Effect of fermentation on selected techno-functional properties of mealworm *(Tenebrio molitor)* and cricket *(Acheta domesticus)* powders.

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● Microbial communities on the surface of cheeses are composed of a wide variety of interacting microorganisms. The structure of these communities, composed of inoculated and non-inoculated microbial strains, remains to be fully understood. Several features indicate that iron acquisition mechanisms play a significant role in microbial growth on the cheese surface and in the structuring of these communities.

This study aimed to investigate the diversity and distribution of iron acquisition systems in cheese microbiomes, in order to understand how these systems contribute to abiotic and biotic selection processes in cheeses. For this purpose, we explored a dataset composed of 135 metagenomes and 1,400 genomes/MAGs (metagenomes assembled genomes) from 44 French PDO cheeses, using an updated set of Hidden Markov Models to detect genes involved in the production and transport of siderophores (chelators able to capture iron from the environment) or in direct iron transport.

A wide variety of iron acquisition systems were identified. Among them, siderophores appear to be key elements for surface-associated microorganisms. We detected about twenty different siderophores biosynthetic pathways, including enterobactin and desferrioxamine. Genomic analyses revealed the main bacterial and fungal siderophore producers, including *Glutamicibacter, Corynebacterium, Staphylococcus,* and *Penicillium* species. Siderophore producers represented only about a quarter of the MAGs. However, we detected siderophore importers in a higher proportion of MAGs, suggesting widespread interactions mediated by siderophore/iron complex uptake. Investigating these interactions may help clarify how microbial communities assemble on cheese surfaces. Ultimately, these findings may also contribute to designing ripening cultures with improved colonization capacities.

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