

# Nutrient Content and Core Microbiota of Packaged Pasteurised Milk Products Characterised during Storage

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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.

**Keywords:** Pasteurised milk • Microflora • Food safety

## Introduction

Not only is pasteurized milk one of the best sources of dairy products, but it is also a complex biological fluid that is great for many microorganisms to grow in. Some pathogenic microorganisms are retained by pasteurized milk processing technology, allowing for the growth of a wide variety of microorganisms under ideal growth conditions. Pasteurized milk is susceptible to deterioration during long-term or long-distance storage and transportation, respectively, compromising its quality and safety in comparison to the long 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 point of fact, recent research has begun to place a greater emphasis on the microorganisms found in raw milk and the connection between these microorganisms and the quality of dairy products. It has been reported that raw milk arriving at dairy processing plants contains *Bacillus* and *Paenibacillus*. The predominant gram-positive spore-forming bacteria isolated from pasteurized cow milk are made up of some of these bacteria [1,2].

## Literature Review

Only a few *Bacillus* species typically grow in similar conditions, whereas the majority of *Paenibacillus* isolates from pasteurized milk can grow at low temperatures. Other studies have demonstrated that *Paenibacillus* is the predominant bacteria during long storage intervals (10 days) and that *Bacillus* is the predominant population during the early shelf-life of pasteurized milk (7 days). 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. Notwithstanding, capacity

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at 8 °C fundamentally expands the wealth of functional ordered units (OTUs) having a place with the family *Bacillus* and the plate count levels of possible *Bacillus cereus*.

Furthermore, Doyle et al. have inspected the impact of refrigeration temperature (2, 4 and 6°C) and capacity span (96 h) on the microbiota creation of crude mass tank milk (BTM). Despite the fact that only a few genera and species, such as *Paenibacillus* spp., possess this ability, and the genus *Pseudomonas*, Milk spoilage in refrigerated storage appears to be primarily due to these strains. 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 [3-5].

## Discussion

The study of microbial ecology has undergone significant transformations in recent years as a result of the rapid advancement 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 conventionally produced data sets. The findings indicate that existing culture methods cannot isolate the vast majority of microorganisms, severely restricting research on these organisms. 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, can now be found in milk thanks to high throughput sequencing methods. As a result, this study makes a significant leap forward 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 reference for preserving the nutritional quality of pasteurized milk, as very few studies have addressed this research area [6].

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. Ding et al. gave instructions on how to extract DNA from pasteurized milk at different storage temperatures. In short, the bacterial 16S rRNA gene's variable regions V3 and V4 were amplified, and the Illumina Miseq platform and a 300 bp paired-end sequencing kit were used to sequence the library. 26 of these samples were subjected to 16S rRNA sequencing after three replicate samples were combined into a single sample [7-9].

When samples were grouped together at different storage temperatures and times, it was found that they shared the same top abundant phyla-phyla with more than 1% of all sequences-but had different relative abundances. *Proteobacteria*, *Firmicutes*, *Tenericutes*, *Bacteroidetes*, *Actinobacteria* and *Saccharibacteria* were among the six dominant phyla identified in the bacterial communities. More than half of the bacterial populations were made up of proteobacteria, which were the most common type of bacteria among the phyla that were found (P 0.01) [10].

## Conclusion

Similar studies have shown that *Firmicutes* and *Proteobacteria* phyla bacteria dominate raw milk, accounting for more than 40% of the population. At 4, 10, and 15 degrees Celsius, the bacterial populations became significantly less diverse over time, with the *Proteobacteria* population expanding as a distinct phylum and the *Tenericute* and *Firmicute* populations gradually decreasing. Additionally, the population differences between the samples were statistically significant, and the abundance of *Proteobacteria* was nearly identical to that of *Firmicutes* when the temperature was set at 25 degrees Celsius for 15 days. This was most likely due to the growth of psychrotrophic bacteria.

## Acknowledgement

None.

## Conflict of Interest

None.

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