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### ► To cite this version:

Mahtab Shoukat, Eric Dugat-Bony, Vincent Hervé, Dominique Swennen, Marjon H.J. Wells-Bennik, et al.. Evaluation of the ability of smear-ripened cheese microbial communities to colonize pea-protein matrix. 7th International ISEKI-Food Conference, Jul 2023, Paris, France. hal-04160030

**HAL Id: hal-04160030**

**<https://hal.science/hal-04160030>**

Submitted on 12 Jul 2023

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

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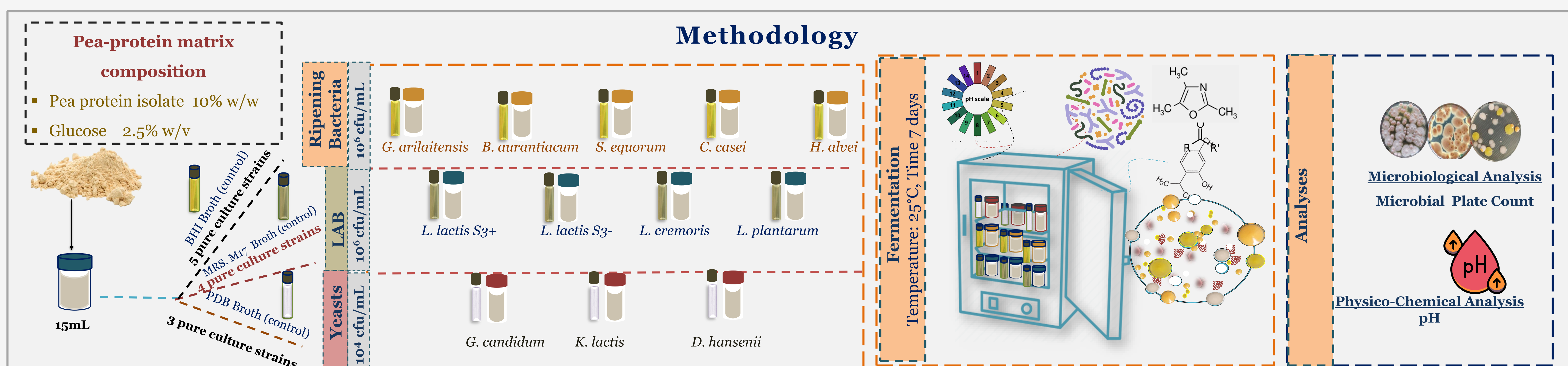
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## Introduction

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.

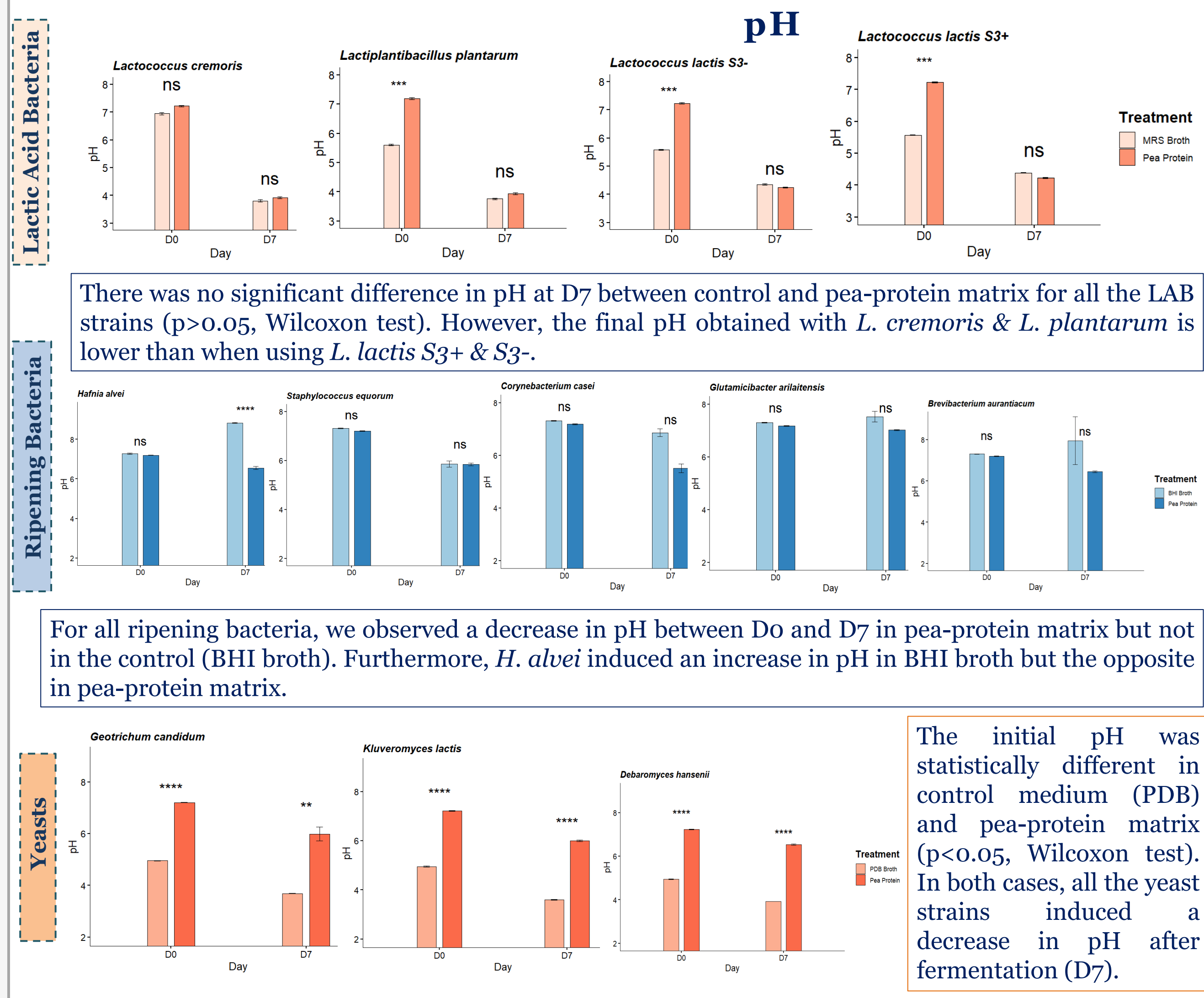
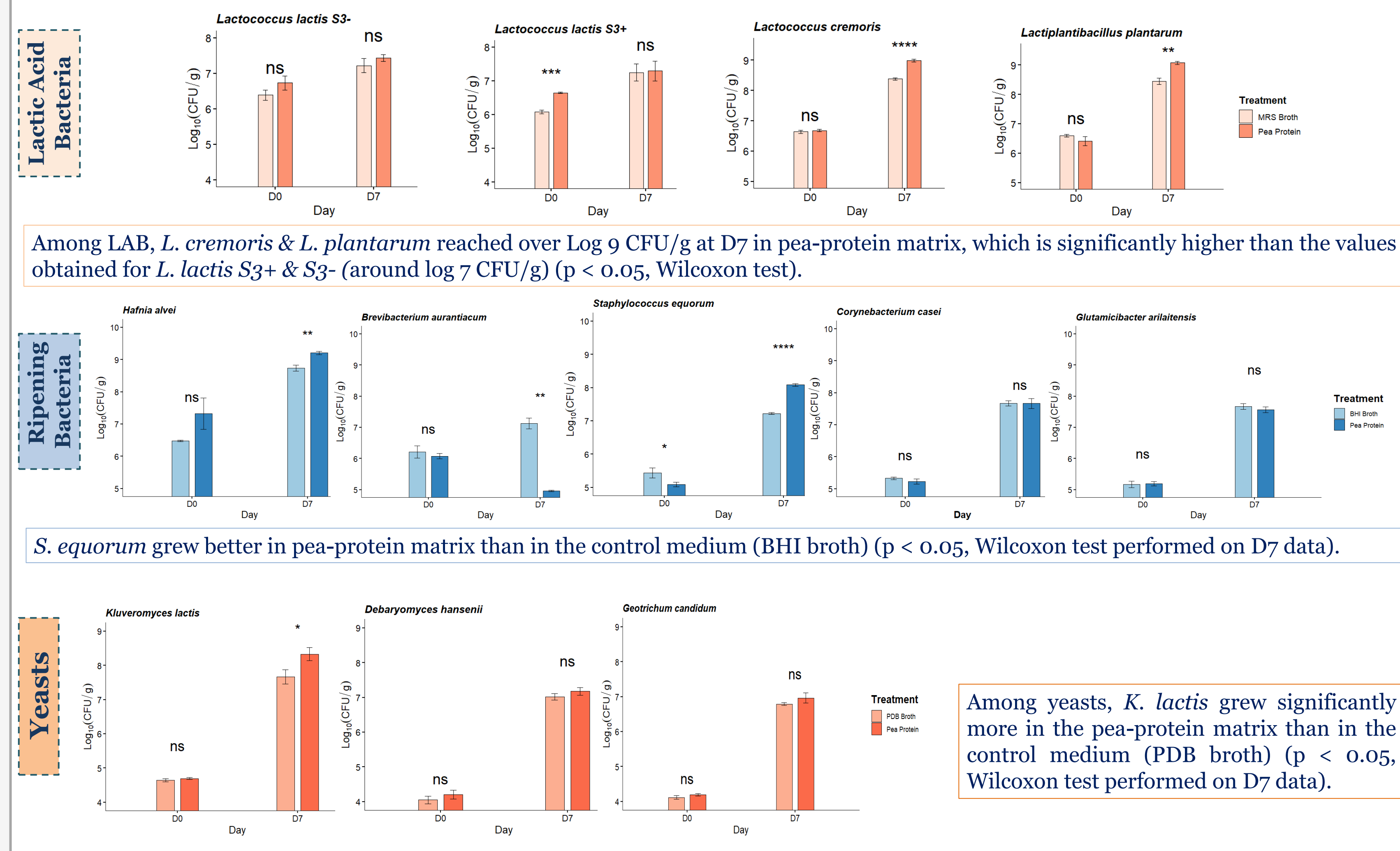
## Aims & Objectives

- 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.



## Microbial Growth

## Results



## Conclusion

- All smear-ripened cheese microorganisms well colonized the pea protein matrix except *Brevibacterium 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

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## 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.

