Impact of a pulse-based vegetarian lunch meal on the modulation of gut bacterial sub-populations

Helena Ferreira[1], Joana Barbosa[1], Célia Costa[1], Marta W. Vasconcelos[1], Ana Gomes[1], Ana M. Gil[2], Elisabete Pinto[1,3]

[1]Universidade Católica Portuguesa, CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Porto, Portugal;
[2]Departamento de Química e Instituto de Materiais CICECO, Universidade de Aveiro, Portugal;
[3]EPIUnit – Unidade de Investigação em Epidemiologia do Instituto de Saúde Pública da Universidade do Porto, Portugal

INTRODUCTION

The current global trend to adopt more plant-based diets is expected to increase the intake of pulses in the near future, given their potential as eco-friendly nutrient-rich alternatives to animal-based protein food sources. Still, more comprehensive data, as well as higher quality food intervention trials, are needed to fully understand the health benefits of such dietary shift, namely at the gut microbiota level. In this context, the use of molecular biology research tools, such as quantitative Polymerase Chain Reaction (qPCR) could be useful to monitor the dietary modulation of gut bacterial sub-populations.

OBJECTIVE

To investigate the modulation of gut bacterial populations after an 8-week pulse-based food intervention using qPCR optimized for 5 bacterial genera.

METHODOLOGY

Twenty-five non-vegetarian healthy young adults (18-45 years) were asked to replace a typical omnivorous lunch meal with a vegetarian pulse-based meal, 5 times per week, for 8 consecutive weeks. Stool samples were self-collected at weeks 0 (T0) and 8 (T8), in a total of 50 samples, and total DNA was extracted using NZY Tissue gDNA isolation Kit (NZYTech, Lisbon, Portugal). A sequence region of the gene 16S rRNA specific for Akkermansia muciniphila, Roseburia spp., Bifidobacterium spp., Clostridium leptum subgroup, and Faecalibacterium prausnitzii, was quantified using qPCR.

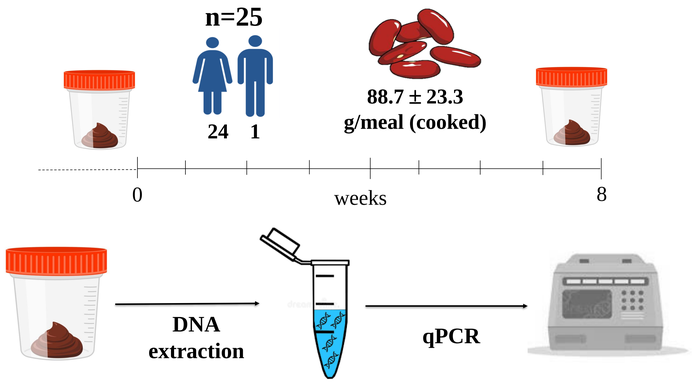


Figure 1. Diagram of study design.

RESULTS

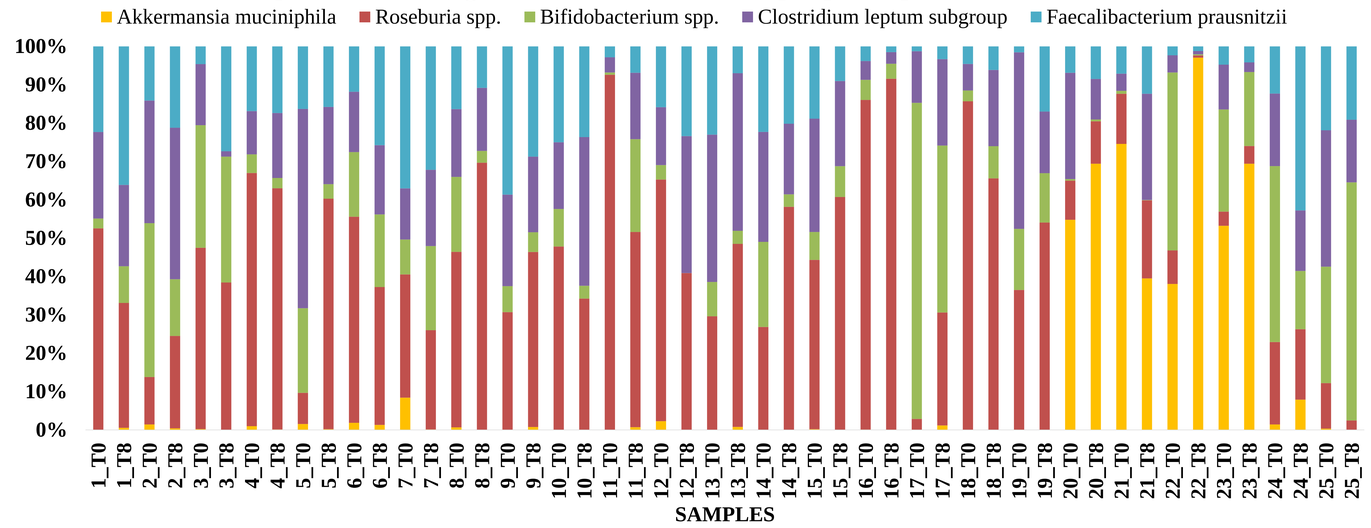
Table 1 represents the 5 bacteria genera variations per participant, between baseline and the end of the 2-month food intervention. In turn, graphic 1 represents the relative abundance of each bacteria genera, expressed as the percentage in relation to the total 5 bacterial sub-populations analyzed. In both cases, the results are expressed as variations in the number of copies of the gene 16S rRNA per ng of DNA. All in all, results reveal an evident interindividual variability after the 8-week pulse-based food intervention, apparently with no clear net tendency on the modulation of the analyzed gut bacterial sub-groups.

Table 1. Bacteria genera variations per participant between T0 and T8.

	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18	P19	P20	P21	P22	P23	P24	P25
ROSE	↓	↑	↓	↑	↑	→	↑	↑	↑	→	↓	→	↑	↑	→	↑	↑	↓	→	→	↑	↓	→	↓	→
BIF	→	↑	↓	↑	↑	→	↑	→	→	↓	↑	↓	→	↓	→	↑	↓	→	↑	→	→	↓	↓	↓	→
CLEP	↓	↑	↓	↑	↑	→	↑	↑	→	↑	↓	↑	→	→	→	↑	→	→	→	↓	↑	↓	↓	↓	→
FPRAU	↓	↑	→	↑	↑	↑	↑	↑	→	→	↓	↑	→	↑	↓	↑	→	→	↑	→	→	→	→	→	→
AKK	↑	→	a	→	↑	→	↓	↓	↑	ND	↑	a	b	ND	↓	↑	↑	→	a	→	→	↑	↓	→	a

AKK - Akkermansia muciniphila; BIF - Bifidobacterium spp.; CLEP - Clostridium leptum subgroup; FPRAU - Faecalibacterium prausnitzii; ROSE - Roseburia spp.
a – below detection limit at T8; b – below detection limit at T0; ND – below detection level at T0 and T8; ↑ - increase $p<0.05$; ↓ - decrease $p<0.05$; → - no statistically significant change.

Graphic 1. Bacteria genera relative abundance per participant at T0 and T8



CONCLUSIONS

An 8-week pulse-based food intervention caused different gut bacteria modulation profiles in each individual, masking any potential generalized effects of the diet. This highlights the need for personalized approaches concerning health and nutrition research fields.

ACKNOWLEDGEMENTS

This work was supported by National Funds from FCT - Fundação para a Ciência e a Tecnologia through project UIDB/50016/2020 and by the project "Transition paths to sustainable legume-based systems in Europe" (TRUE) which has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No. 727973. HF would like to acknowledge FCT for doctoral grant ref. SFRH/BDE/132240/2017. AMG acknowledges the CICECO-Aveiro Institute of Materials project, with references UIDB/50011/2020 & UIDP/50011/2020, financed by national funds through the FCT/MEC and when appropriate co-financed by FEDER under the PT2020 Partnership Agreement. The NMR spectrometer is part of the National NMR Network (PTNMR) and are partially supported by Infrastructure Project Nº 022161 (co-financed by FEDER through COMPETE 2020, POCI and PORL and FCT through PIDDAC).