

FUNglucan

Effects of rich in β-glucans edible mushrooms on the gut microbiota characteristics of healthy elderly: an in vitro study

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INTRODUCTION

Gut microbiota (GM) is the largest and most complex microbial community in the body and is associated with various health promoting activities. Fungal β -glucans, from the cell wall of yeasts and fungi, are non-starch polysaccharides with differences in their chemical structure and bioactivity. Dietary interventions for modulation of GI microbiota by mushrooms rich in β -glucans, have not been widely conducted; nevertheless, increasing experimental evidence supports their potential prebiotic action and their beneficial health effects. The aim of this project is to investigate the impact of edible mushrooms rich in β -glucans on the gut microbiota composition and metabolites production using an *in vitro* batch culture fermentation system inoculated with faecal samples from healthy elderly.

MATERIALS AND METHODS

Mushrooms from six fungal strains rich in β-glucans (genera *Cyclocybe, Pleurotus,* and *Hericium*), cultivated in different substrates, were evaluated for their prebiotic activity.

□ They were fermented *in vitro* in static anaerobic batch cultures with faecal inoculum from eight healthy elderly individuals with no history of gastrointestinal disorders and antibiotics consumption for at least 2 months before entering the study.

- □ The mushrooms (2% w/v) were transferred in sterile basic culture medium and inoculated with 10% (v/v) faecal slurry under anaerobic conditions (37°C, 24 h).
- Samples were taken at 0h, 8h and 24h. Microbial populations (Total Bacteria, Lactobacillus, Bifidobacterium sp., Bacteroides sp., and Clostridium perfringens group) were assessed at baseline and after 24 h of fermentation using qPCR.
- □ The prebiotic indexes for all the mushrooms-substrates were calculated.
- □ Production of short chain fatty acids (SCFAs) was also measured by gas chromatography.

RESULTS



Figure A: Prebiotic Indexes from substrates: INU2 (Inulin), POWS (*P. ostreatus* 1123 – WS substrate), POOLRP (*P. ostreatus* 1123 – OLRP substrate), POLWS (*P. ostreatus* LGM 22– WS substrate), POLTPOMW (*P. ostreatus* LGM 22 – OL:TPOMW 3:1 substrate), PEWS (*P. eryngii* Zheng 216 – WS substrate), PEWSGM (*P. eryngii* Zheng 216 – WS:GM 1:1 substrate), HEBS (*H. erinaceus* – BS substrate), HEOLRP (*H. erinaceus* – OLRP substrate), CC2WS (*C. cylindracea* CC2 – WS substrate), CC505WS (*C. cylindracea* 505 – WS substrate). NC: Negative control



- The Prebiotic Index (PI) describes the relationship between changes of "beneficial" bacteria, such as *bifidobacteria* and *lactobacilli* with those of the "undesirable" bacteria, such as *clostridia* and *bacteroides*, in relation to the changes of the total number of bacteria. The PI gives a quantitative score that describes the prebiotic effect. As shown in figure A, all the treatments of substrates were characterized by positive prebiotic indexes. Substrates PEWS, CC2WS and CC505WS exerted higher PI scores than the positive control inulin.
- Substrates INU2, PEWS and PEWSGM increased significantly the levels of Lactobacillus group, compared to the negative control after 24-h fermentation. Further more Lactobacilli levels from PEWS and PEWSGM were comparable to inulin.
- Bifidobacteria significantly increased after fermentation of INU2, POOLRP and CC505WS, compared to the negative control after 24 -h fermentation. Furthermore, bifidobacterial levels from POOLRP and CC505WS were comparable to inulin.
- It is noteworthy that substrates CC2WS and CC505WS showed significantly reduced levels of *Bacteroides* after 24-h fermentation compared to baseline. A similar effect was noticed in the case of negative control.
- Total concentration of SCFAs was low in all treatments at t=0, while after 24h fermentation all substrates showed increased SCFAs levels compared to negative control.

CONCLUSION

This research highlighted the potential role of certain edible mushrooms, rich in β -glucans as candidate prebiotics. Strains of *Pleurotus* and *Cyclocybe* genera had a beneficial influence on the gut microbiota composition of elderly subjects.

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