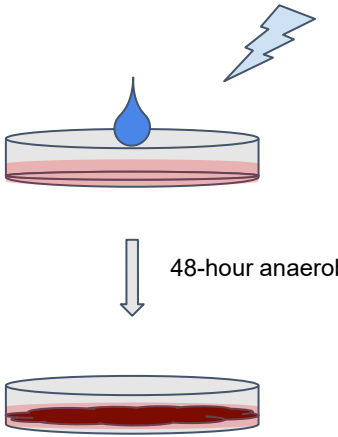
Is *AMY1* CN associated with oral health?

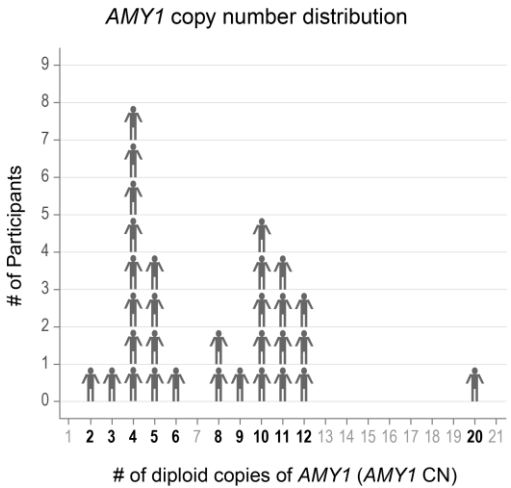
Increased levels of two members of *Porphyromonas* genus in the high *AMY1* copy number group



- Several species of *Porphyromonas* are associated with periodontitis
- Do people with high *AMY1* CN have higher incidence of periodontitis?
- Is oral microbiota response to starch intake dependent upon *AMY1* CN?

Does *AMY1* CN affect microbiota response to starch?





	All participants
Total n	31
Age in years (Mean ± SD)	19-57 (29.5±9)
Sex	
Female	25
Male	6
Gum disease status	
Gingivitis	3
Gum recession	4
Periodontitis	4
None	20

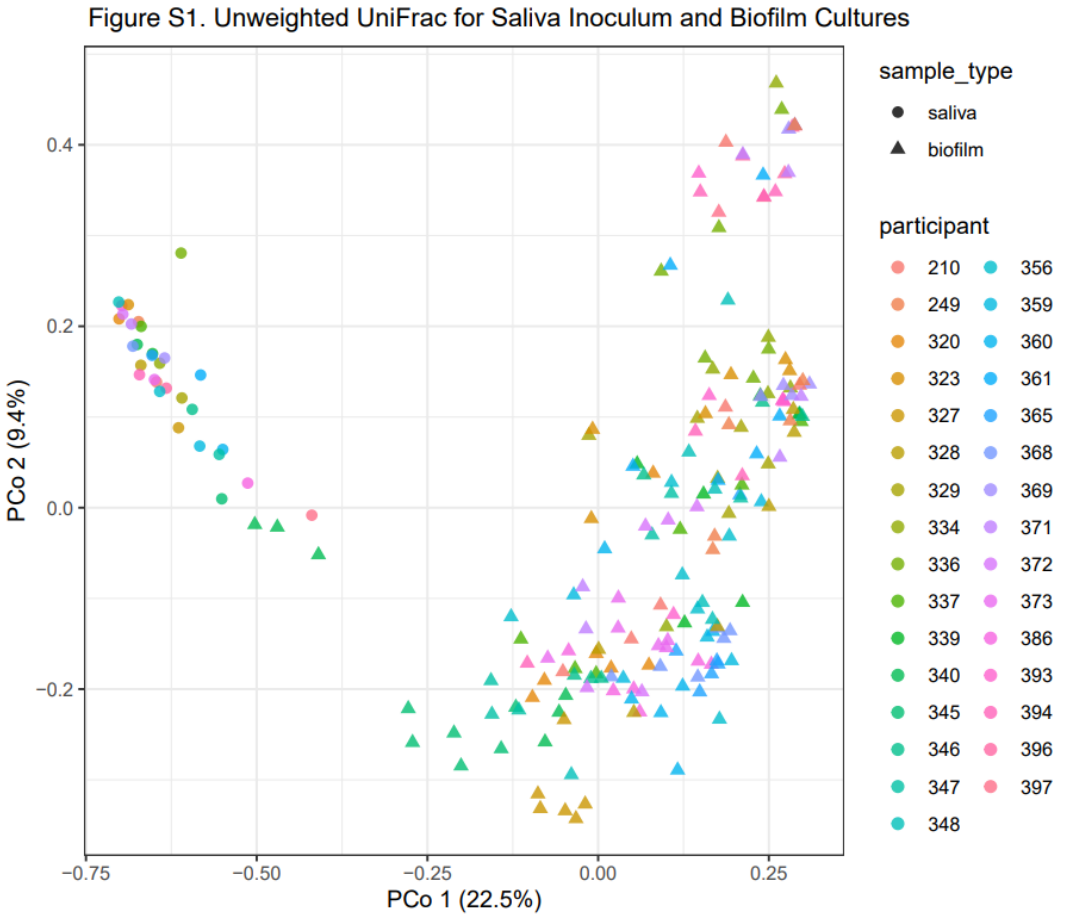
Media
- subSHI
- subSHI+0.1% starch

We used a previously published *in vitro* model

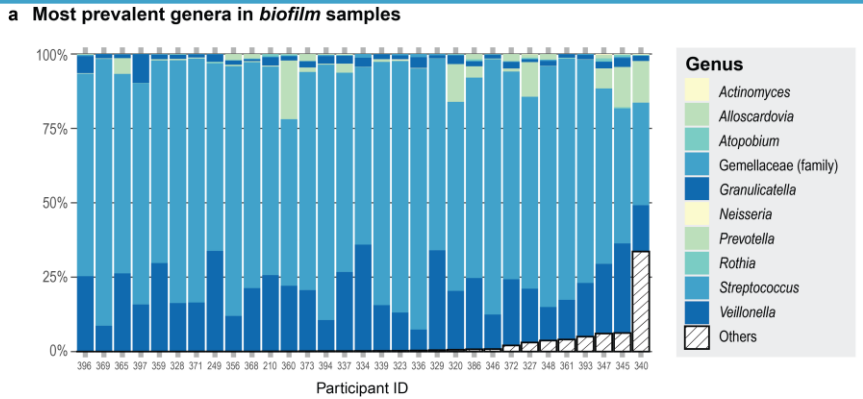
Samples from 31 participants.
Biofilms for each of 2 media grown in triplicates.

Dorothy (Kim)
Superdock

Donor identity is conserved in biofilm samples

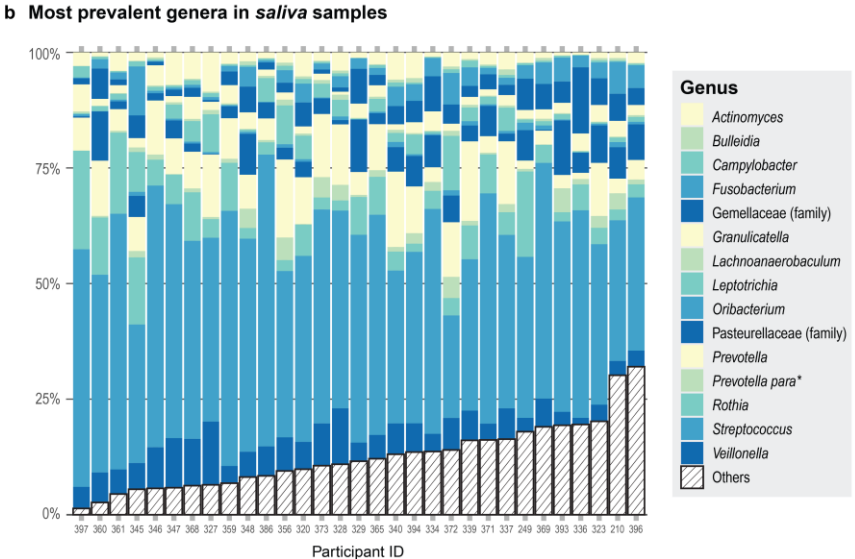


Biofilms mainly comprised of 10 genera



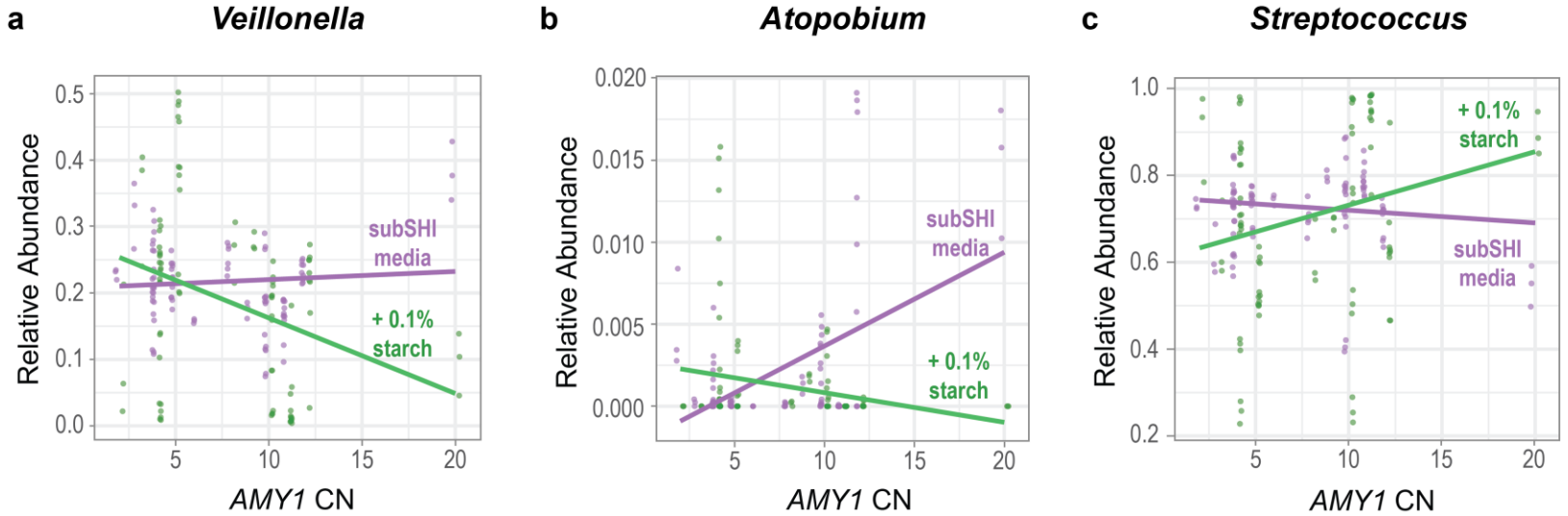
Biofilms

Include 98% of the read counts



Saliva

AMY1 CN affects microbiome response to starch



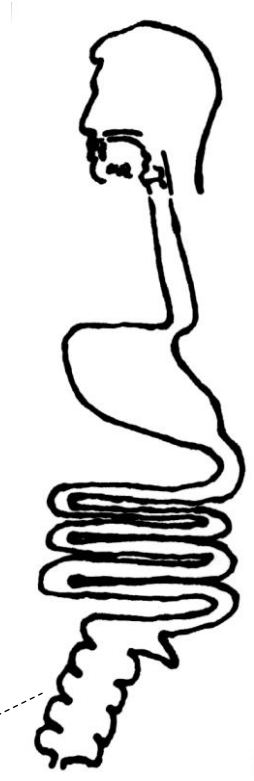
Genus ~ gum_disease + participant_age + AMY1CN*media + (1|participant) + (1|participant:media)

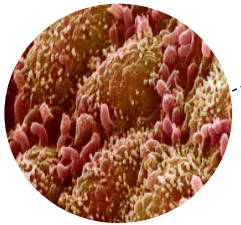
Linear mixed models

Summary

- For higher *AMY1* CN, *Veillonella* and *Atopobium* have a lower relative abundance in starch supplemented media
- Species within *Veillonella* and *Atopobium* contain carbohydrate-active enzymes
- Competition between host and microbes for starch substrate
- Mechanistically,
  - The species within these 2 genera may differ depending upon the host genotype
  - Other genera correlated with *AMY1* CN may affect the relative abundance of these 2 genera
- *Veillonella sp.* associated with dental caries and periodontitis, and *Atopobium sp.* associated with dental caries

- Carbohydrate intake influences oral and metabolic health partly via
  - Oral microbiota
  - Gut microbiota





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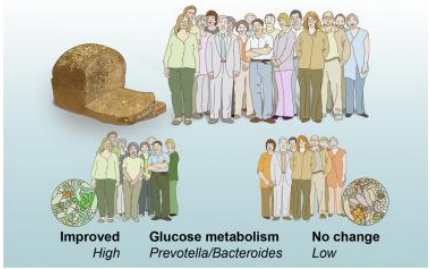
Variable response to dietary fiber supplementation



Dietary Fiber-Induced Improvement in Glucose Metabolism Is Associated with Increased Abundance of *Prevotella*

Petia Kovatcheva-Datchary [1], Anne Nilsson [2], Rozita Akrami [1], Ying Shiuan Lee [1], Filipe De Vadder [1], Tulika Arora [1], Anna Hallen [1], Eric Martens [3], Inger Björck [2], Fredrik Bäckhed [1, 4]

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Nutrition Research
Volume 77, May 2020, Pages 12-28

Variable responses of human microbiomes to dietary supplementation with resistant starch

A. Venkataraman[1], J. R. Sieber[1,2], A. W. Schmidt[1], C. Waldron[1], K. R. Theis[1,3] and T. M. Schmidt[1*]

Review Article

Conserved and variable responses of the gut microbiome to resistant starch type 2

Zachary A. Bendiks [a], Knud E.B. Knudsen [b], Michael J. Keenan [c], Maria L. Marco [a]

Published: 24 April 2014

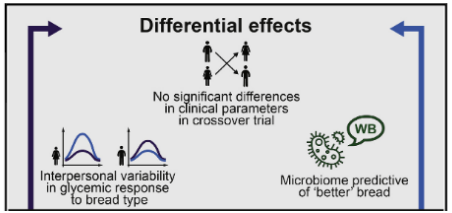
Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men

Anne Salonen, Leo Lahti, Jarkko Salojärvi, Grietje Holtrop, Katri Korpela, Sylvia H Duncan, Priya Date, Freda Farquharson, Alexandra M Johnstone, Gerald E Lobley, Petra Louis, Harry J Flint & Willem M de Vos

The ISME Journal **8**, 2218–2230 (2014) | Cite this article

Bread Affects Clinical Parameters and Induces Gut Microbiome-Associated Personal Glycemic Responses

Graphical Abstract



Authors

Tal Korem, David Zeevi, Niv Zmora, ..., Avraham A. Levy, Eran Elinav, Eran Segal

Correspondence

avi.levy@weizmann.ac.il (A.A.L.), eran.elinav@weizmann.ac.il (E.E.), eran.segal@weizmann.ac.il (E.S.)

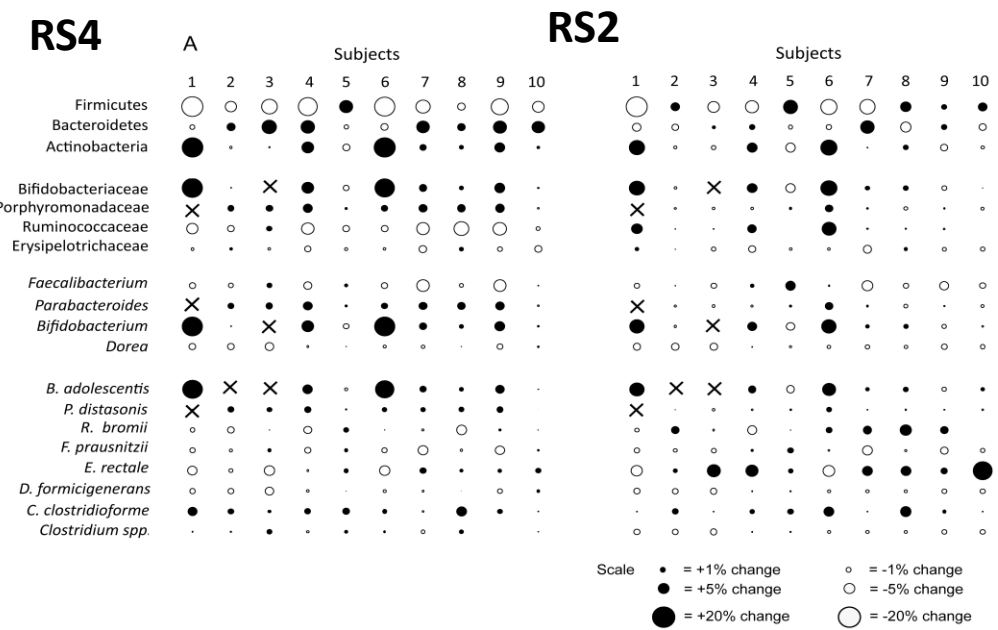
In Brief

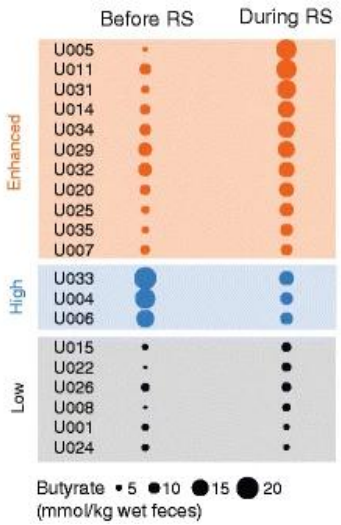
Resistant Starches Types 2 and 4 Have Differential Effects on the Composition of the Fecal Microbiota in Human Subjects

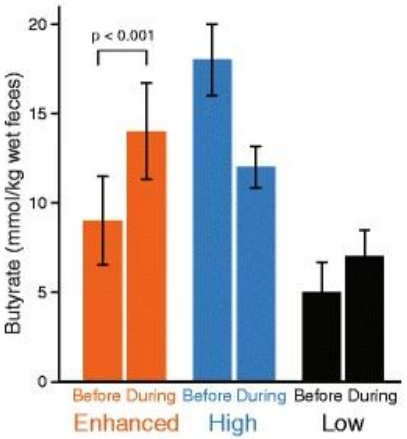
Inés Martínez, Jaehyoung Kim, Patrick R. Duffy, Vicki L. Schlegel, Jens Walter*

Department of Food Science and Technology, University of Nebraska, Lincoln, Nebraska, United States of America

Variability in gut microbiome response







PMID: 21151493
PMID: 27357127

Research question

Can we identify factors that predict gut microbiota response to resistant starch types 2 and 4 (RS2 and RS4)?

- Conflicting results from RS supplementations regarding glucose improvement outcomes
- Variability in gut microbiome response to RS2 and RS4 supplementation

Resistant Starches Types 2 and 4 Have Differential Effects on the Composition of the Fecal Microbiota in Human Subjects

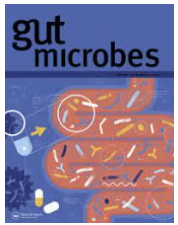
Inés Martínez, Jaehyoung Kim, Patrick R. Duffy, Vicki L. Schlegel, Jens Walter*

Department of Food Science and Technology, University of Nebraska, Lincoln, Nebraska, United States of America

Variable responses of human microbiomes to dietary supplementation with resistant starch

A. Venkataraman[1], J. R. Sieber[1,2], A. W. Schmidt[1], C. Waldron[1], K. R. Theis[1,3] and T. M. Schmidt[1*]

Sri Devarakonda



PMID: 38913541

Dorothy (Kim) Superdock

Dietary supplementation with 3 types of crackers

Formulations for the crackers were matched for total carbohydrate
Starches were provided by Ingredion
Crackers (~22,000) were baked by The National Food Lab
Following ramp up period of 3 days, 7 days of 30g RS per day

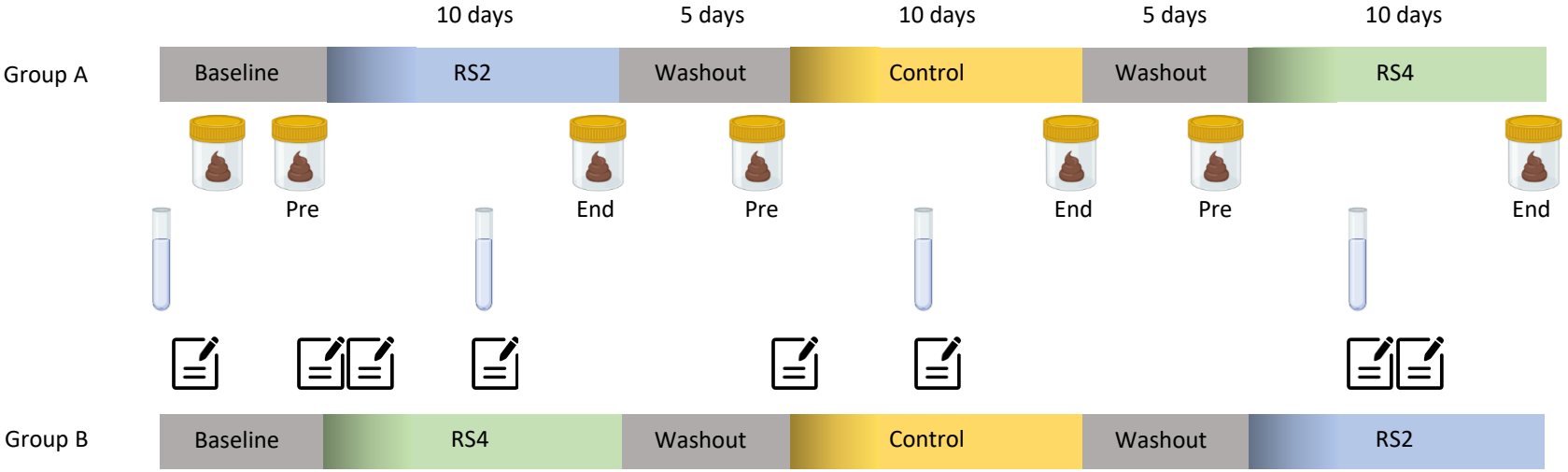
Ingredient	Control (digestible starch)	RS2	RS4
Bread flour	49.85%	29.40%	45.27%
Amioca TF starch	24.72%	-	-
HiMaize 260	-	44.78%	-
VersaFibe 1490	-	-	29.95%
Unsalted Butter	17.89%	17.59%	18.05%
Sugar	2.41%	2.36%	2.44%
Salt	1.15%	1.12%	1.15%
Water	3.99%	4.76%	3.14%
TOTAL	100.0%	100.0%	100.0%

Crossover study design

Stool sample collected

Saliva sample collected

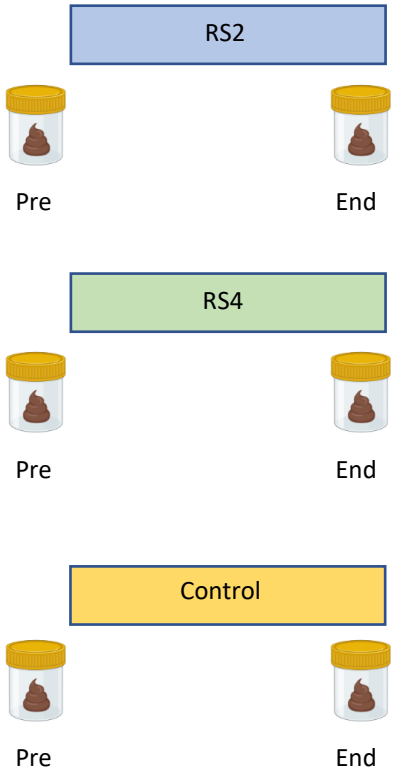
Dietary record collected (ASA24)

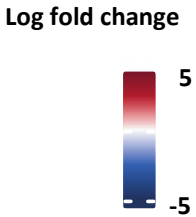


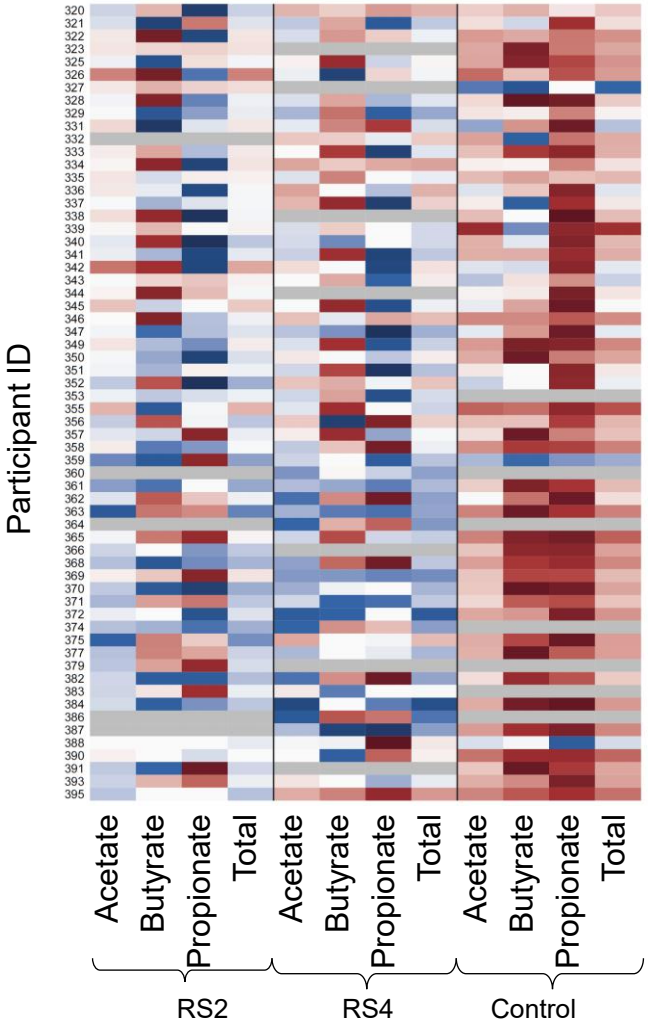
All 59 participants ate all 3 types of crackers: control, RS2, RS4

Half of the participants began with RS2, the other half began with RS4

Interindividual variability







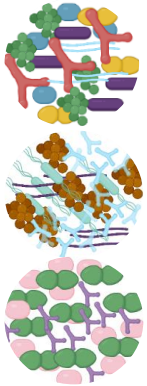
Candidate predictors of SCFA response

Genetics

- ❑ Salivary amylase gene copy number (*AMY1* CN)
- ❑ High versus low *AMY1* CN (group)

Dietary intake

- ❑ Mean salivary amylase activity
- ❑ Dietary fiber intake



Different baseline gut microbiome compositions

- ❑ Group: order of treatment
- ❑ Alpha diversity prior
- ❑ Presence or abundance of species prior

Candidate predictors of SCFA response

Genetics

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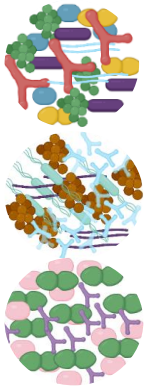
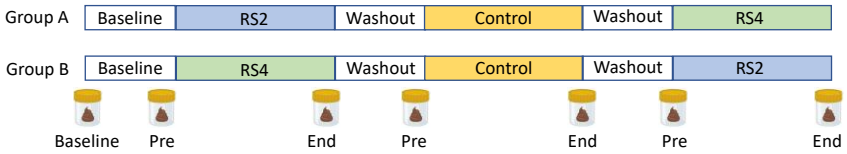
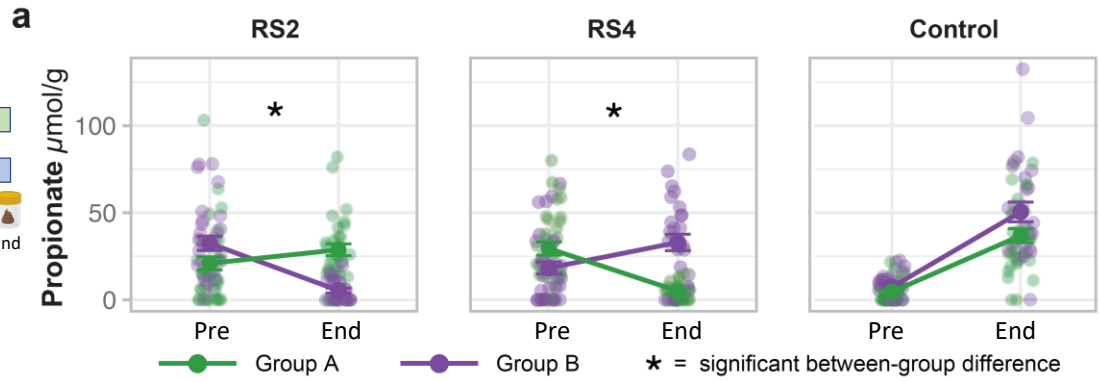


Different baseline gut microbiome compositions

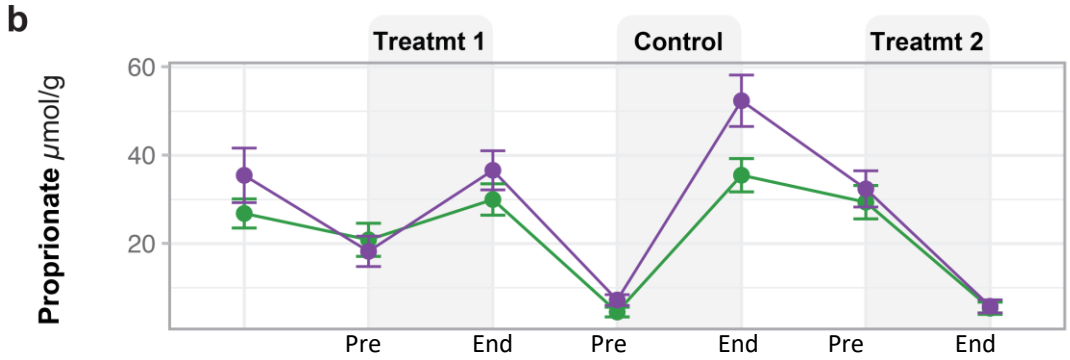
- ✓ Group: order of treatment
- ✓ Alpha diversity prior
- ✓ Presence or abundance of species prior

Group predicts propionate response





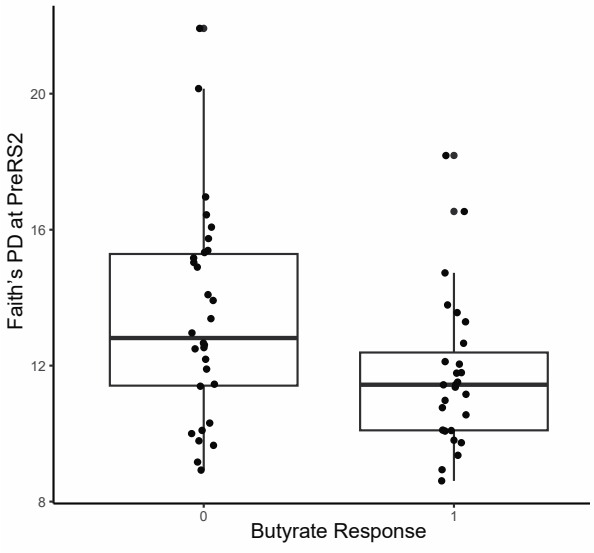
Propionate concentration more likely to increase during the first RS treatment than the third RS treatment

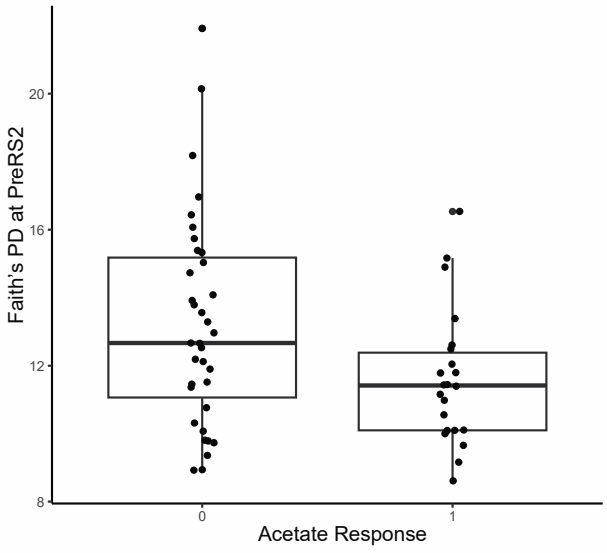


Method: Linear regression

Alpha diversity predicts butyrate and acetate response to RS2

Lower Faith's PD at PreRS2 associated with a significantly higher odds of an increase in butyrate and acetate by EndRS2





0 = No change or decrease
1 = Increase

For every unit increase in Faith's PD at PreRS2, the odds of an increase in butyrate and acetate were each 22% **lower**

Method: Logistic regression

Significant predictors of SCFA change = Log(End/Pre)

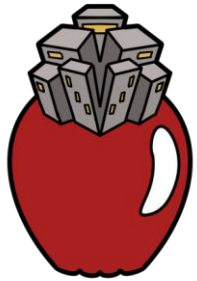
What combination of accounts the variability in SCFA response to RS supplementation?

- Treatment order (Group A vs Group B)
- Subset of microbes at Pre time points

Method: LASSO

Perspective

- Remaining questions
  - Reproducibility of predictors across populations
  - Impact on other gut microbial metabolites
  - Impact on metabolic health
  - Predict responses to whole food sources of dietary fiber
  - In vitro systems to study oral and gut microbiota
- Long-term applications
  - Manipulation of oral microbiota to prevent pathology
  - Dietary changes that maximize benefits of dietary fiber intake
  - Outcomes: lower PPGR, lower blood lipids, weight loss
  - Predictors: host genotype, microbiome, lifestyle factors
  - Implementation: translation, accessibility, adherence



Precision Nutrition New York

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LAB MEMBERS:

Sri Devarakonda
Dorothy (Kim) Superdock
Jennifer Ren
Alexis Loinard-González
Jacqueline Anaeto
Belle Lin
Janice Liu
Alizeh Khan
Shuai Mann
Megan Eno

COLLABORATORS AND CONSULTANTS:

Lynn Johnson
Erica Bender
Meghan Witherow
Christopher Loss
Catalin Moraru
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Tory Hendry

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