Precision Nutrition Model Predicts Postprandial Glucose Response Following Potato Intake

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ABSTRACT

Background: Individual glycemic responses following dietary intake result from complex physiological processes. These processes can be influenced by physical properties of foods, such as increased resistant starch (RS) from retrogradation of starch in foods upon cooling after cooking. Predictive equations are needed to provide personalized recommendations for those most at risk for poor metabolic outcomes.

Methods: Overweight women with no comorbid conditions participated in a randomized crossover trial, in which they consumed 250g of hot (boiled) or cold (baked and chilled 5 days) potatoes. Baseline characteristics included demographics, 10-d dietary records, body composition, and the relative abundance (RA) and Simpson α-diversity of gut microbiota. Elastic net regression using 5-fold cross-validation predicted postprandial glucose response (PPGR) following the potatoes, determined by incremental $AUC_{0-120min}$ (iAUC).

Results: Thirty participants (29.6 ± 6.0 years; BMI 32.8 ± 3.7 kg/m^2) consumed 250 g of Russet potatoes: ~9.2g of RS from the hot potato and ~13.7g of RS from the cold potato (p=0.009). Most women (70%) showed a favorable PPGR to the cold potato. The model explained 32.2% of the variance in iAUC glucose with the equation: 547.65 x (0 [if cold potato], x 1 [if hot potato])* + (BMI [kg/m^2] x 40.66) - (insoluble fiber [g] x 49.35) + (*Bacteroides* [RA] x 8.69) - (*Faecalibacterium* [RA] x 73.49)* - (*Parabacteroides* [RA] x 42.08) + (α-diversity x 110.87) + 292.52 (* indicates p=0.01, all else NS).

Conclusion: Gut microbiota and potato preparation method significantly predicted PPGR following potato intake in overweight females. This model provides a better understanding of factors driving interpersonal variation in PPGR and offers a tool to optimize dietary recommendations for a commonly consumed food.

PURPOSE

The purpose of this project was to better understand subject characteristics and baseline features contributing to differences in PPGR following potato intake among subjects. We developed a model to predict the PPGR that can be used for personalized recommendations in women with a BMI 25-40 kg/m^2. We focused on the same type of potato (Russet) and manipulated the RS content through cooking to demonstrate the functional aspect RS has on PPGR.
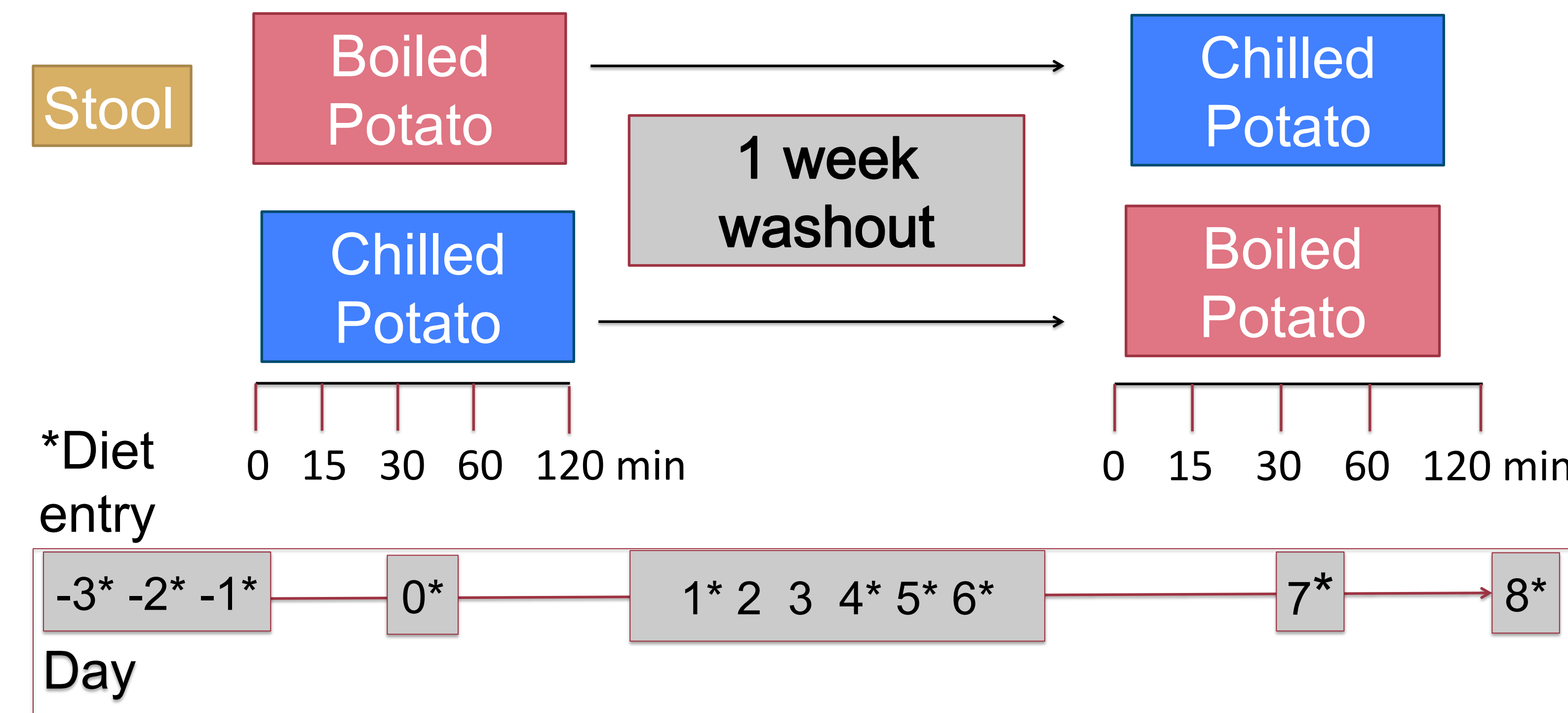
METHODS

Figure 1. Study flow of the crossover design

Blood glucose was collected immediately before each potato intervention and at 15, 30, 60 and 120 min postprandially. Stool was collected prior to any intervention. The Nutrition Data System for Research was used for dietary analysis. Pearson's correlations were performed between PPGR and baseline characteristics (**Table 1**), with a Bonferroni correction applied to microbiome data. Stata v16.1 was used for data analysis; p<0.05 was considered significant.

RESULTS

Most women showed a lower PPGR following the cold potato compared to the hot potato, likely due to the higher RS concentration in the cold potato. Baseline features that were correlated with glucose iAUC were different between potatoes, with dietary intake correlating only with the cold potato. No demographic or microbiota characteristics correlated with PPGR after Bonferroni correction.

Table 1. Significant correlations between postprandial glucose (iAUC) and baseline characteristics

	Glucose – Hot Potato		Glucose – Cold Potato	
	Rho	P value	Rho	P value
Height, cm	-0.38	**0.04**	-0.23	0.23
Insoluble fiber, g	-0.20	0.28	-0.37	**0.04**
Kcals from fat, %	-0.13	0.49	0.39	**0.03**
Kcals from protein, %	-0.20	0.30	0.50	**0.005**
Actinobacteria*	-0.16	0.67	-0.40	**0.04**
*Faecalibacterium**	-0.44	**0.02**	0.03	0.87

*No longer statistically significant after Bonferroni correction

RESULTS
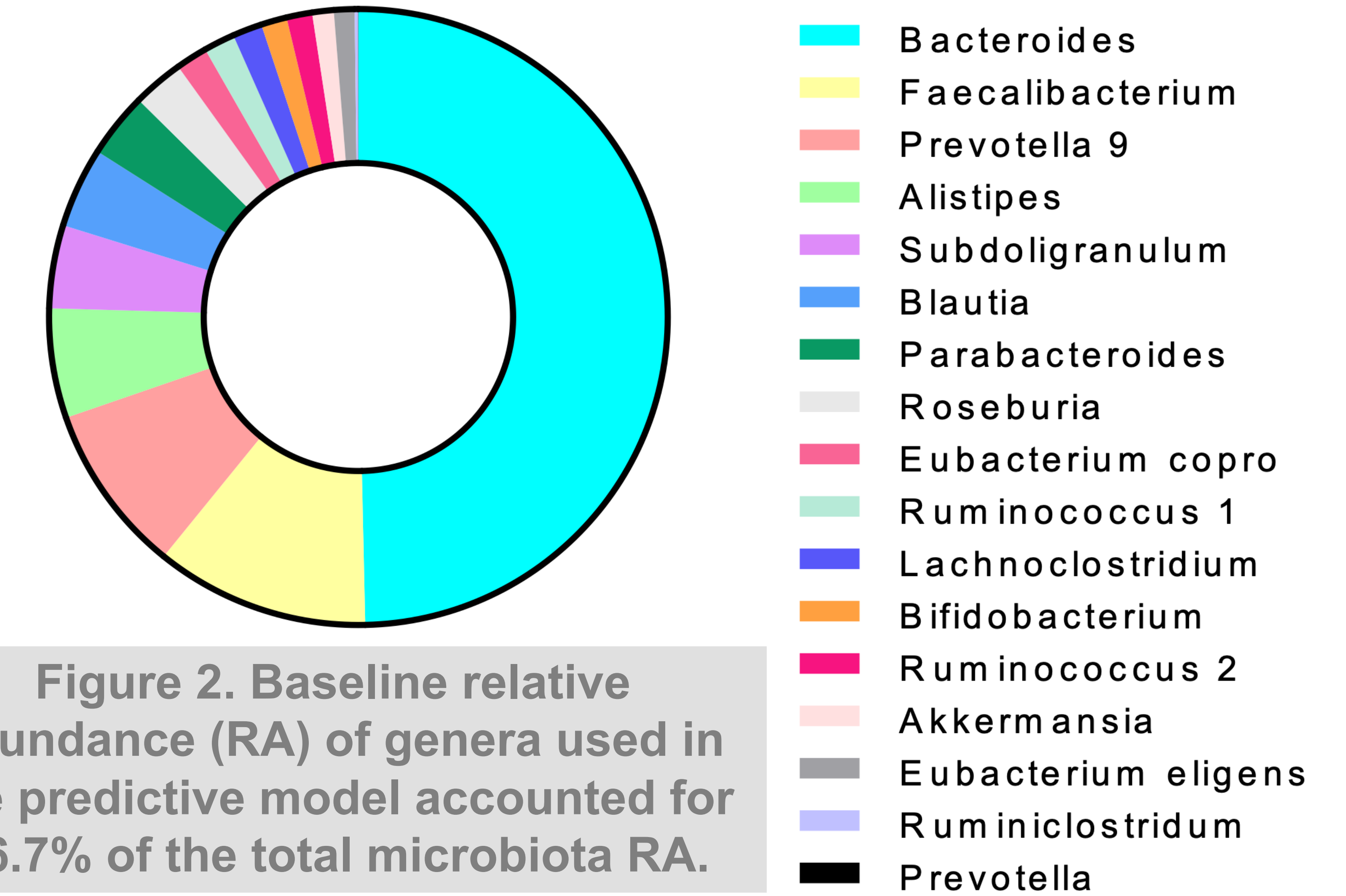

Figure 2. Baseline relative abundance (RA) of genera used in the predictive model accounted for 66.7% of the total microbiota RA.

- Bacteroides
- Faecalibacterium
- Prevotella 9
- Alistipes
- Subdoligranulum
- Blautia
- Parabacteroides
- Roseburia
- Eubacterium copro
- Ruminococcus 1
- Lachnoclostridium
- Bifidobacterium
- Ruminococcus 2
- Akkermansia
- Eubacterium eligens
- Ruminiclostridium
- Prevotella

Most participants had a microbiome profile abundant in *Bacteroides* and *Faecalibacterium* (**Figure 2**). Only the potato type (hot vs cold) and *Faecalibacterium* relative abundance significantly contributed to the model (**Table 2**). The model accounted for 32.2% of the PPGR variance.

Table 2. Baseline characteristics to predict PPGR, multivariate regression

	β coef. (95% CI)	P value
Hot (vs cold)	547.65 (131.61, 963.68)	**0.01**
Faecalibacterium	-73.49 (-128.51, -18.47)	**0.01**
Bacteroides	8.69 (-14.33, 31.72)	0.45
BMI	40.66 (-54.21, 135.54)	0.39
Alpha diversity, Simpson	110.87 (-10,209.57, 10,431.30)	0.98
Insoluble fiber, g	-49.35 (-116.56, 17.86)	0.14
Parabacteroides	-42.08 (-136.35, 52.18)	0.37
Intercept	292.52 (-9,705.98, 10,291.01)	0.95

CONCLUSION

Factors that influence the PPGR to potatoes is cooking method, likely due to the higher RS content in the cold potatoes, and *Faecalibacterium*. Future studies should investigate other populations and perform shotgun sequencing to determine specific species that impact PPGR.

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