Evaluation of the prebiotic potential of *Coriolus versicolor*-Effect on the human gut microbiota

C.M. Costa[1*], S. Silva[1], L. Pimentel[1] and M.M. Pintado[1]

[1]Universidade Católica Portuguesa, CBQF – Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Rua Arquiteto Lobão Vital 172, 4200-374 Porto, Portugal

*corresponding author: celiamsfcosta@gmail.com

CATÓLICA
FACULTY
OF BIOTECHNOLOGY
PORTO

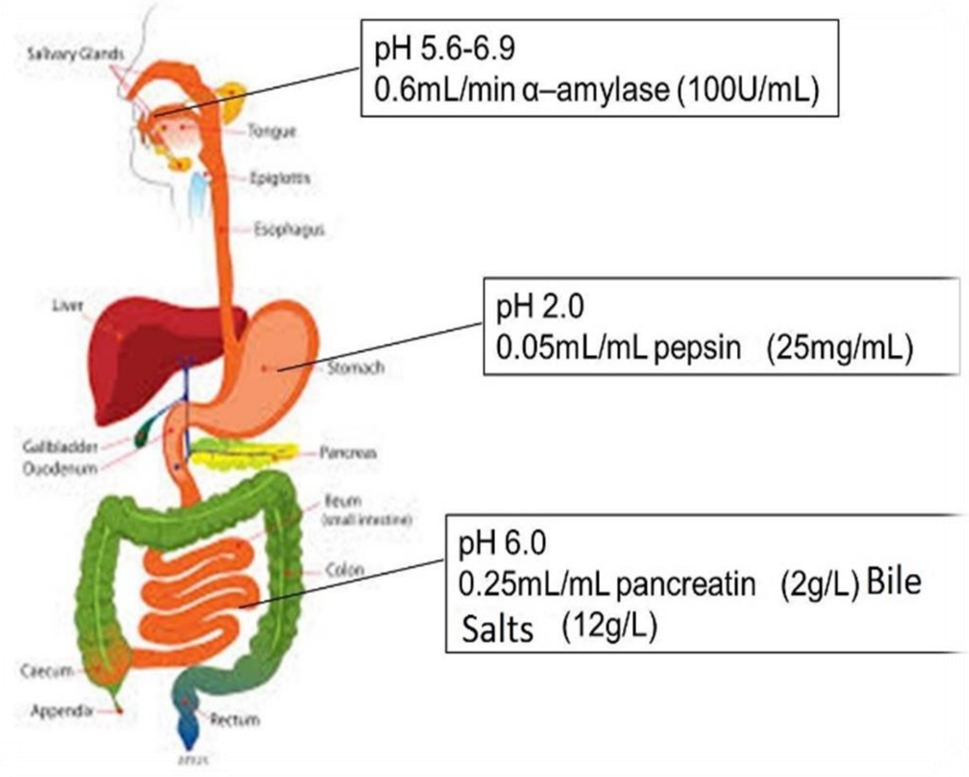
6th World Congress on
Targeting Microbiota
Towards Clinical Revolution
October 28-30, 2018 · Porto, Portugal

Introduction

The human gut microbiota has become increasingly relevant when studying human health and disease due to its connection with the immune system and metabolism. Several factors are known to shape the microbiota composition, such as age, diet or genetic markers. Furthermore, the gut microbiota can be actively modulated by prebiotics, which pass through the gastrointestinal tract and are then fermented by colonic bacteria, leading to the production of metabolites and to changes in the microbial population dynamics'[1]. In parallel, mushroom's consumption has becoming more relevant in western diets. *Coriolus versicolor* is a mushroom known for its immunomodulatory properties but has also displayed prebiotic-like activity in previous studies[2,3]. The main goal of the present work was to evaluate the prebiotic potential of a commercial supplement of *C. versicolor* biomass through *in vitro* faecal fermentations, using fresh faecal samples from five healthy donors, and to perform the subsequent analysis of changes in the bacterial population as well as concerning the production of short chain fatty acids (SCFA).

Methods

- **Simulation of gastrointestinal tract digestion and dialysis**

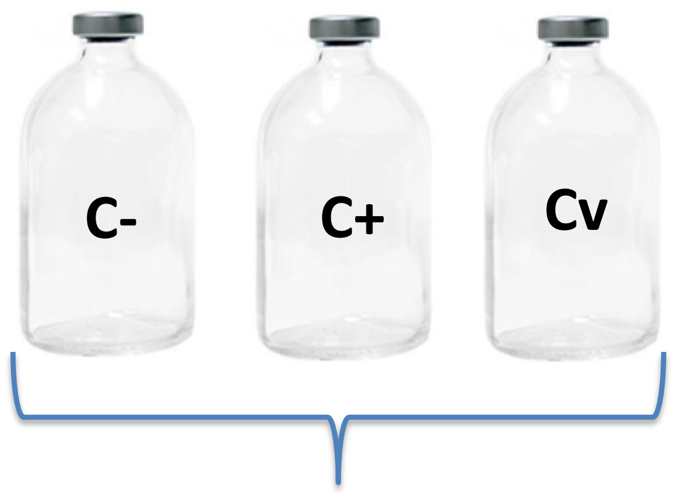


pH 5.6-6.9
0.6mL/min α–amylase (100U/mL)

pH 2.0
0.05mL/mL pepsin (25mg/mL)

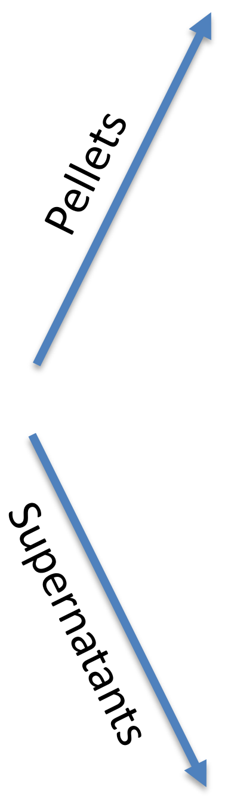
pH 6.0
0.25mL/mL pancreatin (2g/L) Bile Salts (12g/L)

- **Faecal fermentations**



Negative control (C-): only medium and faecal inoculum;
Positive control (C+): medium, faecal inoculum and FOS;
Cv: medium, faecal inoculum and *C. versicolor* digested biomass powder.

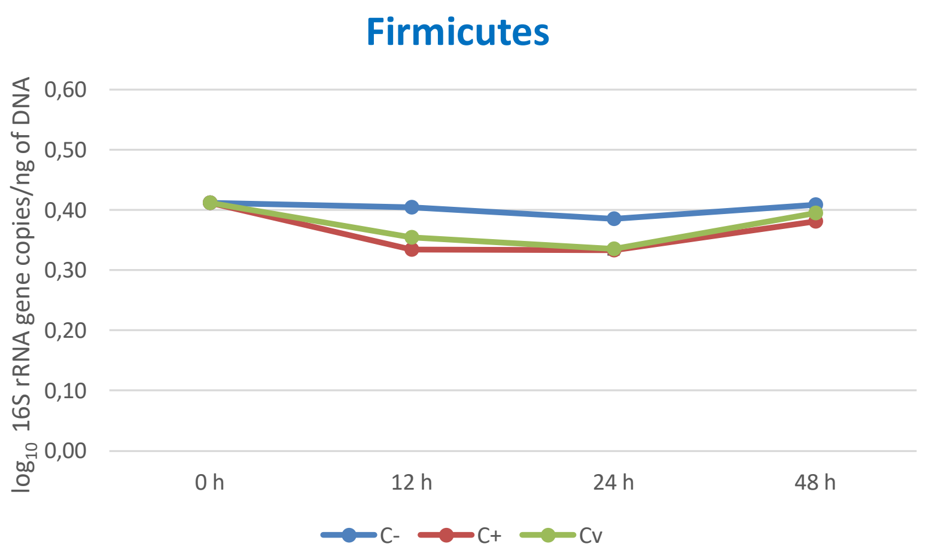
Sampling at **0, 12, 24** and **48 h; pH values** measurement and centrifugation

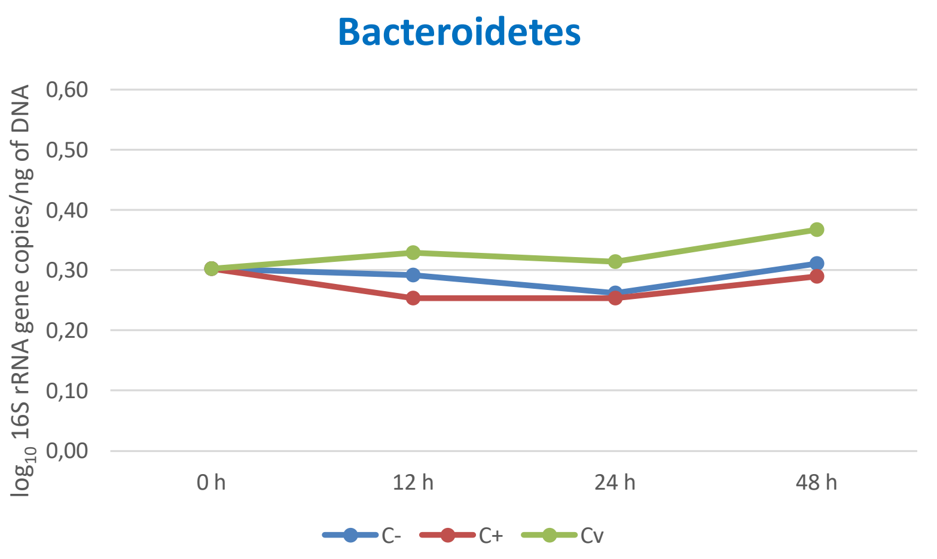


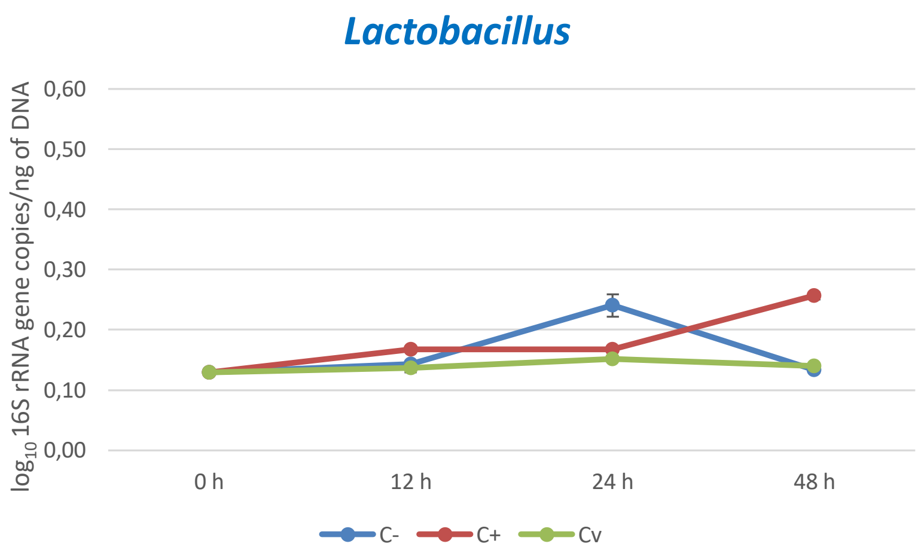
- After DNA extraction of the samples collected, **the bacterial population** was analyzed through **qPCR**

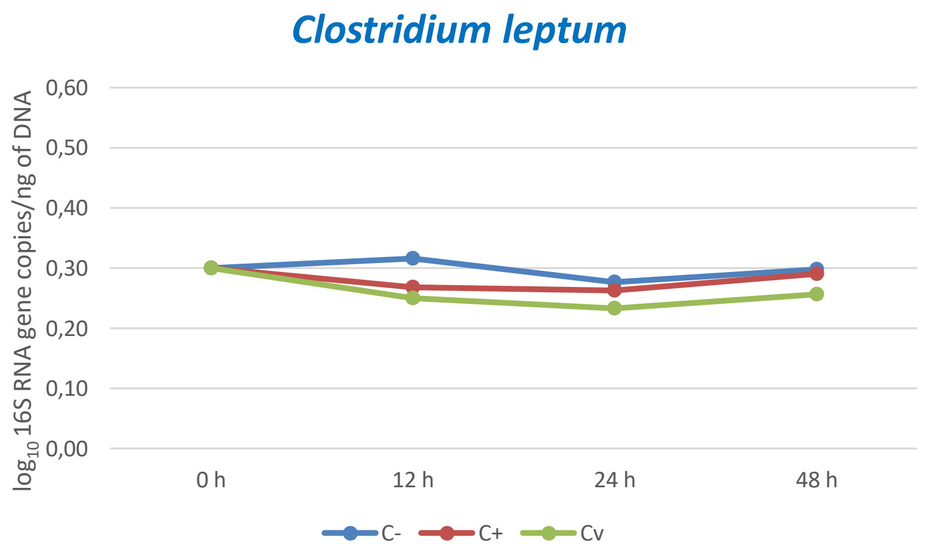
- **Sugar consumption** and **SCFA production** evaluated through **HPLC**

Results









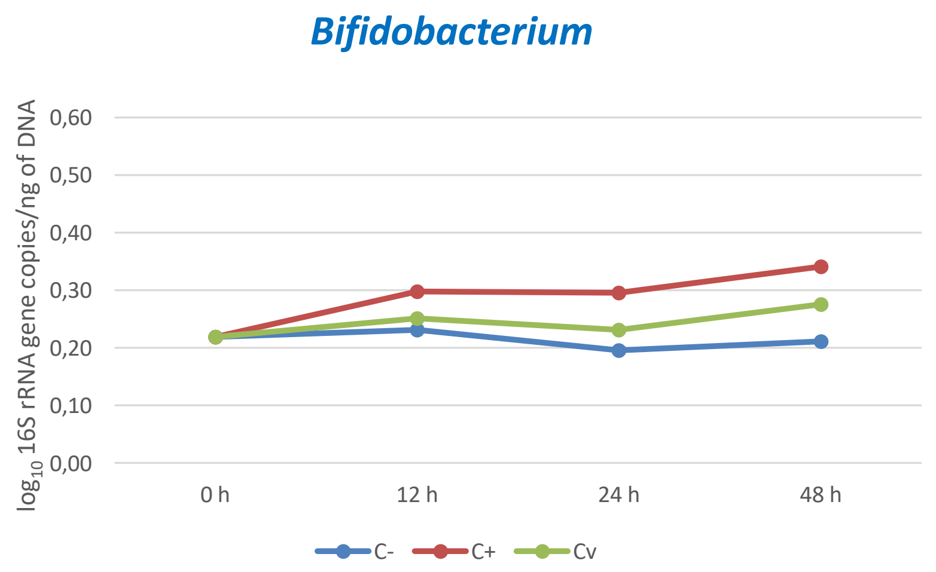


Figure 1. Variation of microbiota in one of the donors. Values presented as $\log_{10}$ 16S rRNA gene copies per ng of DNA through time. Assays done in quintuplicate.

Table 1. Overall **s**ugar consumption and short chain fatty acids production (mg.mL^{-1}), along with pH values for controls and *Coriolus versicolor* digested biomass, at each sampling time, for the five donors (mean±standard deviation).

	0 h	**12 h**			**24 h**			**48 h**		
	C-; C+; Cv	C-	C+	Cv	C-	C+	Cv	C-	C+	Cv
Glucose	0.199 ± 0.023	0.238 ± 0.028	nq	0.940 ± 0.266	0.220 ± 0.027	nq	0.733 ± 0.191	0.214 ± 0.016	nq	0.577 ± 0.270
Frutose	nd	nd	3.45 ± 1.306	nd	nd	3.240 ± 0.731	nd	nd	2.64 ± 1.762	nd
Sucrose	nd	nd	0.178 ± 0.006	nd	nd	0.184 ± 0.009	nd	nd	0.190 ± 0.013	nd
Arabinose	nd	0.373 ± 0.224	nd	0.275 ± 0.079	nd	nd	0.281 ± 0.057	nd	nd	0.266 ± 0.094
Propionic	nd	nd	nd	0.0312 ± 0.002	0.0136 ± 0.004	nd	0.048 ± 0.028	0.0299 ± 0.007	nd	0.0184 0.007
Lactic	nd	nd	0.0177 ± 0.005	nd	nd	0.0841 ± 0.056	0.034 ± 0.026	nd	0.0971 ± 0.064	0.0320 ± 0.022
Acetic	nd	0.126 ± 0.033	0.135 ± 0.079	0.0975 ± 0.046	0.404 ± 0.092	0.370 ± 0.195	0.171 ± 0.024	0.696 ± 0.339	0.642 ± 0.394	0.212 ± 0.088
Butyric	nd	nd	nd	nd	0.0117 ± 0.001	0.0753 ± 0.111	0.014 ± 0.01	0.0239 ± 0.007	0.0182 ± 0.004	nd
pH values	5.90 ± 0.10	5.89 ± 0.14	4.20 ± 0.04	5.25 ± 0.36	6.15 ± 0.35	3.78 ± 0.27	5.00 ± 0.29	6.40 ± 0.16	3.49 ± 0.18	4.79 ± 0.20

Conclusions

- *C. versicolor* biomass had a bifidogenic effect and induced positive changes in the gut microbiota with Firmicutes and *C. leptum* population as observed for positive control FOS;
- The pH values decreased throughout the 48 h of fermentation thus showing that *C. versicolor* was fermented;
- The fermentation led to the production of SFCA and sugar consumption. Glucose was consumed, and arabinose (a sugar present in mushrooms) was detected but not consumed. Propionic and acetic acid were detected after 12 h, but lactic acid was only detected after 24 h of fermentation;
- These results may open the possibility for its establishment as a prebiotic ingredient.

Acknowledgements

The authors would like to acknowledge the funding provided by Fundação para a Ciência e Tecnologia (FCT, Lisboa, Portugal) through the project UID/Multi/50016/2013 and also by Mycology Research Laboratories (UK)

1. Wang, B., Yao, M., LV, L., Ling, Z. & Li, L. 2017. *The Human Microbiota in Health and Disease. Engineering, 3, 71-82.*
2. Cruz, A., Pimentel, L. L., Rodríguez-Alcalá, L. M., Fernandes, T. & Pintado, M. 2016. *Health Benefits of Edible Mushrooms Focused on Coriolus versicolor: A Review. Journal of Food and Nutrition Research, 4, 773-781.*
3. Yu, Z.-T., Liu, B., Mukherjee, P. & Newburg, D. S. 2013. *Trametes versicolor Extract Modifies Human Fecal Microbiota Composition In vitro. Plant Foods for Human Nutrition, 68, 107-112.*