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Title:

Microbiota dynamics and their impact on the metabolite in lupin oat yoghurt analogues

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Abstract: (Your abstract must use **Normal style** and must fit in this box. Your abstract should be no longer than 300 words. The box will 'expand' over 2 pages as you add text into it.)

Preparation of Your Abstract

1. The title should be as brief as possible but long enough to indicate clearly the nature of the study. Capitalise the first letter of the first word ONLY (place names excluded). No full stop at the end.

2. Abstracts should state briefly and clearly the purpose, methods, results and conclusions of the work.

Introduction: Clearly state the purpose of the abstract

Methods: Describe your selection of observations or experimental subjects clearly

Results: Present your results in a logical sequence

Discussion: Emphasize new and important aspects of the study and conclusions that are drawn from them

The growing demand for nutritious, flavour-rich plant-based yoghurt analogues calls for innovative fermentation strategies. This study examined the impact of three probiotic combinations- Y1 (*Lactobacillus delbrueckii subsp. bulgaricus*, *Streptococcus thermophilus* and *Lactobacillus rhamnosus*), Y2 (*Lactobacillus delbrueckii subsp. bulgaricus*, *Streptococcus thermophilus* and *Lactobacillus paracasei*) and Y3 (*Lactobacillus plantarum* and *Bifidobacterium sps*)- on microbial dynamics and metabolite formation in lupin-oat yoghurt analogues, using unfermented milk analogues as a control. Samples were assessed during fermentation and throughout 28 days of refrigerated storage (4 °C) using microbial enumeration, 16S rRNA sequencing, acidification profiling, and mass spectroscopy-based metabolomics. Fermentation increased volatile compounds, from 23 in the control to 28 (Y1), 41 (Y2) and 54 (Y3). Probiotic combination Y3 exhibited the most complex and stable aroma profile, enriched in pleasant volatiles such as butanoic acid, phenylacetaldehyde, and butyl esters which effectively masked off-flavours like hexanal and heptanal. Microbiota analysis revealed stable formulation-specific communities, with- *Streptococcus* dominating in yoghurt analogues Y1 and Y2, and *Bifidobacterium* prevailing in yoghurt analogues Y3. KEGG-based functional prediction linked these transformations to microbial enzymatic activities within metabolic pathways. Notably, *Bifidobacterium* dominance in Y3 facilitated enhanced ester biosynthesis and conversion of aldehydes to acids, highlighting the “bifid shunt” as a key contributor to flavour enhancement. This integrated multi-omics approach highlights the critical role of targeted probiotic selection in modulating fermentation biochemistry, microbial ecology, and sensory attributes in plant-based lupin-oat yoghurt analogues. Notably, *Bifidobacterium*- driven fermentation in Y3 offers a promising strategy for improving the flavour profile and consumer acceptance of lupin-oat yoghurt analogues.