



Advanced Techniques in Cheese Fermentation

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DESCRIPTION

Microorganisms that are intentionally added (raw or manufactured beginnings and/or supplementary cultures) or that penetrate the milk or cheese surface as contaminants make up a complex microbial ecology in cheese (secondary or adventitious microbiota). In internally ripened cheeses with a medium to long ripening period, Lactic Acid Bacteria (LAB), including starter and non-starter LAB, are the principal ripening agents. Externally ripened cheeses, on the other hand, have a variety of bacteria, yeasts, and molds on their surfaces. More complex volatile profiles and higher scores for diverse sensory qualities have been linked to indigenous LAB recovered from milk or cheese, as well as surface bacteria and yeasts derived from raw-milk cheeses or traditional brines. Development of heritage approaches based on high-throughput sequencing (e.g., targeting 16S rRNA or metabolic genes) is enabling a more targeted approach to starter/adjunct selection for cheese quality enhancement.

Cheese-related foodborne infections, on the other hand, have been observed worldwide in the recent decade. *Listeria monocytogenes*, *Salmonella* spp., *Escherichia coli*, and *Staphylococcus aureus* are the main pathogens of concern when it comes to cheese safety. Although molecular techniques such as real-time quantitative PCR have made it possible to detect and identify foodborne pathogens quickly, it appears that detecting these bacteria in their early stages of growth, as well as obtaining reliable and standardised data to develop predictive microbiological models, is still necessary. The microbial interactions between the technical microbiota and contaminating pathogens should also be considered in these models. The use of non-thermal technology and new biopreservation strategies should also be studied.

Enzymatic coagulation of milk is followed by protein separation, carbohydrate elimination, and an extended bacterial fermentation in the process of creating cheese. The amount of factors that determine cheese quality in this complex process is so huge that developing new manufacturing processes is difficult. Several models have been created to miniaturise the

cheese making process in order to cut screening expenses. However, the throughputs required for systematic screening procedures are incompatible with these models. Furthermore, results identical to those seen in industrial cheese were observed in single-strain supplemental starter cultures designed to overexpress key flavor-related enzymes. When compared to industrial cheese made from the same raw materials, the proteolytic breakdown products and flavour profiles were found to be very similar.

These microcheeses, or small cheeses, open up new avenues for research into various elements of cheese manufacturing, which will not only speed up product creation but also allow for a more systematic investigation into the intricate biochemistry and microbiology of cheese production. Understanding the dynamic biochemical and microbiological responses in cheese will require the use of genomes and proteomics. Understanding the dynamics and evolution of the microbiota during cheese manufacture and ripening. The use of high-throughput DNA sequencing technology has aided in the more precise identification of the cheese microbiome, as well as the extensive investigation of its potential functionality and contribution to the formation of specific organoleptic qualities. Amplicon sequencing, whole-metagenome shotgun sequencing, metatranscriptomics, proteomics, and, most recently, metabolomics are examples of these technologies. However, in recent years, the use of multiple meta-omics approaches in combination with data integration analysis enabled by advanced computational and bioinformatics tools has paved the way for a better understanding of the cheese ripening process, revealing significant associations between the cheese microbiota and metabolites, as well as their impact on cheese flavour and quality.

CONCLUSION

Cheese is a complex microbial environment, and most cheese varieties generate a complex microflora. Cheese ripening is influenced by microflora, and choosing the right strains allows the cheese maker to control or adjust flavour development. However, strain selection for flavour improvement is not always

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clear due to the intricacy of the flora and the interactions that occur between various components of it and the cheese environment. The development of molecular tools for studying cheese microflora will result in a significant improvement in our knowledge of this environment, which will be used to manage

cheese ripening. Genomes and proteomics will be used in the future to better understand the dynamic biochemical and microbiological reactions in cheese. It will be possible to better understand the molecular connections that determine cheese texture and functionality.