The prebiotic effect of Australian seaweeds on bacterial abundance and short chain fatty acid production in a simulated gut model

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Introduction

Diet is known to affect the composition of the human gut microbiota and the bacterial production of short chain fatty acids (SCFA), which impacts the health of the host [1]. Whole seaweeds (WH) and their extracts contain prebiotic components such as polysaccharides (PS) and polyphenols (PP) that can be digested by gut bacteria. In this study, the Australian brown seaweeds, *Phyllospora comosa* and *Ecklonia radiata*, the green seaweed, *Ulva ohnoi*, and their PS and PP extracts were assessed for potential prebiotic activities using an *in vitro* gut model with human faecal inoculum. Seaweeds are an underutilised source of prebiotics which may be developed as functional foods for gut health.

Methods

Fig. 1 Australian seaweeds under study

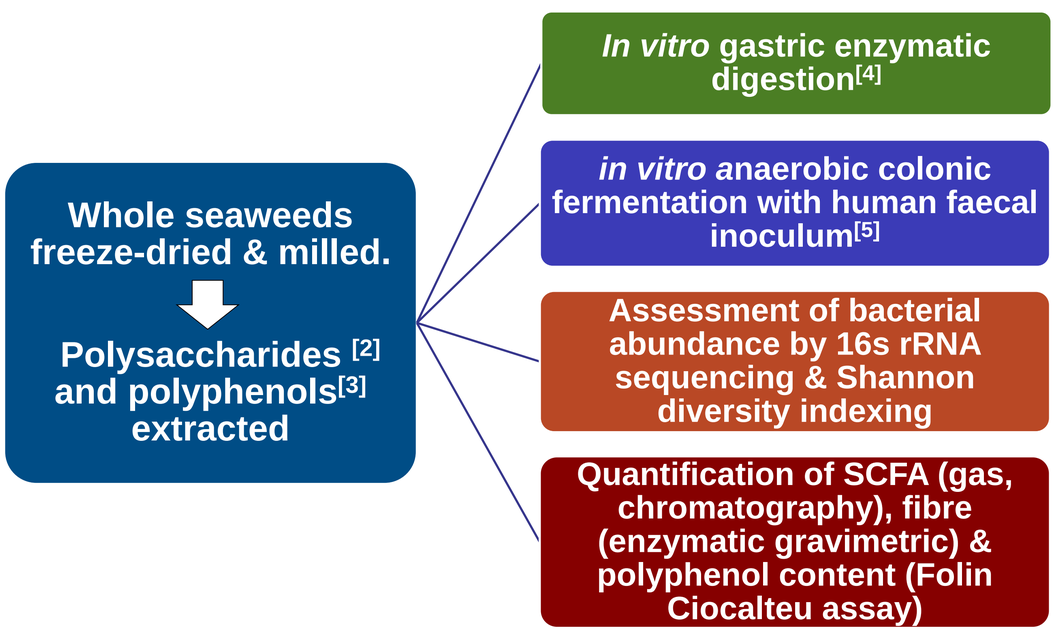

Fig. 2. Experimental process

- Pepsin (porcine, 2,000 U/mg), pancreatin (porcine, 100 U/g protease, 60 U/g lipase, 200 U/g amylase) and amyloglucosidase (*Aspergillus niger*, 30 U/mg) were used to simulate gastrointestinal digestion.
- Fresh faecal samples were collected and pooled from three individual healthy volunteers on no dietary restrictions who had not taken antibiotics for at least 3 months prior to donating.
- Inulin (INU) was used as a positive polysaccharide control, cellulose as a negative, and epigallocatechingallate (EGCG) as a positive polyphenol control.

Results

ENHANCEMENT OF BACTERIAL ABUNDANCE

At Phylum level, Bacteroidetes, Firmicutes, Actinobacteria and Proteobacteria comprised 98.6% of the total bacterial population (Fig. 3). After 24 hr, compared to the INU and EGCG controls, several taxa within the phylum Firmicutes, including the lactic acid producing order Lactobacillales, particularly Enterococci and Ruminococcaceae; and the chief butyrate-producing genera Faecalibacteria, Roseburia and Butyricicoccus, were significantly ($P \leq 0.05$) enhanced by WH & PS extracts. PP extracts enhanced the abundance of some families within the phylum Actinobacteria, namingly Bifidobacteriaceae and Eggerthellaceae; and the genera Blautia and Barnesiella. Bacteroidetes and total Actinobacteria were reduced by all seaweed extracts compared to INU, while Proteobacteria increased. The Shannon Diversity Index and species richness increased in the presence of the WH, PS & PP extracts compared to INU and EGCG controls.

Table 1. **Gastric digestibility**

Seaweed	Gastric digestibility (% DW)
***P. comosa* WH**	**20.28 ± 0.93**
***E. radiata* WH**	**41.98 ± 1.84**
***U. ohnoi* WH**	**26.90 ± 1.07**

Table 2. **Fibre content (% DW)**

	Soluble fibre	Insoluble fibre
***P. comosa* WH**	23.47 ± 0.60	37.41 ± 0.72
***P. comosa* PS**	31.37 ± 0.56	50.49 ± 1.81
***E. radiata* WH**	13.46 ± 0.45	27.82 ± 0.21
***E. radiata* PS**	30.86 ± 0.96	63.09 ± 1.74
***U. ohnoi* WH**	15.05 ± 0.48	32.01 ± 0.34
***U. ohnoi* PS**	28.32 ± 0.30	59.61 ± 1.17

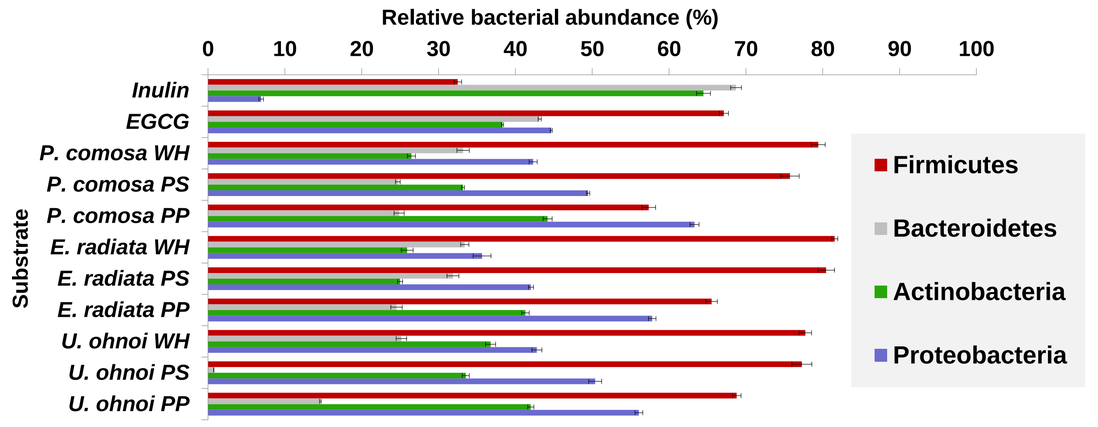

Fig. 3 Relative bacterial abundance at phylum level

ENHANCEMENT OF SCFA PRODUCTION

Total and individual SCFA, particularly butyric, acetic and propionic acids produced by bacteria fermented with *E. radiata* PS and PP; and *U. ohnoi* WH, PS and PP were significantly greater those in INU and EGCG controls (Fig. 4).

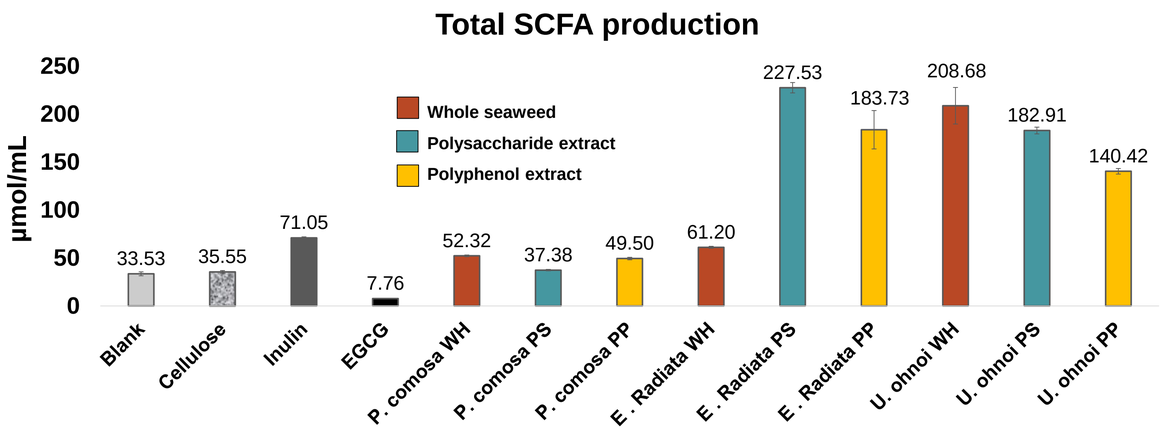

Fig. 4. Total SCFA production by gut bacteria after 24 hr fermentation with each substrate

Conclusion

Whole seaweeds and their polysaccharide and polyphenol extracts showed prebiotic activities in the simulated gut model with up to three-fold increases in SCFA production, and enhancement of bacterial abundance in taxa associated with gut homeostasis, mucosal barrier regulation, SCFA production, immune modulation, and anti-inflammatory effects [6,7]. However, the total abundance of Actinobacteria decreased, while Proteobacteria increased, both of which has been found to occur in the gut microbiota of individuals with gastrointestinal and systemic diseases [8,9]. This study shows that whole seaweeds and their polysaccharide and polyphenol extracts may have potential as prebiotic functional food supplements to maintain normal gut function and alleviate dysbiosis, however, *in vitro* results are not fully representative of the biological fate or impact of dietary prebiotics and must be validated in animal and human trials.

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