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Topic: Food Microbiology

AN HIGH-THROUGHPUT MOLECULAR TOOL FOR HIGHLIGHTING THE EUKARYOTIC FOOD MICROBIAL COMMUNITIES: APPLICATION ON 12 FRENCH CHEESE VARIETIES

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Cheese fermentation process is deeply related to culture and tradition. Indeed, the manufacturing processes shapes the chemistry and microbiology of cheeses, which contribute to express their organoleptic properties. France alone represents almost 1000 different cheese varieties harboring each a specific, dense microbiota ($2-3 \times 10^9$ cells/g cheese). Recently, the use of metagenomics combined with high-throughput sequencing (HTS) technologies offer the opportunity to profile cheese microbial populations on a large scale. Even if the knowledge associated with the bacterial communities of cheeses is well documented, it remains still missing for the eukaryotic fraction.

The GenoScreen company and the French National Institute for Agricultural Research (INRA) associated their expertise to develop a HTS tool for investigate the eukaryotic microbiota associated with 60 cheeses belonging to 12 traditional French cheese varieties. The high throughput ITS2 amplicon sequencing associated with bioinformatic processing was used to characterize the fungal community composition down to the species level.

The results showed that major differences were observed between rind and core samples and also according to cheese varieties and manufacturing processes. Occurrence analysis revealed the presence of widespread taxa as well as operational taxonomic units (OTUs) specific to one or several cheese varieties. We highlighted as well some cheese varieties such as Saint-Nectaire and Soumaintrain still hosted unknown species that may account for a large proportion of the total community.

Finally, this molecular tool could be employed as a large-scale microbial inventory in food-related habitats to identify microbial taxa without reference to food isolates.

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