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Marine Penland, Monika Coton, Jerome Mounier, Sandrine Parayre,
Emmanuel Coton, Hélène Falentin, Stéphanie-Marie Deutsch

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Microbial diversity of Pélardon, an artisanal raw goat milk cheese

^{1,2} Marine PENLAND, ¹ Monika COTON, ¹ Jérôme MOUNIER, ² Sandrine PARAYRE, ¹ Emmanuel COTON, ² Hélène FALENTIN, ² Stéphanie Marie DEUTSCH

Context

Pélardon is a Protection Designation of Origin (PDO) French artisanal soft rind cheese, produced in mountainous areas in southern France. It is exclusively produced from raw goat's milk using a back slopping method for inoculation. Its manufacture and unique organoleptic properties rely on the autochthonous microbiota and their activities. The aim of this work is thus to study Pélardon microbial (fungal & bacterial) ecology and dynamics during cheese-making process by culture-dependent and -independent approaches.

Strategy

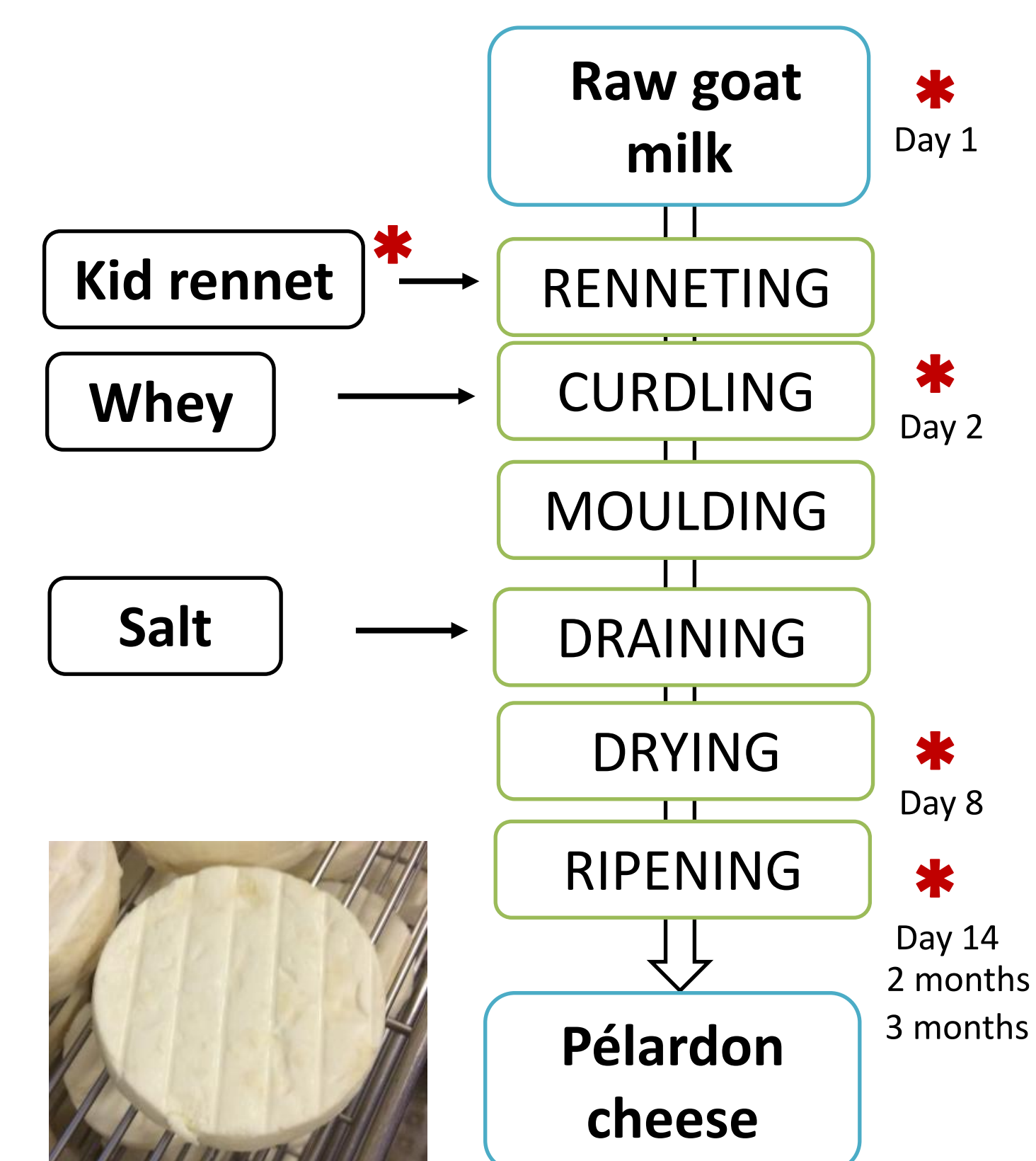
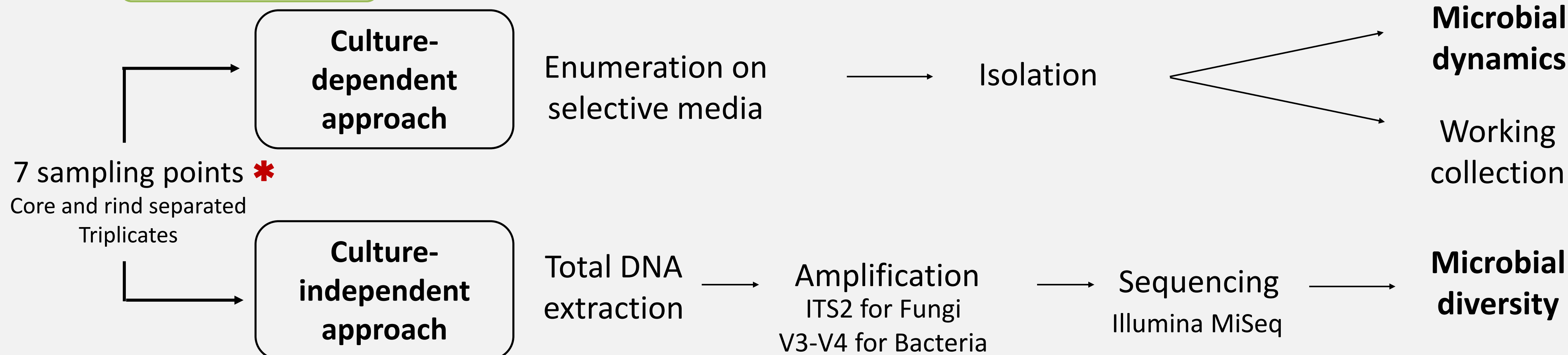


Figure 1. Pélardon cheese-making process. Red stars correspond to the sampling points.

Microbial dynamics during cheese-making

Culture-dependent analyses used to monitor microbial dynamics during Pélardon cheese-making process in both rind and core

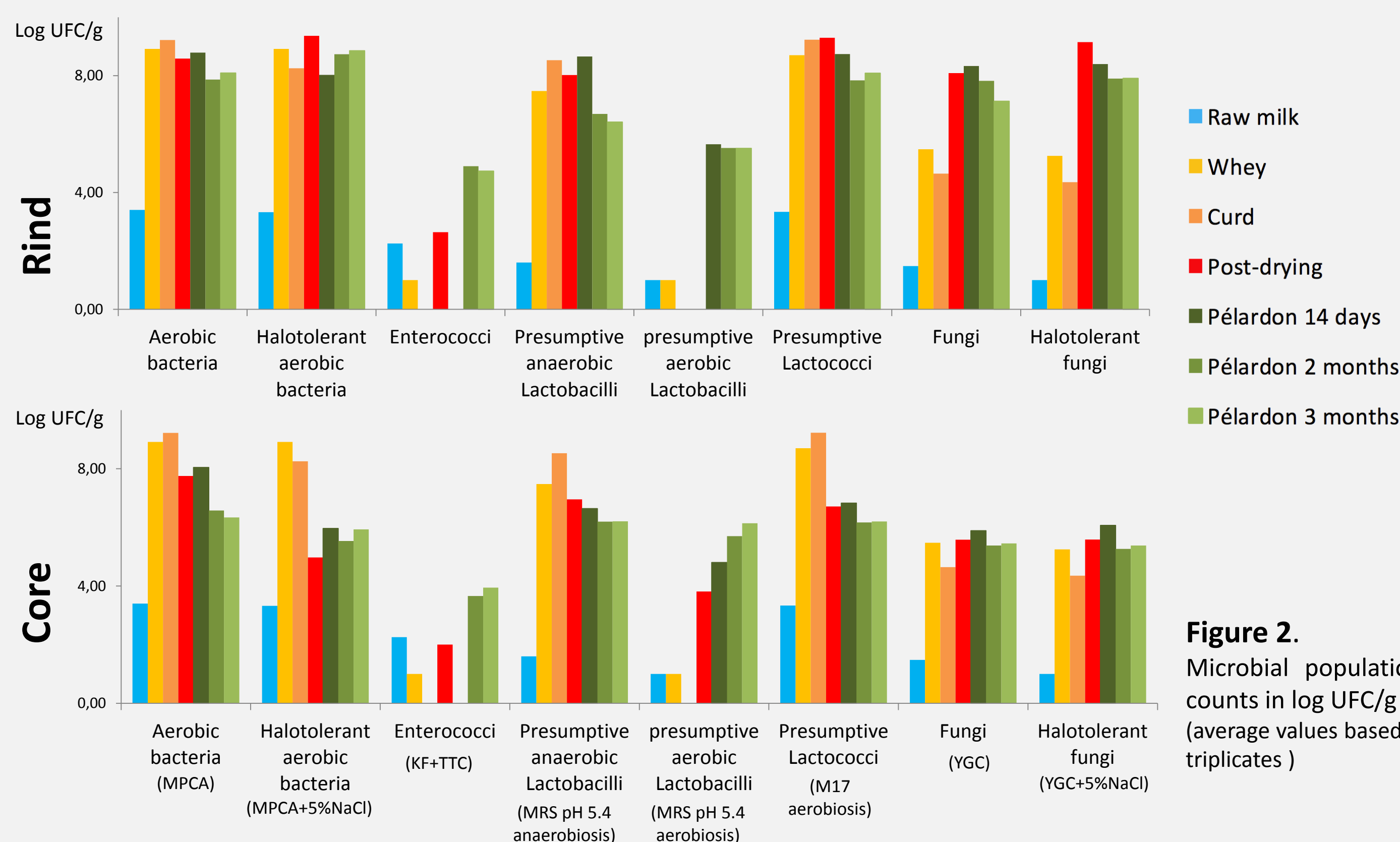


Figure 2. Microbial populations counts in log UFC/g (average values based on triplicates)

- Raw milk showed diversified bacterial counts although higher populations were observed in the whey used as an inoculum
- Populations were higher in the rind compared to the core
- As expected, halotolerant fungi and bacteria populations increased in both sample types after salting and drying

Creation of a working collection (n= 2829 isolates) representative of the diversity

Conclusion

An entire Pélardon cheese production was monitored using culture-dependent and -independent methods. First results highlighted the importance of the whey used as inoculum for bacterial and fungal populations and metagenetic analyses provided a first glance of the microbial diversity and dynamics.

Metagenetic analyses of microbial diversity

Preliminary metagenetic analyses performed on curd (day 2) and 3-month ripened cheese from a previous batch

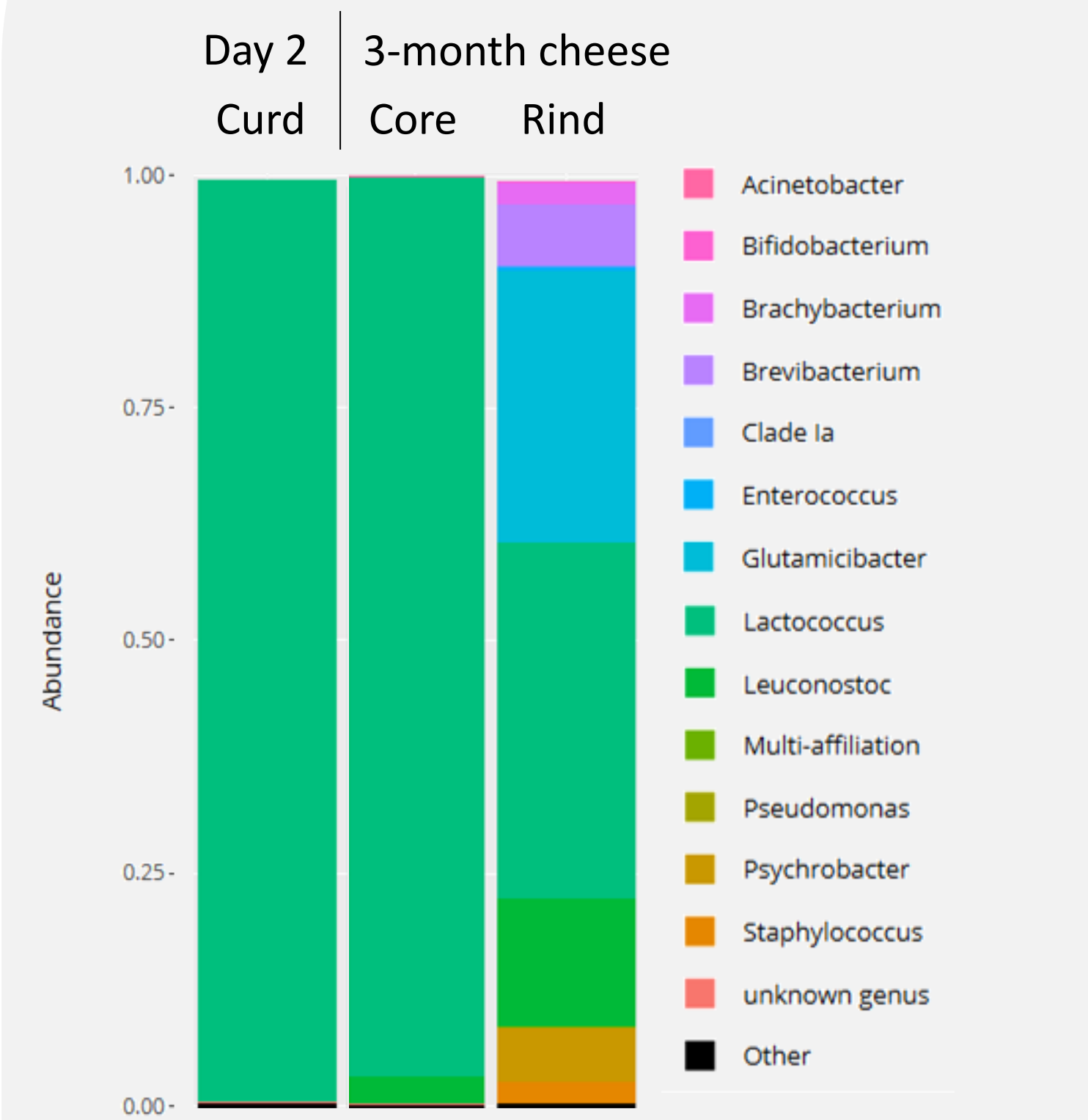


Figure 3. Bacterial composition of the samples at the genus level. Data were analysed using FROGS pipeline and Silva132 database.

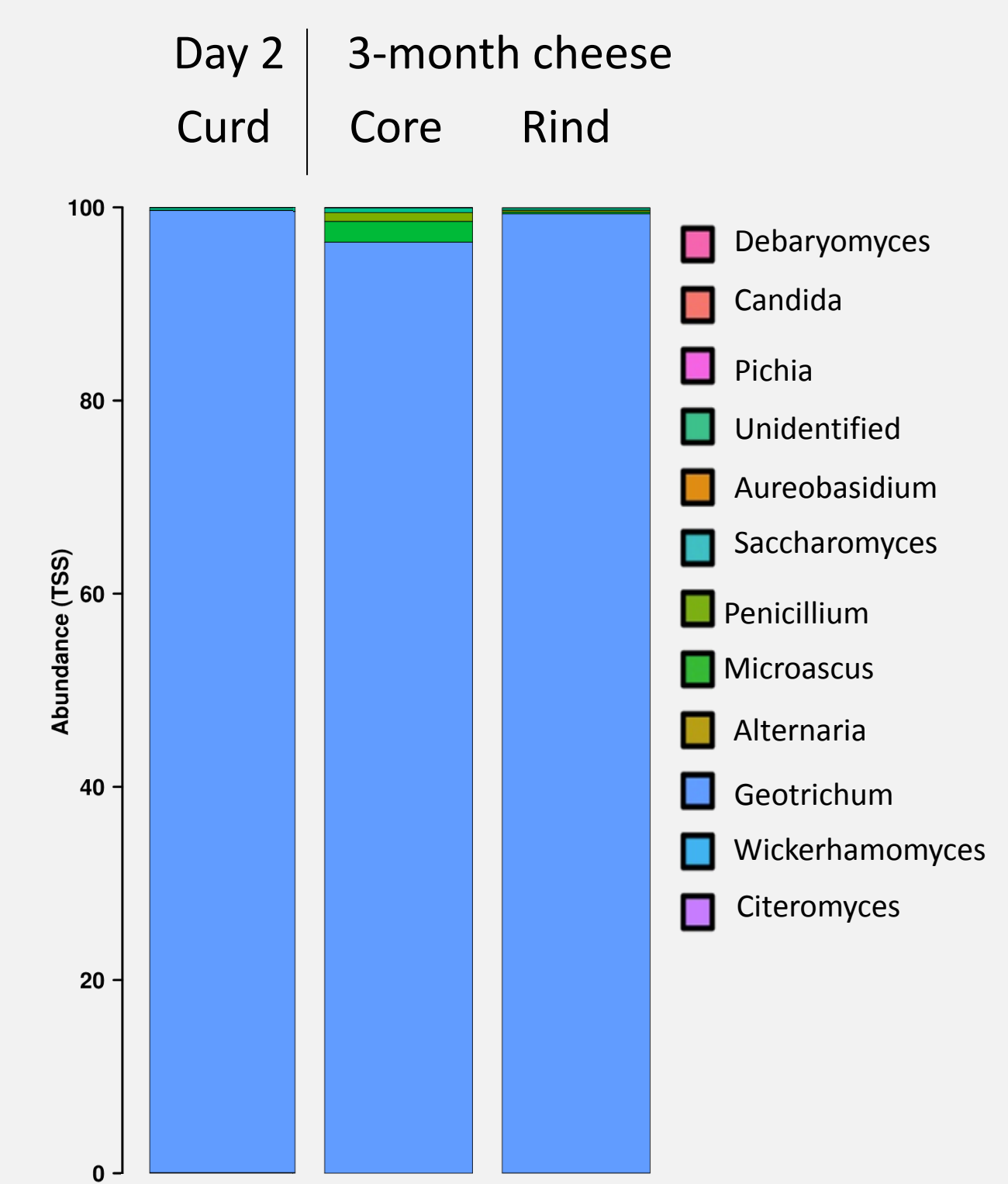


Figure 4. Fungal composition of the samples at the genus level. Data were analysed using an intern Qiime pipeline and UNITE database.

- Lactic acid bacteria dominating in curd are also highly abundant in core samples during ripening
- Higher bacterial diversity in rind: up to 6 taxa, mainly Corynebacteria and Gram-negative bacteria (relative abundance >2%)
- Fungal populations dominated by *Geotrichum*

On-going work

Representative isolates collected during production will be identified and metagenetic analyses will be performed for all sampling points. All results will be correlated and give us a better understanding of the diversity of the microbial populations and their evolution over time. In the long term, shotgun analyses will be used to investigate potential metabolic roles of the different populations during cheese production.

Acknowledgements

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