

Synthesis and impact of sweet dietary fibres on faecal microbiome composition and activity

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Objectives

Formulate sweet dietary fibres that combine clean flavour profiles with gut microbiome modulation activity.

Methods

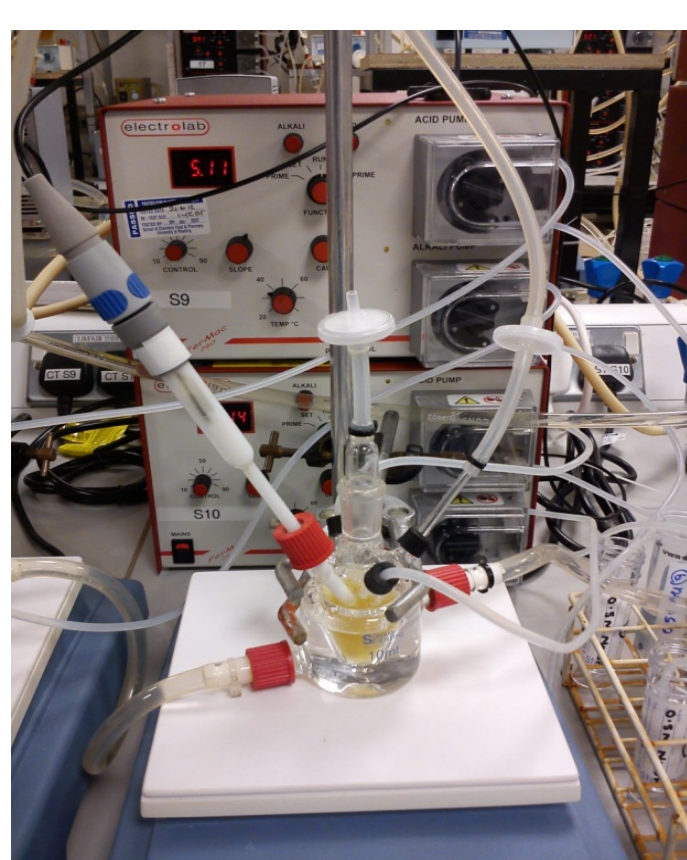
Steviol glycosides (SG) and Mogrosides (MV) were enzymatically modified by fructosyltransferases and β -galactosidases to:

- improve flavor profiles
- reduce sweetness intensity
- add gut microbiome modulation ability

Structure determination was carried out by HPLC-DAD, GC-MS and MALDI-TOF.

Flavour profiles were determined, before and after enzymatic modification, by a panel of 12 expert flavourists.

Gut microbiome modification was determined in 24h, anaerobic, pH controlled, micro-scale faecal cultures.

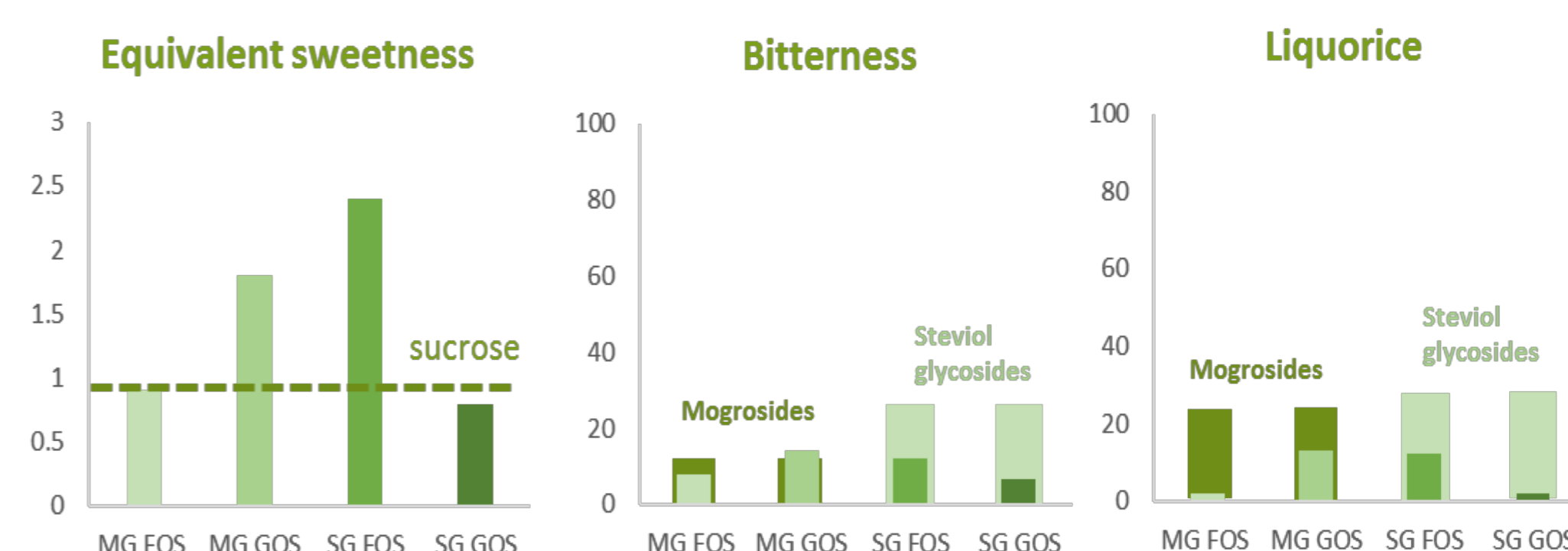
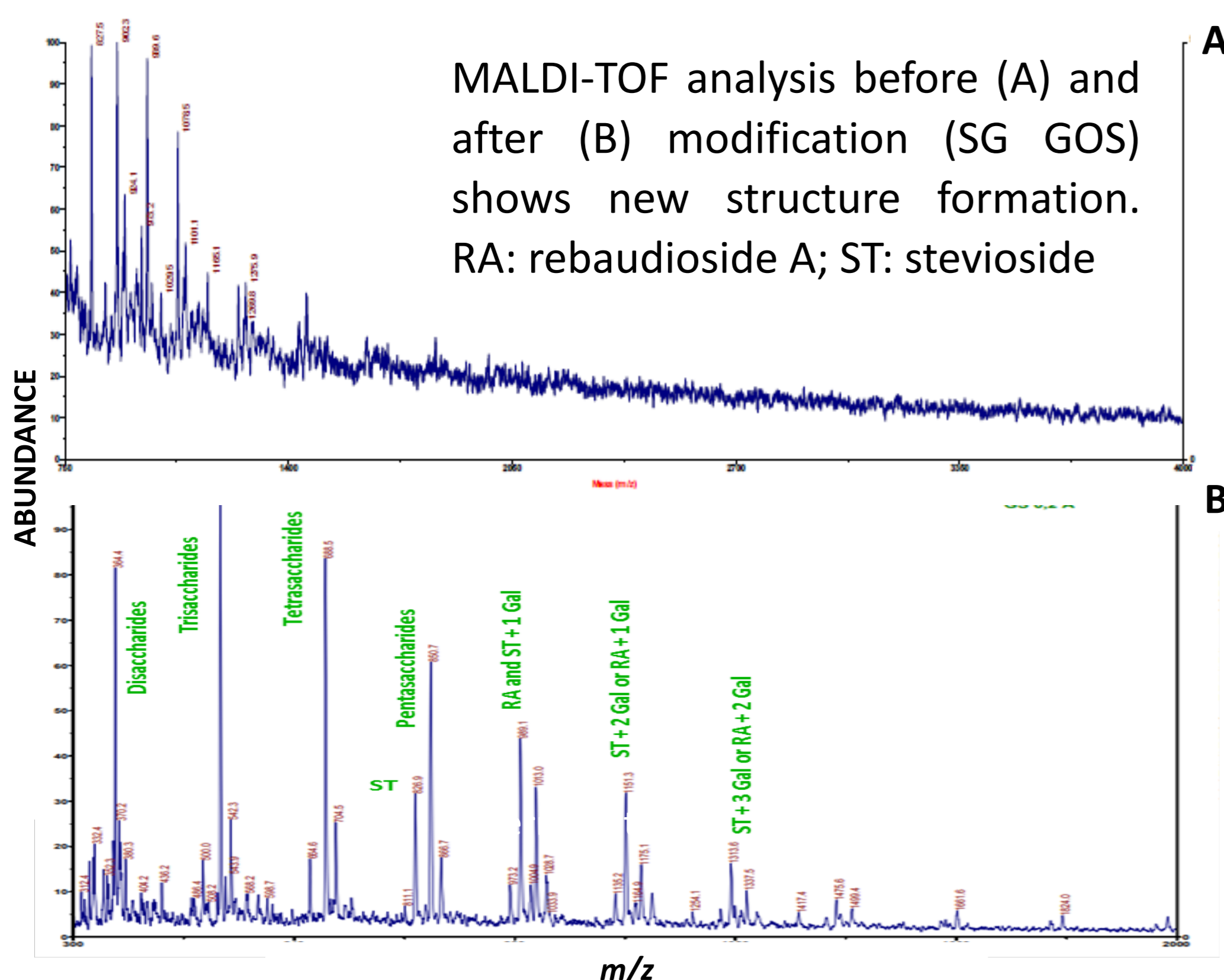


Tests:

- SG FOS: SG modified by fructosyltransferases
- SG GOS: SG modified by β -galactosidases
- MV FOS: MV modified by fructosyltransferases
- MV GOS: MV modified by β -galactosidases

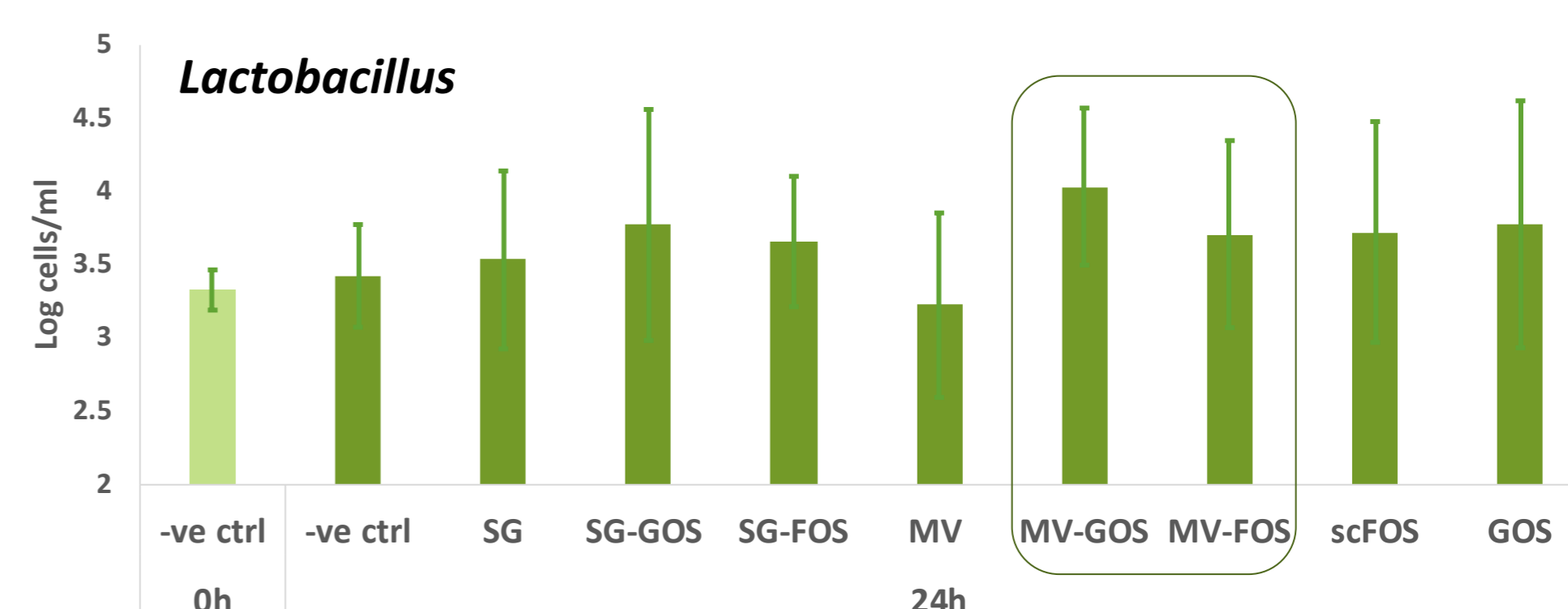
Bacteriology was carried out by real-time PCR and organic acid concentrations were determined by GC-FID.

Results

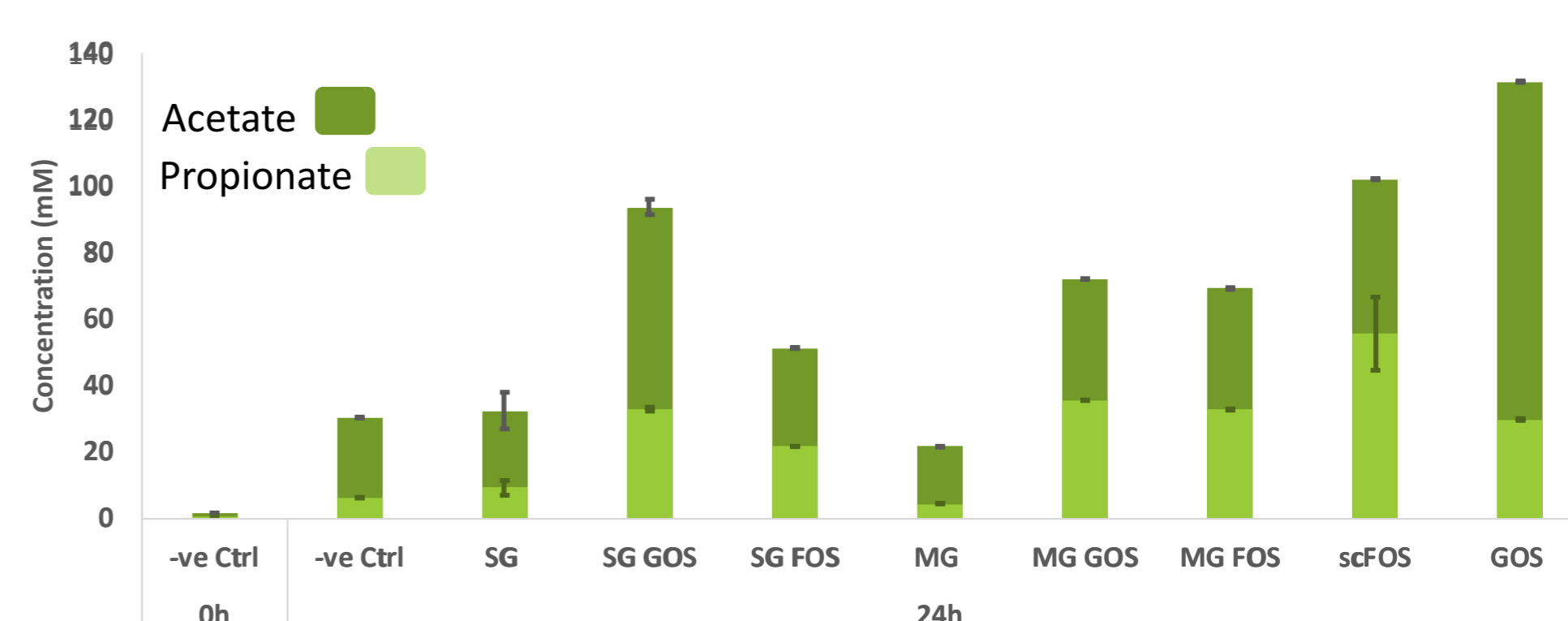


Enzymatic modification significantly reduced:

- Bitterness aftertaste of steviol glycosides
- Liquorice aftertaste of mogrosides



Enzymatically modified MV significantly increased *Lactobacillus* and *C. coccoides* compared to negative control and native MV after 24h faecal culture. Trends for increase in *Bifidobacterium* were also noted.



Enzymatically modified SG and MV significantly increased acetate and propionate compared to negative controls and parent compounds after 24h faecal culture.

Study Highlights

Enzymatic modification of SG and MV generated sweet dietary fibres which:

Significantly **reduced SG bitterness**

Significantly **reduced MV liquorice aftertaste**

MV and SG dietary fibres: significantly increased acetate and propionate and health positive gut bacterial groups, combining **sweetness with health functionality**.