Evaluation of the ability of smear-ripened cheese microbial communities to colonize pea-protein matrix

Mahtab Shoukat, Eric Dugat-Bony, Vincent Hervé, Dominique Swennen, Marjon H.J. Wells-Bennik, Pascal Bonnarme

Evaluation of the ability of smear-ripened cheese microbial communities to colonize pea-protein matrix

Mahtab Shoukat[1], Eric Dugat-Bony[1], Dominique Swennen[1], Vincent Hervé[1], [2]Marjon H. J. Wells-Bennik & Pascal Bonnarme[1]*

[1] Université Paris-Saclay, INRAE, AgroParisTech, UMR SayFood, 91120 Palaiseau, France, [2] NIZO, Ede, Netherlands

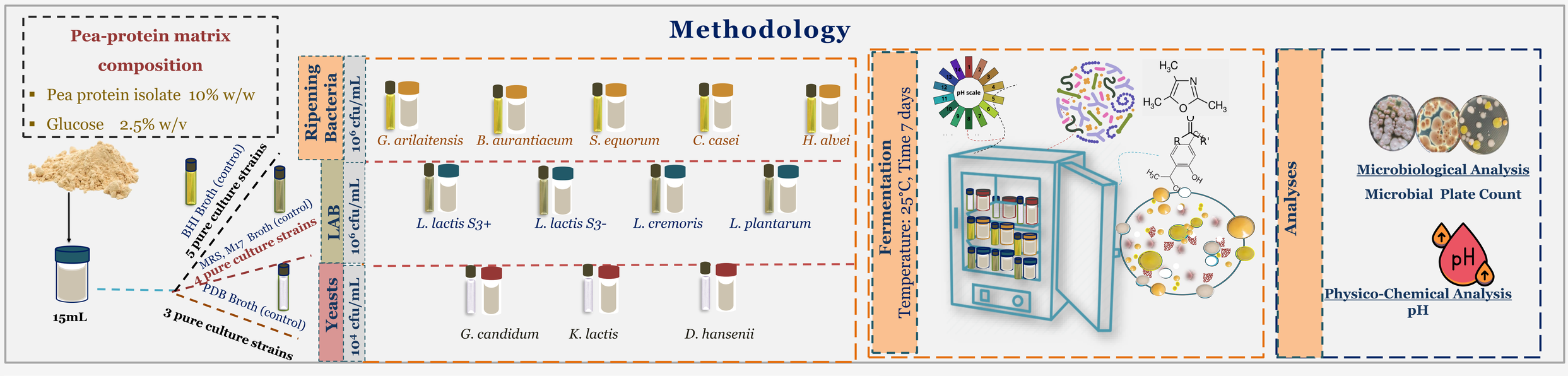
Introduction

Plant-based substitutes for dairy and meat products have been one of the key innovative drivers since the last decade due to concerns about sustainability, lifestyle, and dietary limitations (El Youssef *et al.*, 2020). Pea protein is one of the most preferable plant-based protein to develop plant-based substitutes due to its high nutritional value (Masiá *et al.*, 2022). However, **microbial safety** and **sensory attributes** of these plant-based products are the main technological and scientific challenges for the food industry (Ben-Harb *et al.*, 2022). **Fermentation** and **ripening processes** may help to enhance the microbiological safety, nutritional, physicochemical, and sensory characteristics of plant-based products (Ben-Harb *et al.*, 2020). However, to understand the evolution and behaviour of microorganisms during these processes is crucial for the development of plant-based products with desired characteristics.

Aims & Objectives

- To evaluate the ability of smear-ripened cheese microbial communities to colonize a pea-protein matrix.
- To understand the growth behaviour of different cheese microorganisms in pure culture fermentation conditions.
- To identify microbial strains with optimum potential for pea-protein based cheese ripening.

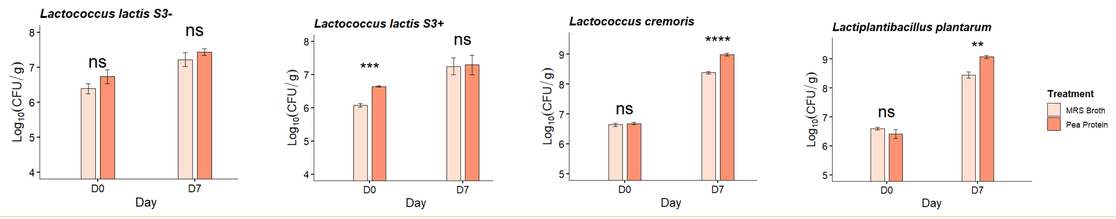
Methodology



Results

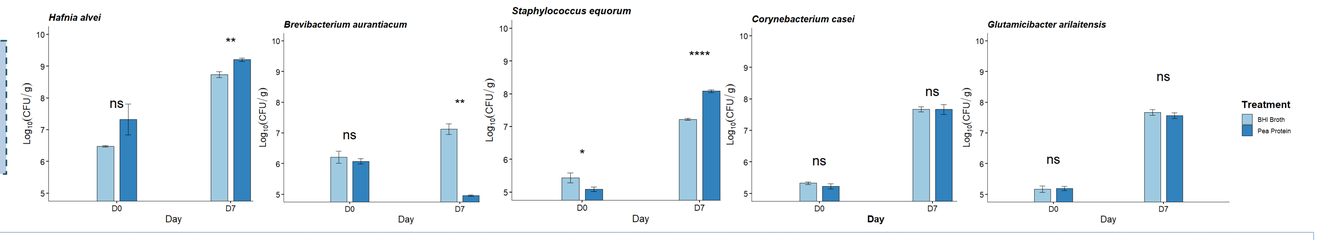
Microbial Growth

Lactic Acid Bacteria



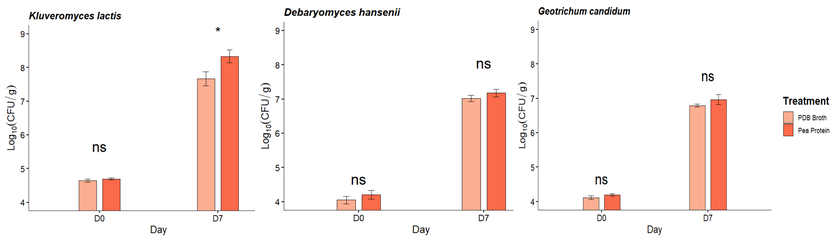
Among LAB, *L. cremoris & L. plantarum* reached over Log 9 CFU/g at D7 in pea-protein matrix, which is significantly higher than the values obtained for *L. lactis S3+ & S3-* (around log 7 CFU/g) ($p < 0.05$, Wilcoxon test).

Ripening Bacteria



S. equorum grew better in pea-protein matrix than in the control medium (BHI broth) ($p < 0.05$, Wilcoxon test performed on D7 data).

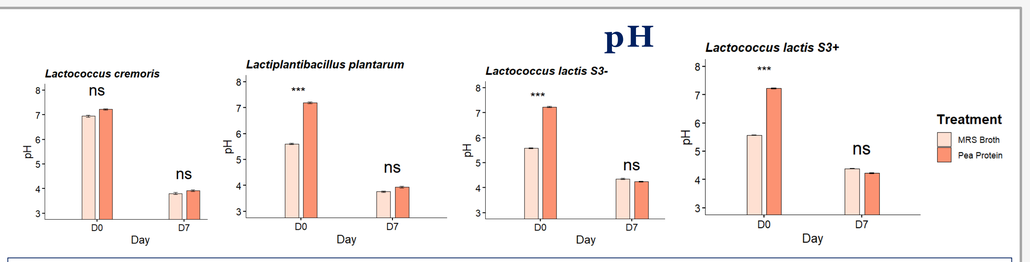
Yeasts



Among yeasts, *K. lactis* grew significantly more in the pea-protein matrix than in the control medium (PDB broth) ($p < 0.05$, Wilcoxon test performed on D7 data).

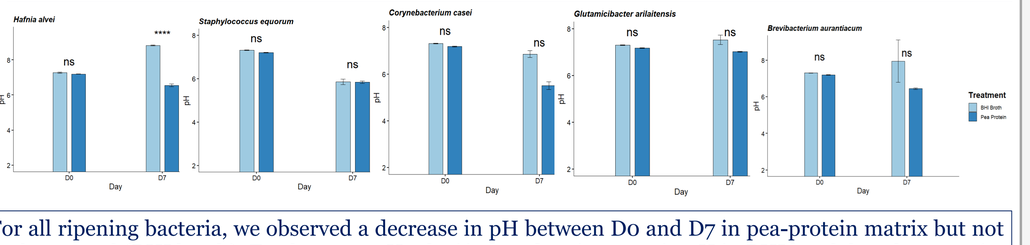
pH

Lactic Acid Bacteria



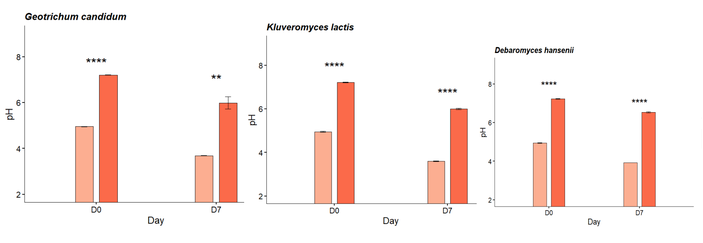
There was no significant difference in pH at D7 between control and pea-protein matrix for all the LAB strains ($p>0.05$, Wilcoxon test). However, the final pH obtained with *L. cremoris & L. plantarum* is lower than when using *L. lactis S3+ & S3-*.

Ripening Bacteria



For all ripening bacteria, we observed a decrease in pH between D0 and D7 in pea-protein matrix but not in the control (BHI broth). Furthermore, *H. alvei* induced an increase in pH in BHI broth but the opposite in pea-protein matrix.

Yeasts



The initial pH was statistically different in control medium (PDB) and pea-protein matrix ($p<0.05$, Wilcoxon test). In both cases, all the yeast strains induced a decrease in pH after fermentation (D7).

Conclusion

- All smear-ripened cheese microorganisms well colonized the pea protein matrix except *Brevivacterium aurantiacum*.
- Among lactic acid bacteria (LAB), *L. plantarum,* and *L. cremoris* showed higher growth tendency compared to *L. lactis* S3+ & S3 strains in pea-protein matrix.
- Most cheese ripening bacteria and yeasts demonstrated the ability to slightly decrease the pH of pea protein matrix especially *H. alvei* and *K. lactis*.

Future Work

- To understand the evolution and behaviour of smear-ripened cheese microorganisms and their interaction in a pea-protein matrix.
- To investigate the effect of iron-deficient and iron-rich conditions on the growth evolution of smear-ripened cheese microbial communities during pea-protein matrix fermentation.
- To identify an optimal synthetic microbial consortia for plant based cheese fermentation.

References

- Masiá, C., Jensen, P. E., Petersen, I. L., & Buldo, P. (2022). Design of a functional pea protein matrix for fermented plant-based cheese. *Foods*, *11*(2), 178
- El Youssef, C., Bonnarme, P., Fraud, S., Péron, A. C., Helinck, S., & Landaud, S. (2020). Sensory improvement of a pea protein-based product using microbial co-cultures of lactic acid bacteria and yeasts. *Foods*, *9*(3), 349.
- Ben-Harb, S., Irlinger, F., Saint-Eve, A., Panouillé, M., Souchon, I., & Bonnarme, P. (2020). Versatility of microbial consortia and sensory properties induced by the composition of different milk and pea protein-based gels. *LWT*, *118*, 108720.
- Ben-Harb, S., Saint-Eve, A., Irlinger, F., Souchon, I., & Bonnarme, P. (2022). Modulation of Metabolome and Overall Perception of Pea Protein-Based Gels Fermented with Various Synthetic Microbial Consortia. *Foods*, *11*(8), 1146.

Acknowledgment

E-MUSE project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement N° 956126.