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Who is doing what on the cheese surface? Overview of the cheese microbial ecosystem functioning by metatranscriptomic analyses

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Cheese ripening is a complex biochemical process driven by microbial communities composed of both eukaryotes and prokaryotes. Surface-ripened cheeses are widely consumed all over the world and are appreciated for their characteristic flavor. Microbial community composition has been studied for a long time on surface-ripened cheeses, but only limited knowledge has been acquired about its in situ metabolic activities. We used an iterative sensory procedure to select a simplified microbial consortium, composed of only nine species (three yeasts and six bacteria), producing the odor of Livarot-type cheese when inoculated in a sterile cheese curd. All the genomes were sequenced in order to determine the functional capacities of the different species and facilitate RNA-Seq data analyses. We followed the ripening process of experimental cheeses made using this consortium during four weeks, by metatranscriptomic and biochemical analyses. By combining all of the data, we were able to obtain an overview of the cheese maturation process and to better understand the metabolic activities of the different community members and their possible interactions. We next applied the same approach to investigate the activity of the microorganisms in real cheeses, namely Reblochon-style cheeses. This provided useful insights into the physiological changes that occur during cheese ripening, such as changes in energy substrates, anabolic reactions, or stresses.