

# Characterising the Essential Microbiota and Nutrient Makeup of Packaged Pasteurised Milk Products While they are Being Stored

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## Abstract

Microbial communities in pasteurized milk are intricate and influenced by storage and sterilization conditions. Pasteurized dairy products may be highly susceptible to spoilage due to this intricate microflora. High-throughput sequencing was used to identify microorganisms in packaged pasteurized milk products taken from dairy processing factories in China and stored at 0, 4, 10, 15, and 25°C for 15 days. As a result, the majority of the microbiota was classified into six phyla and 44 genera. In addition, principal component and multi-factor analyses were used to examine the changes in the pasteurized milk's nutritional composition, which included 8 chemical constituents, 7 taste values and 16 free amino acids. *Pseudomonas*, *Aeromonas*, *Paenibacillus*, and *Serratia* were found to be the core functional microbiota that has a significant impact on the nutritional content of pasteurized milk by Pearson correlation analysis. As a result, the findings provide a comprehensive understanding of pasteurized milk's safety and shelf life when stored. Pasteurized milk is not only one of the most nutritious sources of dairy products, but it is also a complex biological fluid that is an excellent growth medium for many microorganisms

**Keywords:** Pasteurized milk • Storage conditions microbiota • High-throughput sequencing

## Introduction

Some pathogenic microorganisms are retained by pasteurized milk processing technology, allowing for the growth of numerous different microorganisms under the right conditions. Pasteurized milk is susceptible to deterioration if not properly stored during long-term or long-distance storage and transportation, respectively, compromising its quality and safety in comparison to the lengthy shelf life of thoroughly sterilized milk products. As a result, China's restriction on the production and consumption of pasteurized dairy products has resulted in the dilemma of choosing between nutrition and food safety. In fact, recent studies have begun to focus more and more on the microorganisms in raw milk and how they relate to the quality of dairy products. It has been reported that raw milk that reaches dairy processing plants contains *Bacillus* as well as *P. aenibacillus*. The predominant gram-positive spore-forming bacteria, which were discovered in pasteurized cow milk are made up of some of these bacteria [1-3].

Only a few *Bacillus* species typically grow in similar conditions, but the majority of *P. aenibacillus* isolates from pasteurized milk can grow at low temperatures. Other studies have demonstrated that *P. aenibacillus* is the predominant bacteria during long storage intervals (10 days) and that *Bacillus* is the predominant population during the early shelf-life (7 days) of pasteurized milk. Product packaging parameters have an impact on dairy products' microbiota as well. The bacterial composition of milk remains stable throughout

the product's shelf life when stored in cartons at 4°C. However, the plate count levels of the presumed *Bacillus cereus* and the abundance of operational taxonomic units (OTUs) belonging to the genus *Bacillus* both significantly rise when stored at 8°C [4].

Furthermore, Doyle et al. have investigated how the microbiota composition of raw bulk tank milk (BTM) is affected by storage time (96 hours) and refrigeration temperatures (2, 4 & 6°C). Despite the fact that only a few genera and species, such as *P. aenibacillus* spp., possess this ability, and the genus *Pseudomonas* Under refrigerated storage conditions, these strains appear to be the primary cause of milk spoilage. The microorganisms that remain unidentified in packaged pasteurized dairy products under various storage conditions may have distinct effects on product quality and safety due to the fact that these strains are not completely consistent among the various studies. As a result, addressing issues pertaining to food safety and quality in the dairy industry may benefit from conducting a comprehensive study of the core strain population and the dynamic changes that occur during storage [5,6].

The research field of microbial ecology has recently undergone revolutionary changes as a result of the rapid development of high-throughput sequencing technology. Numerous previously unknown non-cultivable microorganisms have been identified, along with their functions. However, in both research and industry, culture-dependent methods have always been used to evaluate the milk microbiota in the traditionally produced data sets. The outcomes show that a greater part of microorganisms can't be disconnected utilizing existing society procedures, which significantly restricts the exploration on these microorganisms. As a result, it stands to reason that prior knowledge of the microorganisms found in pasteurized dairy products and the dynamic shifts in their population during storage may not have been sufficient. As a result, the microbial dynamics of pasteurized dairy products during storage must be reexamined and reevaluated. *Pseudomonas* and *Aeromonas*, two genera of bacteria previously thought to be unrelated to milk, have now been identified in milk using high throughput sequencing methods. As a result, this study makes a significant advancement in the study of microorganisms in dairy products by providing a more in-depth analysis of the diversity of microbial species found in dairy products. The correlation between the core microorganisms and the nutritional properties of pasteurized milk during storage will also provide a

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reference for preserving the nutritional quality of pasteurized milk, as very few studies have addressed this research area [7,8].

As a result, the purpose of this study was to examine the core functional microbiota that are related to the nutrient composition and safety of pasteurized milk, as well as the dynamic changes in nutritional compounds and microbiota profiles in packaged pasteurized milk products. Additionally, it was hoped that the findings would provide new insights into examining the differences and differences in the safety of storage conditions. Milk sampling From Chinese dairy processing facilities in Shenyang, Liaoning Province, China, samples of packaged pasteurized milk (n = 78) that were produced on the same day were collected. In order to prepare for the follow-up test, samples (78 500 mL each) were immediately placed in liquid nitrogen tanks and sent back to the laboratory, where they were kept in incubators at 0, 4, 10, 15, and 25°C. The samples were taken from the dairy storage tank every three days until the end of the 15th day. Each sample from each pasteurized milk product was examined in three different ways. For every one of the examples dissected, the milk tests were likewise put away at -80°C as reinforcements [9,10].

## Conclusion

During the same measurement session, conventional laboratory methods were used to examine the milk samples' physicochemical and nutritional properties in terms of pH, acidity, and chromatic aberrations like brightness, redness, and yellowness. In order to confirm the formula and process control, a 120 dairy comprehensive component index analyzer was used to measure the milk's fat, protein, and solids-not-fat (SNF) content. According to von Neubeck et al., an analysis of the free amino acid (FAA) content of pasteurized milk stored at various temperatures approach. Different dairy products were stored at various temperatures and times using electronic tongue technology. The average value was determined by measuring each sample five times. The liquid sample's comprehensive taste information served as the basis for quantitative analysis of the tested sample.

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## Conflict of Interest

None.

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