Community Composition Changes of Feta Cheese during Processing and its Relationship to the Use of Different Starter Cultures

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Abstract

People have been making cheese for many years as a way to preserve milk for its nutritional value (Beresfod 2001). Raw milk has its own microbial community which can undergo desirable fermentation reactions (Quigley 2011). Combining ingredients such as rennet, microorganisms, and salt to milk, followed by heating of the milk mixture, draining the whey, and ripening over a period of time result in cheese being produced. (Beresford 2001).

Probiotics have recently become a buzzword used by yogurt manufacturers. Probiotics have been classically defined as microorganisms that are non-pathogenic and when digested provide a positive benefit to the host both in health and physiology (Marteau & Shanahan 2003). Some positive benefits include aiding in digestion, maintaining bowel regularity, and inhibition of pathogen binding by microbial antagonism (Zago et.al. 2011).

Cheese has recently been studied for its possible probiotic advantages over yogurt due to its longer shelf life and higher pH, which may retain probiotic viability through the acidic gastrointestinal tract (Sharp 2008). In cheese making, a variety of different starter cultures containing an assortment of bacterial mixtures are typically used. These bacteria grow and thrive in many tissues of the body and are commonly found on the epithelial cells in the intestinal tract (Bauman 2009).

The objective of our study was to monitor the microbial community composition of homemade cheese using yogurt as starter cultures. We hoped to determine if the original probiotic strains were still apparent in the final cheese product.