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Evaluation of the microbiological quality of some dairy products

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Abstract. Owing to their nutrient composition, dairy products ensure a favourable environment for different microorganisms. In our study, we investigated the microbiological quality of 22 different commercially available dairy products obtained from local stores and the open-air public market. Among the studied samples four were salty type soft cheese, two were fresh cheese, one was soft cheese (Mascarpone), one was feta-like cheese (Telemea), five were varieties of processed cheese, one was mozzarella, one was a semi-hard cheese, one was smoked cheese, five were cottage cheese, and one was a dairy spread. Samples were evaluated for the presence of *Pseudomonas* sp., total coliforms, *Escherichia coli*, *Salmonella* sp., S*taphylococcus aureus*, *Bacillus cereus* and *Clostridium perfringens*, yeast, and microscopic fungi.

Contamination level of the evaluated dairy products varied widely. Among the dairy samples one salty soft cheese, a processed cheese and one cottage cheese were the most contaminated, while low microbiological load was detected in the other samples.

Keywords and phrases: dairy products, microbiological load, pathogenic bacteria, spoilage

Based on our results, it can be concluded that the microbiological quality of the most studied samples is satisfactory, but there are samples with marginal characteristics too. In turn, three products can be declared potentially hazardous.

1 Introduction

Before consumption, food products are exposed to microbial spoilage during harvest, manufacture, storage, and distribution. The spoilage of foods threatens human health and leads to enormous economic loss. Worldwide, about 15–25% of foodstuffs deteriorate (*Deák & Farkas*, 2013).

Due to their nutritional value, especially the high protein and lipid content, dairy products are a suitable growth environment for a range of microorganisms. The type of dairy product mainly determines the type of the spoilage microorganism. The microbiological load of a product correlates with the steps of manufacturing. Cream cheese and processed cheese are associated with fungi, spore-forming bacteria. Psychrotrophs, coliforms, fungi, lactic acid bacteria, and their enzymatic degradation are responsible for the spoilage of soft, fresh cheese types. The typical types of spoilage microorganisms of cottage cheese are the psychrotrophs, coliforms, yeasts, and moulds (*Ledenbach & Marshall*, 2009).

Generally, in the microbial deterioration of dairy products, two main microorganism groups play a central role: psychrotrophs that grow at 5–7 °C and thermodurants that survive pasteurization. In dairy products, diverse bacterial species can be detected belonging to different genera: both Gram-positive (*Bacillus*, *Clostridium*, *Corynebacterium*, *Microbacterium*, *Micrococcus*, *Streptococcus*, *Staphylococcus*, and *Lactobacillus*) and Gram-negative species (*Pseudomonas*, *Aeromonas*, *Serratia*, *Acinetobacter*, *Alcaligenes*, *Achromobacter*, *Enterobacter*, *Flavobacterium*, *Burkholderia*, *Sphingomonas*, *Stenotrophomonas*). The predominant species altering milk and dairy products are considered those belonging to the genera *Pseudomonas* sp. The alteration is the result of the activity of a wide range of enzymes, such as protease or lipase, or the result of the production of organoleptic spoilage (*Raposo et al.*, 2017). *Pseudomonas* strains with pigment production are also involved in several cases of spoilage of dairy products. In fresh low-acid cheese, *P. fluorescens*, *P. brassicacearum*, and *P. putida* pigment compounds (indigoidine, pyoverdine) discolour the product (*Andreani & Fasolato*, 2017).

In addition to spoilage bacteria, dairy products may be carriers of pathogenic bacteria such as *Bacillus cereus*, *Brucella* sp., *Campylobacter jejuni*, *E. coli*

O157:H7, *Coxiella burnetii*, *Listeria monocytogenes*, *Mycobacterium paratuberculosis*, *Salmonella* sp., *Yersinia enterocolitica*, or *Staphylococcus aureus*. Some of this bacterial species have been associated with milkborne outbreaks (*Lu & Wang*, 2017; *Suilaiman & Hsieh*, 2017).

Among dairy products, cheese or cheese-related products have been mostly contaminated by different microbes. It was reported that cheese is very susceptible to *Salmonella* sp. (*Suilaiman & Hsieh*, 2017). According to *Suilaiman & Hsieh* (2017), between 1998 and 2014, several dairy outbreaks in the United States resulted from the consumption of raw milk or cheese contaminated with Shiga-like toxins producing *E. coli*. The presence of *E. coli* and total coliform bacteria refers to poor hygiene conditions.

Regarding the safety of dairy products, another foodborne pathogen is the enterotoxin-producing *Staphylococcus aureus*. The pathogenicity of these bacteria is mainly linked to toxin-mediated virulence, invasive capacity, and antibiotic resistance (*Carfora et al.*, 2015).

Species of *Bacillus cereus*, able to produce different toxins (cereulide, cytotoxin K, haemolysin BL, and non-hemolytic enterotoxin) are responsible for food poisoning. These bacteria are thermoduric spore formers, therefore challenging the dairy industry. Dairy products are on the *B. cereus*-contaminated food list (*Tirloni et al.*, 2017; *Grutsch et al.*, 2018).

Some species of yeast, such as *Geotrichum candidum*, *Pichia* sp., and *Candida* sp., contribute to a variety of defects in cheese. The production of their metabolites, such as sulphides and other compounds, results in off-flavours and gas production as well (*Lu & Wang*, 2017).

There are few studies on the prevalence of spoilage and foodborne bacteria in locally available dairy packed products or dairy products sold by weight. The aim of the present study was the evaluation of the microbiological quality and safety of different dairy products originated from local stores or the open-air public market.

2 Materials and methods

During our work, 22 different dairy products (salty type soft cheese, fresh cheese, soft cheese, feta-like cheese, processed cheese, mozzarella, semi-hard cheese, smoked cheese, cottage cheese, dairy spreads) have been studied microbiologically with cultivation methods. The selection of the dairy product samples was made at random. Detection of the bacteria important for spoilage or for health and hygienic reasons, such as *Pseudomonas* sp., total coliforms,

Escherichia coli, *Salmonella* sp., *Staphylococcus aureus*, *Bacillus cereus*, or *Clostridium perfringens*, has been carried out with bacteriological cultivation methods on different selective culture media. One gram of each sample was aseptically transferred into a 9 ml physiological solution. From this, serial dilutions to 10^{-1}–10^{-2} were prepared, and a volume of 0.1 ml was spread on the selective agar mediums. The inoculated culture media have been incubated for 48 h at 37 °C and 44 °C for total coliforms and *Clostridium perfringens* respectively. The following selective culture media were used during the determination of the bacteria: Pseudomonas Selective Agar (Biolife), ChromoBio^{R} Coliform (Biolab), TBX Chromo-Agar (Carl Roth), Brilliance^{TM} Salmonella Agar Base (Oxoid), Mannitol Salt Agar (Oxoid), ChromoBio^{R} Cereus Base (Biolab), and Clostridial Differential Broth (Fluka Analytical).

In the case of detecting microscopic filamentous fungi, the studied samples have been inoculated on Czapek-Dox Agar (Oxoid) nutritive medium, and the determination has been done based on colony and cell morphology properties, with the help of microscopic preparations.

Statistical Analysis

Principal component analysis (PCA) has been performed using PAST Software for graphical description and to categorize the studied samples based on microbiological quality. The first three principal components from the microbiological counts of the dairy products have been obtained with PCA.

3 Results and discussion

During this study, we have evaluated the microbial contamination of 22 different commercially available dairy products obtained from local stores and the open-air public market. Among the studied samples, four were salty type soft cheese, two were fresh cheese, one was soft cheese (Mascarpone), one was feta-like cheese (Telemea), five were processed cheese varieties, one was mozzarella, one was a semi-hard cheese, one was smoked cheese, five were cottage cheese, and one was a dairy spread.

Samples have been analysed for the presence of *Pseudomonas* sp., total coliforms, *Escherichia coli*, *Salmonella* sp., *Staphylococcus aureus*, *Bacillus cereus*, *Clostridium perfringens*, yeast, and microscopic fungi. The results of the bacteriological evaluation are presented in *Table 1.* Contamination level by bacteria of the evaluated dairy products varied widely.

Table 1: Bacteriological results of dairy products

Studied samples	Sample code	*Pseudo-monas* sp.	Coliforms	*Escherichia coli*	*Salmonella sp.*	*Staphylococcus aureus*	*Bacillus cereus*	*Clostridium perfringens*
				CFU/g				
Salty type soft cheese 1	SSFC1	$3{\cdot}10^3$	$1{\cdot}10^4$	$5{\cdot}10^3$	$2{\cdot}10^3$	<10	$3{\cdot}10^2$	-
Salty type soft cheese 2	SSFC2	4·10	n	$>3{\cdot}10^2$	<10	<10	$>3{\cdot}10^2$	-
Fresh cheese 1	FC1	$9{\cdot}10^2$	$4{\cdot}10^3$	$7.5{\cdot}10^3$	<10	<10	<10	-
Fresh cheese 2	FC2	$2{\cdot}10^2$	n	$>3{\cdot}10^2$	1·10	$2{\cdot}10^2$	$>3{\cdot}10^2$	-
Soft cheese Mascarpone	M	1·10	$2{\cdot}10^3$	1·10	$2{\cdot}10^2$	$3{\cdot}10^3$	<10	-
Feta-like cheese –Telemea	F	<10	$1{\cdot}10^3$	<10	<10	<10	<10	-
Processed cheese 1	PC1	1·10	810^2	<10	<10	<10	9·10	-
Processed cheese 2	PC2	<10	4·10	7·10	<10	<10	<10	+
Processed cheese 3	PC3	<10	$8{\cdot}10^3$	<10	<10	$1{\cdot}10^4$	4·10	+
Processed cheese 4	PC4	<10	<10	<10	$6{\cdot}10^2$	<10	<10	-
Processed cheese 5	PC5	<10	n	<10	<10	$>3{\cdot}10^2$	$>3{\cdot}10^2$	-
Dairy spread	DS	<10	$4{\cdot}10^2$	<10	3·10	3·10	<10	-
Mozzarella	MO	<10	$5{\cdot}10^3$	<10	<10	<10	<10	-
Smoked cheese	SC	<10	7·10	<10	<10	5·10	<10	-
Semi-hard chees	ShC	<10	n	<10	<10	10	$>3{\cdot}10^2$	-
Cottage cheese 1	CC1	$8{\cdot}10^2$	$7{\cdot}10^2$	$3{\cdot}10^3$	7·10	<10	<10	+
Cottage cheese 2	CC2	<10	<10	$1{\cdot}10^2$	<10	<10	6·10	-
Cottage cheese 3	CC3	<10	4·10	$1{\cdot}10^4$	$1{\cdot}10^3$	<10	$2{\cdot}10^2$	-
Cottage cheese 4	CC4	<10	$1.{\cdot}10^3$	<10	$2{\cdot}10^3$	$1{\cdot}10^3$	$3{\cdot}10^2$	-
Cottage cheese 5	CC5	<10	n	<10	<10	1	$9{\cdot}10^3$	-
Salty type soft cheese 3	SSFC3	<10	$8{\cdot}10^2$	<10	<10	<10	<10	-
Salty type soft cheese 4	SSFC4	4·10	n	<10	<10	$2{\cdot}10^2$	$>3{\cdot}10^2$	-

n: not evaluated

The *Pseudomonas* sp. on selective agar have been detected in eight samples. The number of this bacterial species varied between 10 and $3{\cdot}10^3$ CFU/g. The most contaminated product proved to be a salty type soft cheese with $3{\cdot}10^3$ CFU/g. In the case of both types of fresh cheese obtained from the open-air market, this bacterial isolate has also been detected. Among the five varieties of the studied processed cheese samples, only one (PC1) turned out positive for *Pseudomonas* sp. (10 CFU/g). Among the five evaluated samples, only one (CC1) has been detected $8{\cdot}10^2$ CFU/g. The physico-chemical properties (including pH, salt content) of cottage cheese support the growth of this group of bacteria. Also, they determine the shelf life of the product (*Ledenbach* & *Marshall*, 2009). In the case of a salty type soft cheese (SSFC2) obtained from the store, 4·10 CFU/g *Pseudomonas* sp. has been detected.

Pseudomonas sp. are the most dominant psychrotrophic microorganisms isolated from milk. Low temperatures like 3–7 °C and the ability to use large lipid and protein molecules favour their growth. It has been shown that these bacteria can reduce the diacetyl content of some dairy products, resulting in a green or yogurt-like flavour. The appearance of *P. fluorescens* strains is due to post-process contamination. The refrigeration and protein-rich content of the product is beneficial for this microorganism (*Ledenbach* & *Marshall*, 2009; *Andreani* & *Fasolato*, 2017; *Brasca et al.*, 2018).

It has been shown that different species of *Pseudomonas* genus caused the enzymatic spoilage of dairy products; *P. fluorescens*, *P. fragi*, and *P. putida* caused an alteration in the texture of soft and fresh types of cheese (*Andreani* & *Fasolato*, 2017).

The cell number for the initiation of spoilage by psychrotrophs is about 10^6 CFU/ml (*Brasca et al.*, 2018). In our studied samples, the incidence of *Pseudomonas* sp. did not reach this cell count. For the inhibition control of this group, the suggested solution is the proper combination of time and temperature (*Brasca et al.*, 2018).

Besides pseudomonads, coliform bacteria represent a quality indicator in the dairy industry. Among the evaluated samples, only two were free of coliforms. The highest total coliform load has been determined in the case of the salty type soft cheese from the open-air market, containing 10^4 CFU/g. In six dairy products, the coliform level has been 10^3, varying between $1{\cdot}10^3$ and $8{\cdot}10^3$ CFU/g. In the case of four products, the number of coliforms has been around $4{\cdot}10^2$–$8{\cdot}10^2$ CFU/g. In the case of a variety of processed cheese and a cottage cheese, the detected total coliform number has been 4·10 CFU/g (CC3), while in the case of smoked cheese it has reached 7·10 CFU/g (SC). The coliforms cause blowing defect in different types of brined cheese (*Pintado*

et al., 2015). Among the studied samples, the salty dairy products reached high counts of this group.

The presence of a coliform group in a dairy product reflects the unhygienic conditions of the production process. Coliforms could be eliminated by compliance with personal hygiene and sanitation processes. This group of bacteria includes bacterial species of *Escherichia*, *Enterobacter*, *Klebsiella*, *Proteus*, *Serratia*, *Hafnia*, *Citrobacter* genera (*El-Ziney*, 2018; *Moatsou* & *Barbaros*, 2015), and many others. The negative impact of this group consists in their enzymatic activity and the production of metabolic by-products influencing the quality of the dairy product. The reduction of coliforms in cheese can be achieved by the reduction of temperature and drop in pH (*Martin et a*l., 2016). *Trmčić et al.* (2016) revealed that the presence of coliforms in a wide variety of cheese made from different kinds of milk is correlated with water activity. They also concluded that the type of the milk influenced the prevalence of this group of bacteria.

Escherichia coli represents a hygienic indicator organism in cheese production, reflecting faecal contamination. In reference to specific virulence factors and phenotypic characteristics, these bacteria have different groups such as enterohaemorrhagic *E. coli* (EHEC), enteropathogenic *E. coli* (EPEC), and so on. Globally, *E. coli* O157:H7 serotype is responsible for foodborne disease outbreaks (*Law et al.*, 2017). 13 dairy samples have turned out free of *Escherichia coli*. The presence of *E. coli* has been found in nine studied samples. In the case of six samples, CFU/g of this bacterium has been higher than 300. Mascarpone contains 10 CFU/g, and in one of the processed cheese types 7·10 CFU/g (PC2) contamination has been found. Different serotypes of *E. coli* with virulence genes have been detected in dairy products by *Douëllou et al.* (2016).

Dairy products can be contaminated with *Salmonella* sp. Species of these bacteria are the major foodborne pathogens. Eight dairy products have been contaminated with *Salmonella* sp. The detected CFU/g of this bacteria varied between 10 and 10^3. The highest total *Salmonella* sp. load has been found in the case of one cottage cheese (CC4). Among the cottage cheese types, two were free of this bacteria. In the case of one salty type soft cheese (SSFC1), the *Salmonella* sp. colony counts have reached 10^3 CFU/g, in dairy spread, (DS) it was 3·10 CFU/g, while in one cottage cheese (CC1) the analysis indicated $7 \cdot 10$ CFU/g.

Species of the genus of *Staphylococcus* are proteolytic enzyme producers in milk and milk-derivate products yet also bacteria of potential danger concerning public health. *Staphylococcus aureus* is a zoonotic pathogen, causing differ-

ent infections (*Biswas & Mandal*, 2017). Based on coagulase production, they are divided in coagulase-positive and coagulase-negative strains. Coagulase-positive strains harbour virulence factors such as a heat-resistant nuclease, catalase, coagulase, haemolysins, protein A, lipase, leukocidin, staphylokinase, toxic shock toxin, or exfoliative toxins A and B. Some of these factors have also been detected in coagulase-negative strains (*Chajęcka-Wierzchowska & Zadernowska*, 2017).

The presence of *Staphylococcus aureus* has been found in seven dairy products. In this case, the highest bacterial load has been detected in two varieties of processed cheese (PC3, PC5), where the CFU/g resulted higher than 300. This bacterial isolate has also been present in Mascarpone (M $3 \cdot 10^3$) and a fresh cheese (FC2) obtained from the open-air market ($2 \cdot 10^2$ CFU/g). The value of 10^4 CFU/g is associated with the result of foodborne illnesses (*Biswas & Mandal*, 2017). In the case of our samples, this critical cell number has been detected in two varieties of processed cheese (PC3, PC5).

According to *Al-Khafaji* and *Flayyih* (2015), in three hundred milk and cheese samples, *Staphylococcus aureus* was the predominant species. This bacterium can originate from humans or biofilms, possibly from insufficient acidification during cheese production (*Kümmel et al.*, 2016). With the control of temperature, time, and pH, the growth and toxin production of this bacterium can be prevented.

The spore-forming bacterium *Bacillus cereus* is one of the most dominant spoilage microorganisms in the dairy industry. Alteration caused by these bacteria appears due to the enzyme activities, such as proteinases, lipases, or phospholipases, also determining the off-flavours of products. In the case of cheese, a negative impact of *Bacillus* sp. consists in the reduction of nitrate to nitrite that limits its preservative effectiveness. A wide variety of dairy products, including cheese and processed cheese, was contaminated by this bacterium (*Lopez-Brea et al.*, 2017). Nine dairy products turned out to be free from *Bacillus cereus*. High counts of this bacteria has been found in four of the studied samples, where the CFU/g resulted higher than $3 \cdot 10^2$ CFU/g. Also, a low contamination level has been detected in two cases of processed cheese (PC1, PC3) (9·10 and 4·10 CFU/g). *B. cereus* is also responsible for the emergence of foodborne diseases on a level of 5 log to 8 log cells/spores/g food. It has been shown that rapid cooling, low pH, and water activity contribute to the inhibition of this bacterium (*EFSA*, 2005).

The spoilage microbiota constituent of milk and dairy products under anaerobic conditions is *Clostridium perfringens*, which is one of the most common foodborne pathogens with low generation time (*Lopez-Brea et al.*, 2018). The

presence of *Clostridium perfringens* has been detected in three dairy samples: in two varieties of processed cheese (PC2, PC3) and one cottage cheese (CC1). The species of *Clostridium* genus are responsible for the late swelling spoilage of different types of cheese. One spore per millilitre milk can already cause alteration. These microorganisms metabolize the residual sugar and citrate with the production of organic acids. Discolouration of soft ricotta cheese has been caused by *Bacillus cereus* and *Clostridium* sp. (*Andre et al.*, 2017; *Remize*, 2017; *Ledenbach & Marshall*, 2009).

The pH and the nutritional characteristics of fermented dairy products favour the growth of yeasts, resulting in fungal spoilage. In these products, yeasts metabolize diacetyl, causing off-flavour, yeast taste, and alteration in colour and texture. In these cases, yeast count can reach 10^5–10^6 CFU/g.

In the different types of cheese, yeasts produce CO_2 and alcohol, altering the taste. The ethanol reacts with short-chain fatty acids, resulting in fruity esters. Egg odour can be the result of the sulphides produced by some proteolytic yeast strains (*Ledenbach & Marshall*, 2009).

Alteration in colour can be caused by *Yarrowia lipolytica*, resulting from the formation of pyomelanin, a brown pigment. Some yeasts can also produce biogenic amines (*Garnier et al.*, 2017).

The results of the evaluation of yeasts and moulds are presented in *Table 2*. In the case of our studied samples, yeast has been present in 13 samples. Except for a cottage cheese, the CFU/g has resulted higher than 10^2. The highest yeast contamination has been detected in the case of the salty soft cheese (SSFC3) $2{\cdot}10^4$CFU/g. The CFU/g has also resulted 10^4 in Mozzarella (MO), a variety of processed cheese (PC1), fresh cheese (FC1), and Mascarpone (M). Consequently, it can be summarized that the yeast count is smaller than the number that leads to deterioration. According to *Ledenbach* and *Marshall* (2009), the common spoilage yeast of cheese includes *Candida* sp., *Kluyveromyces marxianus*, *Geotrichum candidum*, *Debaryomyces hansenii*, and *Pichia* sp. The common yeast *Geotrichum candidum* caused spoilage in a variety of cottage cheese.

For moulds, the surface of different types of cheese represents a favourable environment. Due to oxygen availability, the vacuum package inhibits the growth of these microbes, but some species can support low oxygen tension. Microscopic fungi commonly found and growing in vacuum-packaged varieties of cheese include *Penicillium* sp. and *Cladosporium* sp. *Penicillium* is the mould genus most frequently occurring on cheese (*Ledenbach & Marshall*, 2009). Microscopic fungi have been detected in seven studied dairy products.

Table 2: The yeast and microscopic fungi count of some dairy products

Studied samples		Yeasts	Microscopic fungi
		CFU/g	
Salty soft cheese 1	SSFC1	$5{\cdot}10^3$	6·10
Salty soft cheese 2	SSFC2	$3{\cdot}10^2$	10
Fresh cheese 1	FC1	$1{\cdot}10^4$	1·10
Fresh cheese 2	FC2	<10	0
Soft cheese Mascarpone	M	$1{\cdot}10^4$	0
Feta like cheese	F	$8{\cdot}10^3$	0
Processed cheese 1	PC1	$1{\cdot}10^4$	0
Processed cheese 2	PC2	<10	<10
Processed cheese 3	PC3	<10	$1{\cdot}10^3$
Processed cheese 4	PC4	<10	<10
Processed cheese 5	PC5	<10	<10
Dairy spread	DS	$1{\cdot}10^2$	1·10
Mozzarella	MO	$1{\cdot}10^4$	<10
Smoked cheese	SC	$4{\cdot}10^3$	1·10
Semi-hard cheese	ShC	<10	<10
Cottage cheese 1	CC1	$5{\cdot}10^3$	8·10
Cottage cheese 2	CC2	$1{\cdot}10^3$	<10
Cottage cheese 3	CC3	<10	$2{\cdot}10^3$
Cottage cheese 4	CC4	<10	$2{\cdot}10^2$
Cottage cheese 5	CC5	6·10	<10
Salty soft cheese 3	SSFC3	$2{\cdot}10^4$	<10
Salty soft cheese 4	SSFC4	<10	<10

The highest microscopic fungi load has been found in one cottage cheese (CC3) ($2{\cdot}10^3$ CFU/g) and a variety of processed cheese (PC3) ($1{\cdot}10^3$CFU/g).

A negative impact on moulds' deterioration is in the case of products containing sorbate. Some of the microscopic fungi transform it into trans-1,3-pentadiene, causing an alteration in flavour. Some of them can produce mycotoxins.

The heat-resistant microscopic fungi, such as *Byssochlamys nivea*, can deteriorate cream cheese (*Ledenbach & Marshall*, 2009). This microorganism could be detected in our case in two heat-treated products (PC3, DS). For the prevention of the fungal spoilage, control over some factors is considered critical: air treatment, cleaning, and disinfection procedures, heat treatment, water activity reduction by brining, refrigeration, and modified atmosphere packaging (*Garnier et al.*, 2017). In our work based on colony and cell morphology properties, the following microscopic filamentous fungi have been identified: *Aspergillus niger* in the dairy spread, *Penicillium* sp., *Cladosporium* sp., and *Aspergillus* sp. in the cottage cheese, *Penicillium* sp. and *Mucor mucedo* in the salty soft cheese, and *Penicillium* sp. in the smoked cheese sample.

From the analysed samples, not all the products meet the compliance requirements by the European Regulation EC 2073/2005. It can be stated that one of the salty type soft cheese and one fresh cheese sample (both originating from the open-air market) are unsatisfactory. In these two products, the *E. coli* level is higher than the acceptable regulatory criteria. Mascarpone and one of the processed varieties of cheese samples have also been found unacceptable since the *S. aureus* count exceeds the standards. Regarding *Salmonella*, eight products have resulted unsatisfactory.

PCA and cluster analysis are useful methods for the classification of different types of cheese based on their quality (*Eroglu et al.*, 2015). The microbial contamination level of the studied dairy samples has been subjected to PCA. This statistical method reduces the dimensionality of the data, calculating the components that best describe the differences or similarities between samples (*Ercan et al.*, 2014). Three PCs have been established to be significant for the interpretation of microbial content. The eigenvalues and variance of PCs are shown in *Table 3*.

Table 3: Results of PCA analysis of the microbiological count

PC	**Eigenvalue**	**% variance**	**Cumulative variance** (%)
1	2.13042	26.63	26.63
2	1.82792	22.85	49.48
3	1.37301	17.16	66.64
4	1.04405	13.05	79.69
5	0.628574	7.86	87.55
6	0.529612	6.62	94.17
7	0.312203	3.90	98.07
8	0.154219	1.93	100

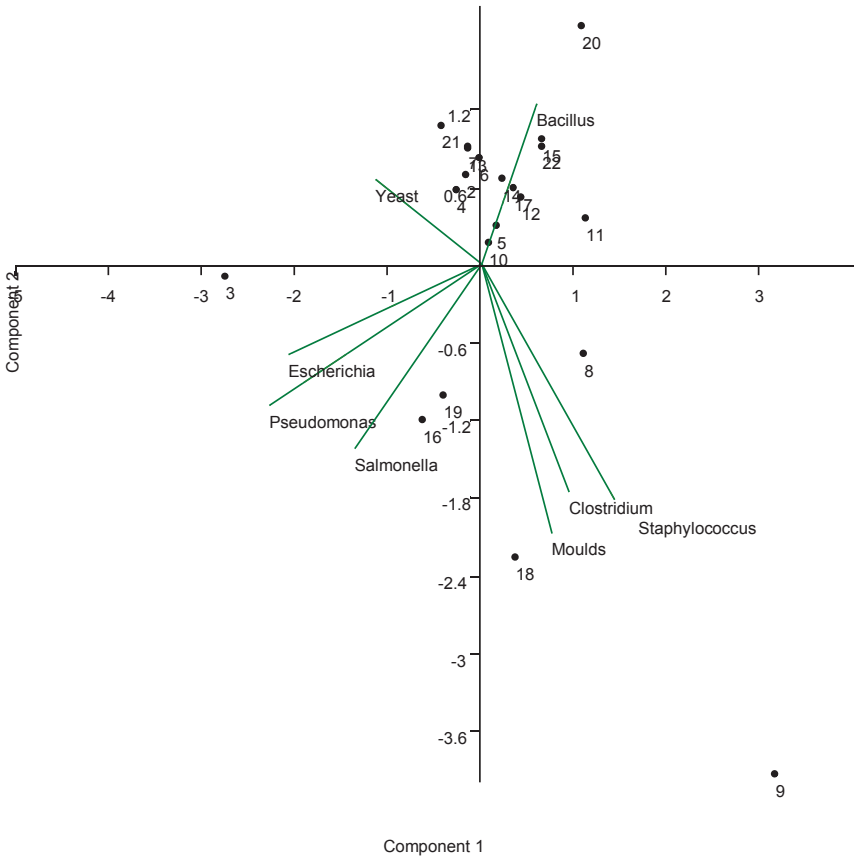
The principal components (PCs) are that eigenvalues resulted higher than 1. These PCs are adequate for the description of the variance. PC1 (26.63%), PC2 (22.85%), and PC3 (17.16%) explain 66.64% of the total variance. The tested variables can be grouped into three new variables (PCs).

According to *Table 4*, the most important variables for the first PC are *Pseudomonas* sp. and *Escherichia coli*, for the second PC, *Staphylococcus aureus* and moulds, and for the third PC *Bacillus cereus* and yeast.

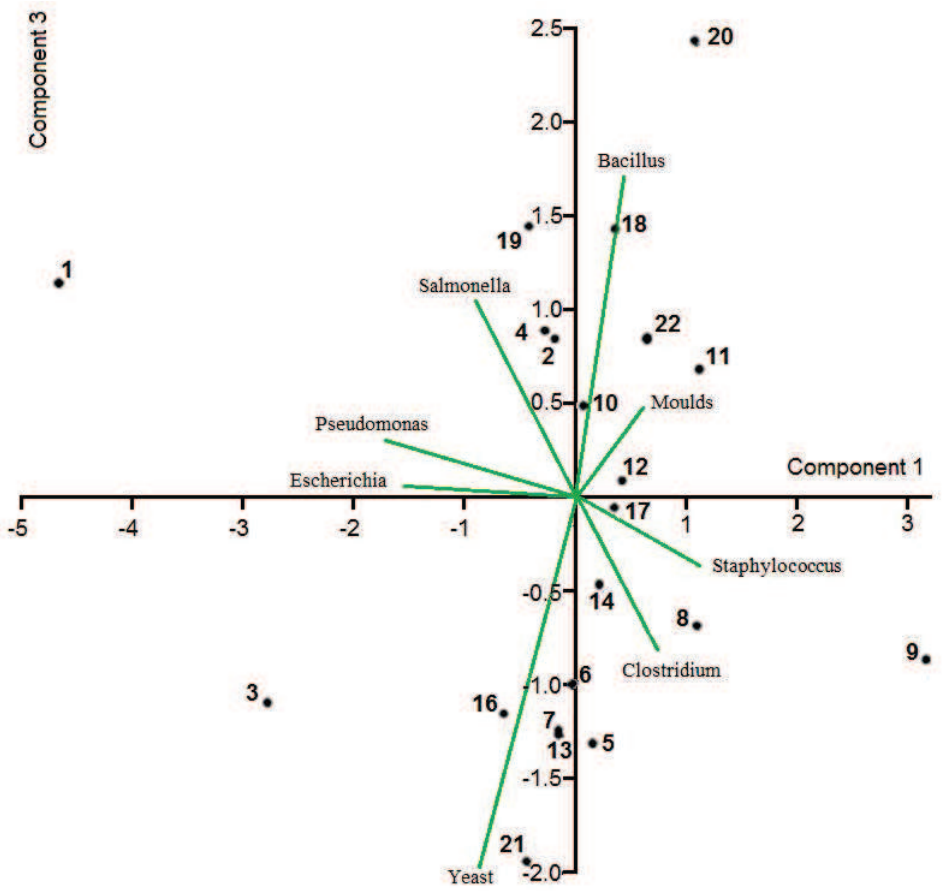
Score and loading plots are shown in *Fig. 1*. Samples coded with 1, 3, 16 (SSFC1, FC1, CC1), and 19 (CC4) are placed on the lower left quadrant (III) of the PC1-PC2 plot. These dairy products are sold by weight and the microbiological quality of these products is not satisfactory.

Table 4: Principal component coefficients (loadings)

	1st loading	2nd loading	3rd loading
Components	**PC1**	**PC2**	**PC 3**
Pseudomonas sp.	**-0.5609**	-0.2703	0.09455
Escherichia coli	**-0.5091**	-0.1721	0.01493
Salmonella	-0.3331	-0.35	0.3814
Staphylococcus aureus	0.3547	**-0.4502**	-0.1228
Bacillus cereus	0.1493	0.3077	**0.5661**
Clostridium	0.2322	-0.433	-0.2676
Yeast	-0.2802	0.164	**-0.6442**
Moulds	0.1863	**-0.5128**	0.1524

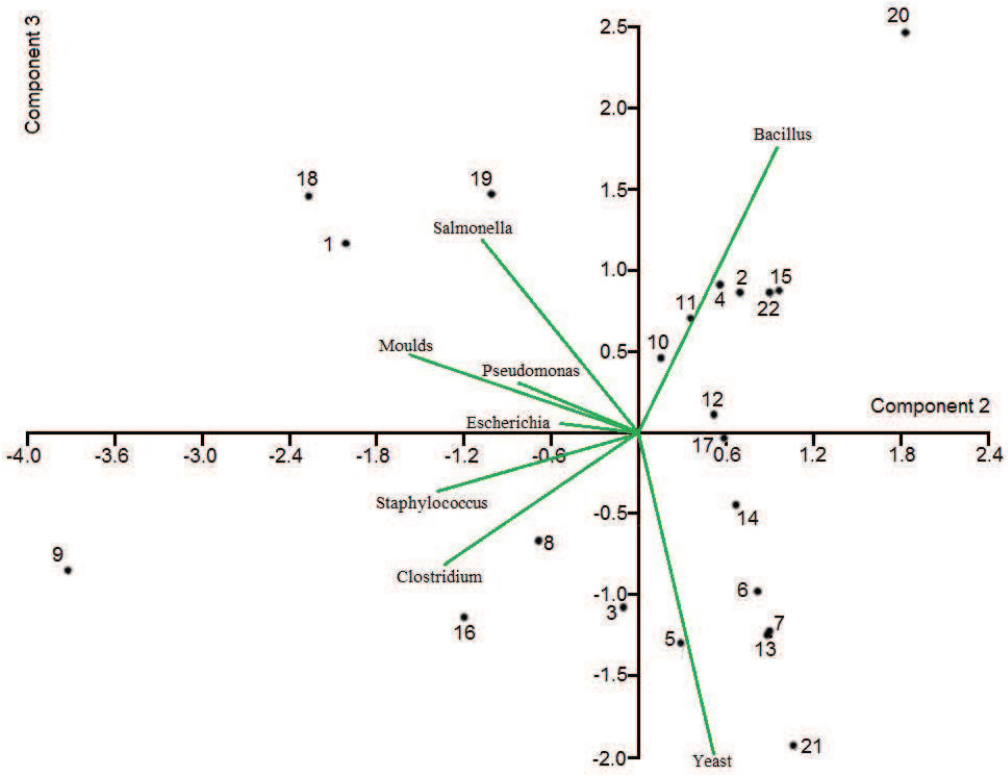


(a)



(b)

The presence of the *E. coli* and *Pseudomonas* in the first three products can originate from milk, from unhygienic conditions during manufacturing. Also, it can be influenced by household practices (*Agarwal et al.*, 2012). Samples coded with 4, 11, 10, 15 (FC2, PC5, PC4, ShC), and 22 (SSFC4) are placed on the upper right quadrant (I) of the PC3-PC2 plot. In four products, except for 10 (PC4), the *Bacillus cereus* count is high. The samples coded with 21, 13, 6, 14 (SSFC3, MO, F, SC), and 17 (CC2) are placed on the lower right quadrant (II) of the PC3-PC2. These products resulted in high yeast counts.



(c)

Figure 1: Score and loading plots of the PCs – (a) PC1-PC2, (b) PC1-PC3, (c) PC2-PC3 – obtained by the principal component analysis (PCA) of microbiological profiles of different dairy products

4 Conclusions

The nutrient content of dairy products favours the growth and development of pathogenic and spoilage microorganisms. Based on our results, the dairy products' microbiological quality varies. We may claim that the majority of the detected microorganisms is due to incorrect food storage, handling, or distribution practices. For maintaining the regulations, the control and prevention of undesirable microbes is also needed after manufacturing, during distribution and storage.

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