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Microbiological Monitoring of Raw Cow Milk in Hungary

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ABSTRACT

Our study aimed to assess the microbiological status of bulk tank milk from dairy farms across Hungary, with a focus on pathogenic microorganisms. In Hungary, raw milk certification involves testing for total germ count, somatic cell count, and the presence of inhibitors, following established standards. However, other pathogenic bacteria are not routinely tested, despite milk being an ideal medium for microbial growth. The increasing consumption of raw dairy heightens the risk of foodborne illnesses and the spread of antibiotic-resistant pathogens. To address this, we sought a comprehensive understanding of the microbiological profile of larger cattle farms in Hungary. Over the course of six months, we collected raw milk samples from 16 locations. We tested them for *Listeria*, *Salmonella*, Coliforms, *E. coli*, *Staphylococcus aureus*, *Clostridium*, and *Enterococcus faecalis*, in accordance with Decree 4/1998 (XI. 11.) of the Ministry of Education and Science. Of the samples, 91.9 % had acceptable total germ counts. However, Coliforms, *Listeria*, and *E. faecalis* exceeded limit values in 14.0 %, 15.5 %, and 20,0 % of samples, respectively. Total germ counts exceeded the threshold in only four counties. Additionally, 13.3 % of samples had *E. coli* bacteria levels above acceptable limits, and *Listeria spp.* was detected in one-third of the analysed samples. These findings highlight the potential health risks associated with foodborne diseases and emphasise the need for periodic testing to ensure the safety of raw milk before consumption.
Keywords: pathogens, monitoring, human health, bulk tank milk

1. INTRODUCTION

Milk is an excellent source of nutrition for humans (Singh et al., 2015), and cow's milk, along with its dairy products, ranks among the most widely consumed foods worldwide. It is one of the best sources of complete protein for human nutrition, boasting outstanding nutritional and biological value due to its rich vitamin and mineral content (Szakály, 2001). However, these nutrients also

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provide an ideal environment for microbial growth (Quigley et al., 2013). The microbiological composition of milk directly affects the microbiological quality of derived products, influencing their food safety properties. It also impacts the organoleptic characteristics, such as taste and texture, of the final product, and may affect its shelf life and quality. Psychrotolerant or psychrotrophic bacteria can grow in refrigerated milk, leading to spoilage (Quigley et al., 2013). The total germ count of milk obtained from a healthy, clean animal is typically 10^3-10^4/ml, remaining stable for 24-48 hours when stored at 4 °C. Several studies have explored the microbiota of cattle milk, describing a complex and diverse community dominated by *Staphylococcus*, *Streptococcus*, *Pseudomonas*, and *Enterococcus* taxa (Oikonomou et al., 2020). These microorganisms can impact animal health and the quality of milk production (Addis et al., 2016). Therefore, understanding the bacterial community in milk is crucial for maintaining a hygienic farming environment and enhancing the quality of dairy products. *Staphylococcus aureus* (*S. aureus*), *Listeria monocytogenes* (*Listeria*), *Campylobacter jejuni*, and *Bacillus cereus*, which are present in milk, not only cause foodborne illnesses but also contribute to milk acidification and spoilage (Willis et al., 2018). Furthermore, their production of lipases and proteases can impair milk quality (Li et al., 2018).

Nowadays, raw milk is becoming increasingly popular as a 'natural and local product' (Loss et al., 2011; Sozańska et al., 2013). However, raw milk can be contaminated by pathogenic bacteria such as coliforms (Godziszewska et al., 2018; Khalid et al., 2024), which can be easily transferred from milk to consumers (Claeys et al., 2013). In a study by Oliver et al. (2005), coliform bacteria were detected in 95 % of bulk tank milk samples collected in 21 U.S. states. The study also showed that pathogenic *Escherichia coli* (*E. coli*) strains often cause human infections (Oliver et al., 2005). A more significant problem is that antibiotic-resistant *E. coli* may also be present in raw milk (Nagy et al., 2021). In New Zealand (Hill et al., 2012), pathogens (*E. coli*, *S. aureus*, *Listeria*, *Salmonella*, and *Campylobacter*) were previously examined in raw milk, where the presence of *S. aureus*, *Listeria*, and *E. coli* was confirmed. In Estonia (Stulova et al., 2010), bulk tank milk was examined, yielding positive results. Specifically, 91 % of the samples were compliant, with *Pseudomonas* being the predominant species in non-compliant milk. The situation in southwestern Ethiopia has deteriorated (Berhanu et al., 2021). Ninety per cent of the 150 milk samples were not suitable, which is a significant problem, as the population consumes raw cow's milk rather than processed cow's milk. In northern Italy, the presence of *Listeria* in raw milk was studied over a three-year period, with a prevalence of 1.66 % in the samples (Dalzini et al., 2016). The examination of milks used in cheese-making in Ireland yielded fairly positive results. *Bacillus cereus*, *S. aureus*, *Listeria*, *Salmonella*, and *E. coli* were observed, and in only 1 of 68 samples was the microbiological status of the raw material unsatisfactory (Lourenco et al., 2020).

Legal requirements apply to microbial criteria for raw cow's milk. In Hungary, these are outlined in the Decree of EüM of 1998 (XI. 11.) on the maximum level of microbiological contaminants that may be present in foodstuffs, as well as Regulation (EC) No 2073/2005. In Hungary, Peles et al. (2008) examined the effect of husbandry technology on milk microbiology and the prevalence and resistance of *S. aureus* in milk from 20 farms (2007). In his dissertation, Jancsó (2015) examined the physico-chemical parameters and total bacterial counts of raw milk. Varga (2016) examined *E. coli* and *S. aureus* in raw cow's milk in his doctoral dissertation. Poor hygiene practices have led to high coliform counts, and other bacteria can also multiply easily (Martin et al., 2023). However, even low levels of pathogens in raw milk can be harmful to consumers (Claeys et al., 2013). For example, it was shown that coliforms can significantly affect the organoleptic characteristics of milk (Godziszewska et al., 2018).

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Environmental pathogens may enter milk through inadequate hygiene of the udder surface, from milking equipment that is not adequately cleaned and disinfected, possibly from milk transport equipment, and from persons, due to either poor milking technique or improper handling. During transport, improper cooling facilitates bacterial growth due to the ideal conditions of nutrients, pH, and water activity (Ndahetuye et al., 2020).

1.1 Microbiological background

Escherichia coli (*E. coli*) is a Gram-negative, aerobic, rod-shaped microbe that resides in the lower part of the gastrointestinal tract. Gram-negative bacteria are most commonly cultured from human samples. Their diarrhoea-causing group often leads to severe epidemics and public health issues. The most commonly studied groups are: enteropathogenic *E. coli* (EPEC), enterohaemorrhagic *E. coli* (EHEC), verotoxigenic *E. coli* (VTEC), enteroaggregative *E. coli* (EAggEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), and diffusely adherent *E. coli* (DAEC). Some of their strains have developed resistance to carbapenems, tigecycline, and colistin (Luo et al., 2020), as well as cephalosporins (Moor et al., 2021), or exhibit multidrug resistance (MDR) to additional antibiotics (Dunn et al., 2019).

Staphylococcus aureus (*S. aureus*) is a Gram-positive bacterium that can cause many infectious diseases (e.g., foodborne illness, skin infections, pneumonia, etc.). It is a significant nosocomial pathogen, and many of its clones also occur in community settings. Due to its virulence factors, it easily evades the host's immune response and is increasingly resistant to antibiotics, making it a highly significant pathogen. It is responsible for many opportunistic infections (bacteraemia, skin and soft tissue infections, surgical infections, abscesses) (Tong et al., 2015; Bencardino et al., 2021). The carotenoids produced by the organism give the yellow colour of its colonies. The Latin term 'aureus' refers to its gold colour (Liu et al., 2005).

Enterococcus faecalis (*E. faecalis*) is a ubiquitous member of the healthy human intestinal flora. However, it is also a common opportunistic pathogen and a leading cause of nosocomial infections. It adapts well to the mammalian host, supports infection, and ensures its survival under diverse conditions. It can easily adjust its metabolism, allowing it to react quickly to new environments (Kao et al., 2019). Several resistant strains have developed, such as vancomycin-resistant (Miller et al., 2020) or linezolid-resistant enterococci (Bi et al., 2018).

Clostridium perfringens is a significant anaerobic, spore-forming pathogenic bacterium affecting humans and animals. A significant proportion of foodborne illnesses is caused by *Clostridium perfringens* enterotoxins (CPE). During infection, it produces protein toxins and forms environmentally resistant endospores. Among them are chloramphenicol-, bacitracin-, lincomycin-, and tetracycline-resistant strains (Adams et al., 2018). Currently, seven different toxin types are known (Rood et al., 2018).

Listeria is a genus of Gram-positive, facultatively anaerobic bacteria that cause listeriosis, resulting in high morbidity and mortality rates. It also causes bacteraemia and meningitis in newborns, primarily through contaminated food. Therefore, it is important to understand its virulence factors (Disson et al., 2021). Six species are classified in the genus.

Salmonella is a genus of rod-shaped, Gram-negative, facultatively anaerobic bacteria belonging to the family Enterobacteriaceae. It is one of the most commonly isolated food pathogens, with food-producing animals as its primary source of infection. People with weakened immune systems are more prone to infection and its more severe course. Almost all of its strains are pathogenic. Upon entering the digestive system, they invade the epithelial cells lining the intestinal wall, encoding

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secretion systems that inject their effectors into the cytoplasm, causing phagocytosis of the intestinal wall. Its clinical manifestations include enteric fever, gastroenteritis, bacteraemia, and other extraintestinal complications. Furthermore, multidrug-resistant strains have been reported in previous studies (Eng et al., 2015).

2. MATERIALS AND METHODS

2.1 Sampling

Samples were obtained by the MTKI Research-Food Testing and Raw Milk Certification Laboratory, collected in accordance with Directive 3-2-1/2004 on the Official Collection of Food Testing Methods of the Hungarian Food Codex (*Codex Alimentarius Hungaricus*) – Sampling and testing methods for the price-consistent classification of raw milk, edition 3 of 2013 (16/2008. (II. 15.) FVM-SZMM). For the examination, samples were requested from at least one dairy farm in each of the 16 counties in Hungary every month. Thus, a minimum of 6 and a maximum of 15 samples were obtained per site (*Table 1*), totalling 135 samples. The samples were delivered from Budapest to Mosonmagyaróvár under refrigerated conditions. Each sample was 100 ml and tested within 10 hours of sampling.

Table 1: Distribution of samples by county

	County	Sample number	Number of dairy farms	Number of cows/1000
1	Baranya	10	2	15,7
2	Bács-Kiskun	9	205	36,3
3	Békés	11	40	27,0
4	Borsod-Abaúj-Zemplén	7	35	23,8
5	Csongrád-Csanád	6	100	19,0
6	Fejér	6	32	22,9
7	Hajdú-Bihar	7	47	55,9
8	Heves	6	11	8,9
9	Jász-Nagykun-Szolnok	13	41	27,5
10	Nógrád	7	14	12,5
11	Pest	15	166	27,1
12	Somogy	6	247	17,1
13	Szabolcs-Szatmár-Bereg	7	34	26,9
14	Tolna	10	20	10,0
15	Vas	7	19	14,2
16	Zala	8	35	12,5

2.2 Examination procedure

Microbiological examinations were conducted in accordance with Annexe 4 to the EüM Decree 4/1998 (XI. 11.) as currently in force in Hungary. Following ISO standards, we determined the presence of *Salmonella* (MSZ EN ISO 6579-1:2017), Coliforms (ISO 4832:2006), *Escherichia coli* (*E. coli*) (ISO 16649-2:2001), *Listeria* (ISO 11290-1:2017), *Staphylococcus aureus* (*S. aureus*) (ISO 6888-1:2021), sulphite-reducing *Clostridium* (ISO 7937:2004), *Enterococcus faecalis* (*E. faecalis*) (ISO

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7899-2), and microbial counts (*Table 2*). All microbial tests were performed in triplicate. According to regulations, two limit values are set: m is the compliance value, and 'M' is the rejection value. A sample is compliant below 'm', acceptable between 'm' and 'M', and non-compliant above 'M'.

Table 2: Limit values for the microbes examined (EÜM Decree 4/1998 (XI.11.)

Bacterial strain	m (CFU/mL)	M (CFU/mL)
Salmonella	-	0/25 g
S. aureus	10^2	$5*10^2$
Listeria	-	0/25 g
Coliform	10	10^2
Total bacterial count	10^5	$3*10^5$
E. faecalis	10	10^2
E. coli	< 1	< 10
Clostridium	10	10^2

2.3 Materials used and standards applied

Plate Count agar, Tryptone-bile-glucuronide agar, Tryptose-sulphite-cycloserine agar, Müller-Kauffmann tetrathionate-novobiocin broth, Brilliant green-phenol red-lactose-sucrose agar, Xylose-lysine deoxycholate agar, Chromobio Coliform agar, ALOA-agar, Oxford agar, Tryptone Soya Yeast agar, Columbia blood agar, Gram stain set, Baird-Parker agar, Kanamycin-esculin-azide agar (all purchased from Biolab), Fraser broth, buffered peptone water (VWR), Rappaport-Vassiliadis broth (Sigma-Aldrich), *Salmonella* whey (Prolab), Bactident Coagulase (Merck), control strains (HNCMB), Petri dishes, pipettes, disposable needles, and flasks (all purchased from AA Laboratories Kft).

2.4 Samples

The MTKI collected samples regularly from 16 counties in Hungary over a six-month period. Each raw milk sample was obtained from a Holstein-Friesian cattle farm, selected based on its leading position in its county for standard lactation milk production and an annual milk yield of 9,000-10,000 kg/cow. The samples were bulk tank milks. They arrived at the examination site properly refrigerated (< 6 °C) and were tested within 10 hours of sampling.

3. RESULTS

In Hungary, raw milk is tested for somatic cell count, inhibitor concentration, and total microbial count in accordance with legislation. Thus, we considered it worthwhile to examine other bacteria as well, given the increasing number of raw milk vending machines and the rising prevalence of antibiotic-resistant pathogens. The following analyses were performed: *Salmonella*, *Staphylococcus aureus* (*S. aureus*), *Listeria*, Coliforms, *Enterococcus faecalis* (*E. faecalis*), *Escherichia coli* (*E. coli*), *Clostridium*, and total germ count. We examined a total of 135 samples of bulk tank milk from dairy farms in 16 counties over a 6-month period (*Table 3*). The 'm' value is the conformity limit, and the 'M' value is the rejection limit. A sample is compliant if it is below the 'm' value; it is acceptable if it is at or above the 'm' value but below the 'M' value. A sample is non-compliant if it reaches or exceeds the 'M' value.

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Table 3: The compliance percentages are presented in percentages and by county

Cow farm*	*Listeria*		*Salmonella*		*E. coli*			*Coliform*			*S. aureus*			*E. faecalis*			Colony plate count		
	> M	< m	> M	< m	m <> M	> M	< m	m <> M	> M	< m	m <> M	> M	< m	m <> M	> M	< m	m <> M	> M	< m
1	20.0	80.0	0	100	10.0	0	90.0	33.0	10.0	57.0	10.0	10.0	80.0	40.0	20.0	40.0	0	0	100
2	33.0	67.0	0	100	0	0	100.0	55.0	0	45.0	11.1	0	88.9	33.3	44.4	22.3	0	0	100
3	9.0	91.0	0	100	18.1	0	81.9	45.4	0	54.6	18.1	9.0	145.5	63.6	9.0	27.4	0	9.0	91.0
4	28.0	72.0	0	100	42.8	0.0	57.2	85.7	0	14.3	28.5	0	114.3	42.8	42.8	14.4	0	0	100
5	33.0	67.0	0	100	33.0	16.6	50.4	66.0	16.6	17.4	16.6	0	116.7	33.3	0	66.7	0	0	100
6	0	100	0	100	50.0	16.6	33.4	50.0	33.0	17.0	33.3	0	116.7	50.0	16.6	33.4	16.6	0	83.4
7	0	100	100	0	28.5	28.5	43.0	100	0	0	42.8	14.2	128.6	71.4	14.2	14.4	0	0	100
8	0	100	0	100	0	0	100	83.3	0	16.7	0	0	100	100	0	0	0	0	100
9	30.7	69.3	0	100	61.5	23.0	15.5	69.2	7.6	23.2	53.8	0	46.2	61.5	23.0	15.5	0	0	100
10	14.0	86.0	0	100	42.8	28.6	28.6	57.1	28.5	14.4	28.5	14.2	57.3	57.1	28.5	14.4	28.5	0	71.5
11	6.6	93.4	0	100	33.0	26.6	40.4	73.3	26.6	0	26.6	0	77.4	73.3	18.1	8.6	20.0	13.3	66.7
12	0	100	0	100	50.0	16.6	33.4	66.0	33.0	0	50.0	0	50.0	50.0	33.3	16.7	0	0	100
13	28.0	72.0	100	0	42.8	0	57.2	57.1	14.2	28.7	57.1	0	42.9	71.4	28.5	0.1	0	14.2	85.8
14	10.0	90.0	0	100	30.0	20.0	50.0	50.0	40.0	10.0	50.0	0	50.0	60.0	20.0	20.0	10.0	0	90.0
15	28.0	72.0	0	100	28.5	14.2	57.3	85.7	0	14.3	28.5	14.2	57.3	71.4	14.2	14.4	0	0	100
16	37.5	62.5	0	100	25.0	12.5	62.5	40.0	12.5	47.5	50.0	0	50.0	50.0	12.5	37.5	0	0	100

*Numbers presented counties as listed in *Table 1*

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When comparing the samples by month, no significant differences were detected in any characteristic.

3.1 *Salmonella* analyses

According to the regulation, the presence of *Salmonella* in milk is not permitted. In contrast, *Salmonella* (*Figure 1*) was found in 2 samples, representing 1.5 % of the samples; therefore, these milks were non-compliant. Based on geographical distribution, the affected samples originated from different but neighbouring counties. For both cattle farms, seven samples were tested, meaning that 14.3 % of the samples were non-compliant.

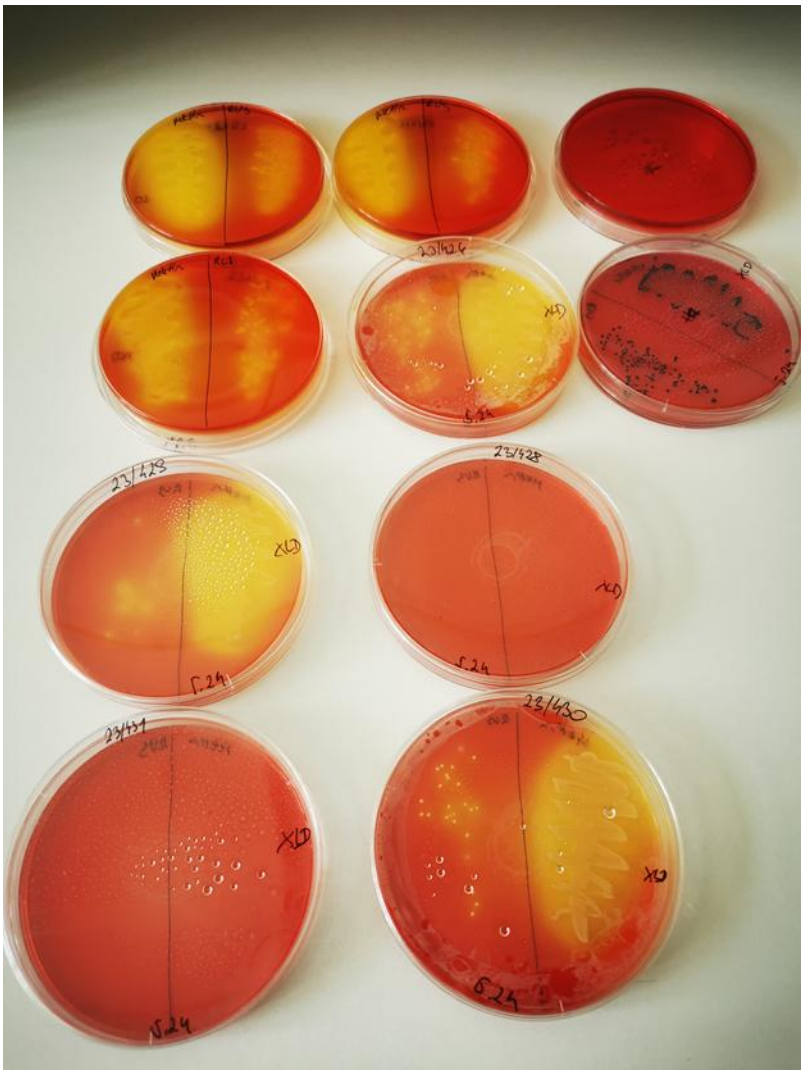

Figure 1: Salmonella tests in Petri dishes

3.2 *Clostridium* analyses

The *Clostridium* analyses showed that none of the samples exceeded the limit value 'm' (10 CFU/ml), indicating that all samples were compliant. Additionally, it is worth noting that we identified the bacterium in 13 samples (9.6 %), primarily in 10 counties (62.5 %), with the majority of cases

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occurring in the central part of the country. The bacterium was detected twice in each of three dairy farms, from 6, 7, and 15 samples.

3.3 *Staphylococcus aureus* analyses

In the *Staphylococcus aureus* (*S. aureus*) analyses, its presence was detected in 5 samples, with 3.7 % of the samples exceeding the limit value 'M' (5×10^2 CFU/ml); consequently, these samples were non-compliant. It can also be stated that the batches that reached the rejection limit were all from different counties. Only the samples from one dairy farm (out of 6 samples) had no objectionable batch, and the number of these bacteria reached the limit value 'm' (10^2 CFU/ml) at least once in the dairy farms of the other 15 counties (*Figure 2*).

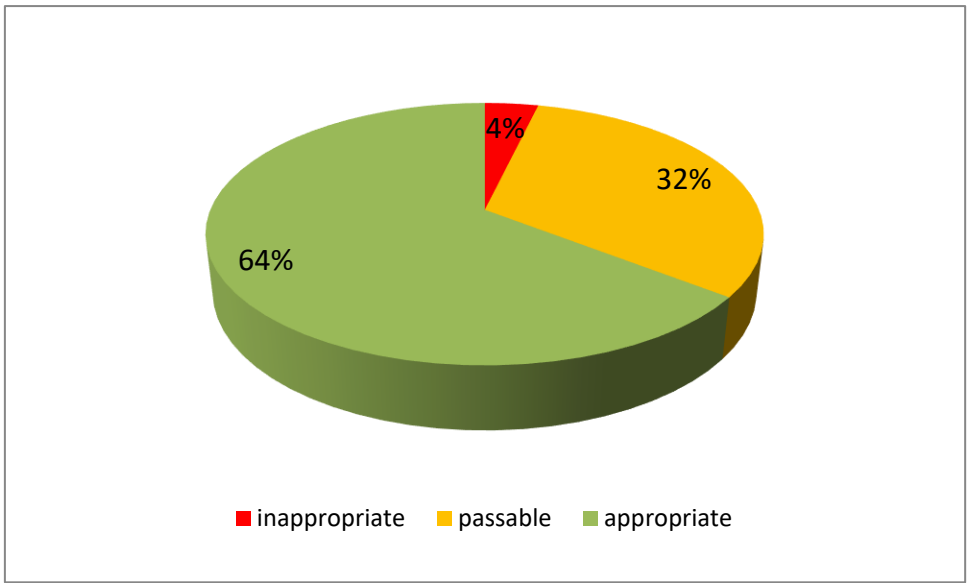

Figure 2: Classification of bulk tank milk based on the occurrence of Staphylococcus aureus nationwide

3.4 *Listeria* analyses

Listeria was present in 21 samples, representing 15.5 % of all samples (135) on a pro rata basis. When analysed by counties, this proportion was very high (33.3 %) in each cattle farm. However, there were cattle farms where no bacteria were detected, but their proportion was very low (2.9 %). Unfortunately, there were also false positive results on ALOA and XLD media, which biochemical tests can verify. These microbes can generally be classified into *Aeromonas*, *Proteus*, and *Serratia* strains. In one sample, we identified the strain of *Serratia marcescens*, a microorganism that is one of the most common opportunistic pathogens (causing nosocomial infections) in the natural environment.

3.5 *E. coli* analyses

The occurrence of *Escherichia coli* (*E. coli*) (*Figure 3*) was also significant in the samples. It was not detected in two cattle farms (12.5 %); in the others, the bacterium was found at least twice. In total, *E. coli* was detected in 60 (44.4 %) of the 135 samples.

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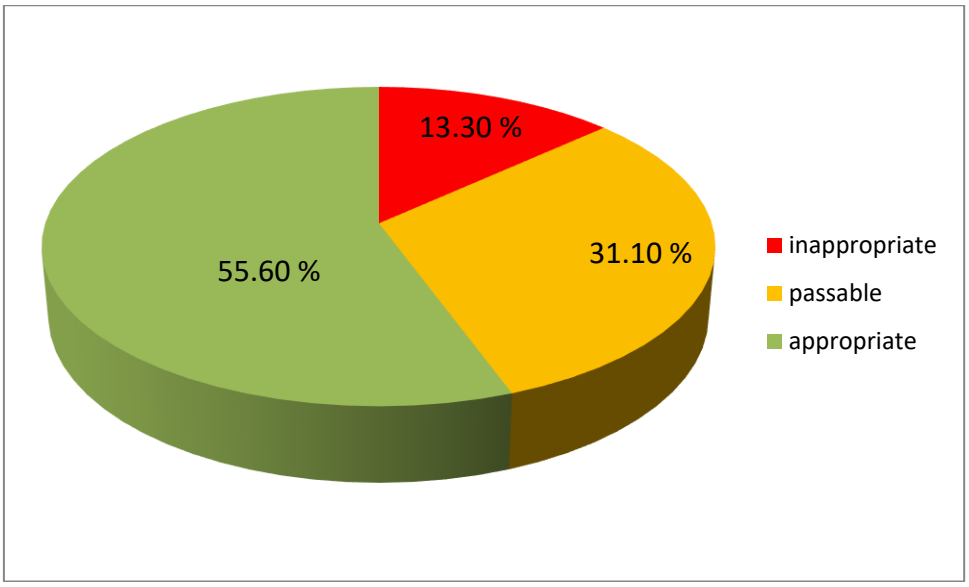

Figure 3: Classification of bulk tank milk based on the occurrence of E. coli nationwide

3.6 Coliform analyses

Coliforms (*Figure 4*) were found in 19 samples (*Figure 5*). The non-compliant samples (14.0 %) originated from 10 counties. Fifty per cent of the samples from one county received a non-compliant rating. In 6 counties (37.5 %), all samples were rated as compliant or acceptable.

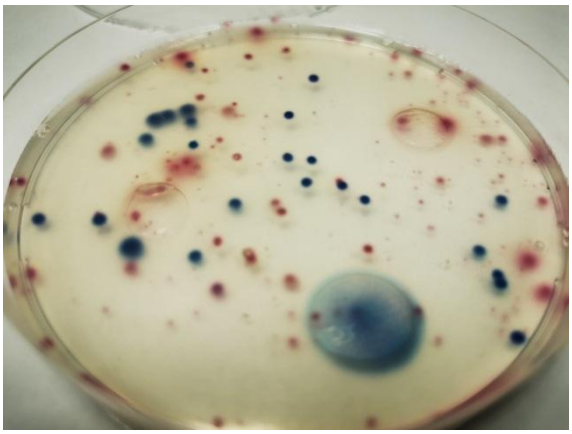

Figure 4: Coliforms in a Petri dish

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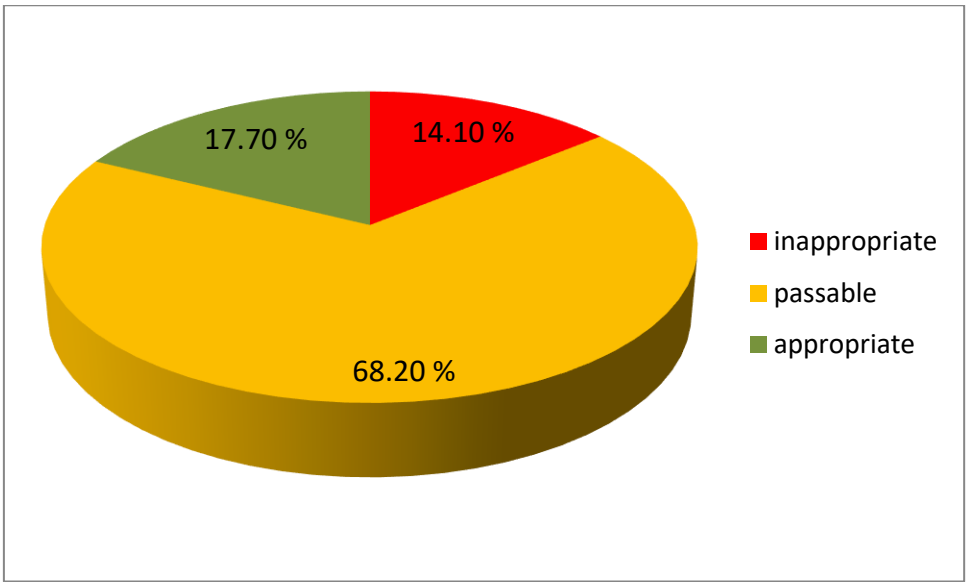

Figure 5: Classification of bulk tank milk based on the occurrence of Coliform nationwide

3.7 *E. faecalis* analyses

Most of the samples examined contained *Enterococcus faecalis* (*E. faecalis*) in excess of the acceptable limit value. Only 24 samples contained an acceptable bacterial count (< 10 CFU/ml). However, only 27 samples received a non-compliant classification (> 10^2 CFU/ml). The percentage distribution is shown in *Figure 6*.

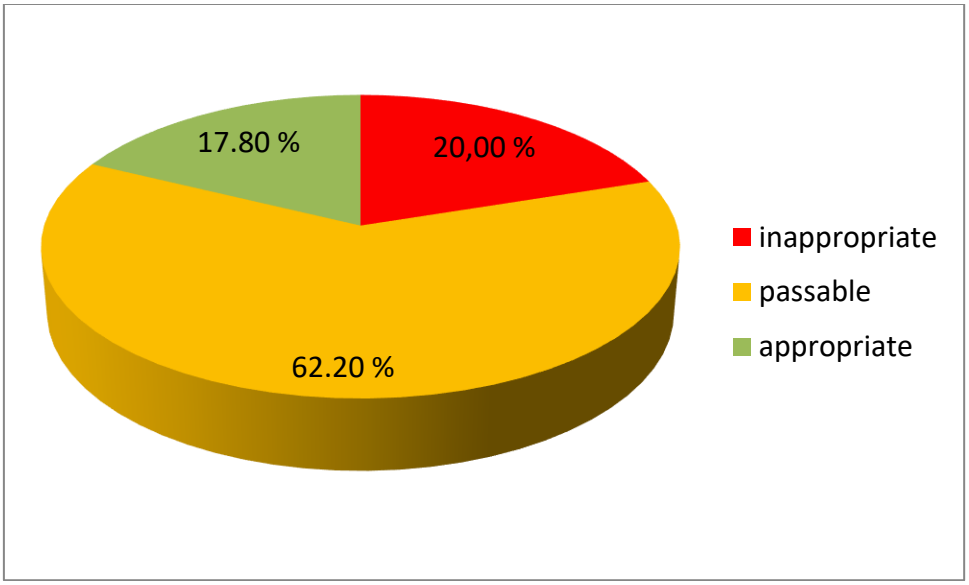

Figure 6: Classification of bulk tank milk based on the occurrence of E. faecalis nationwide

3.8 Total germ count analyses

The total germ count in the milk samples was mostly within the limits defined by law, which is routinely verified. Relevant food safety regulations mandate compliance; therefore, any sample

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exceeding the threshold would not be permitted for market distribution. Non-compliant samples represented approximately 3 % (*Figure 7*). Table 2 presents the compliance percentages by county.

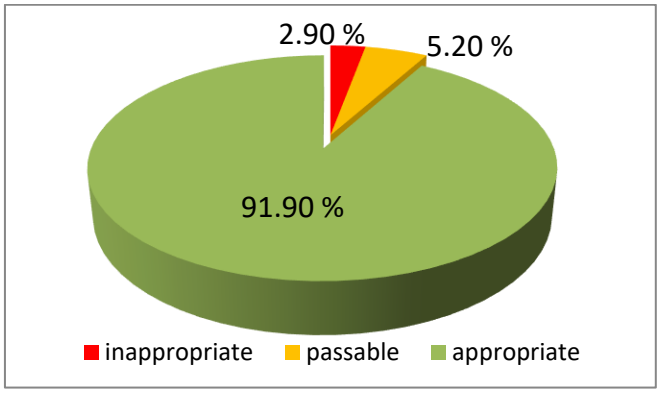

Figure 7: Classification of bulk tank milk based on the occurrence of total germ count nationwide

4. DISCUSSION

Based on the results, it can be concluded that total germ counts, one of the key parameters for classifying raw milk, exceeded the threshold value (> 10^5 CFU/ml) in only four counties. This suggests that, from a general microbiological perspective, the majority of the milk samples were acceptable. However, data from the six-month study indicate that, in numerous cases, the levels of coliform bacteria, *Enterococcus faecalis* (*E. faecalis*), and *Escherichia coli* (*E. coli*) were significantly above acceptable limits. Furthermore, the detection of *Listeria* spp. presents a notable concern, as it was detected in one-third of the analysed samples from one cattle farm. These findings highlight potential health risks. On a more positive note, according to Peles et al. (2007), *Staphylococcus aureus* (*S. aureus*) was detected in 70 % of samples, whereas in our study, it was found in only 4 %. Due to the unavailability of hygiene data from the farms, we infer, based on findings from previous studies (Peles et al., 2008), that hygiene conditions may have contributed to the elevated pathogen levels observed.

5. CONCLUSIONS

Our study aimed to assess the presence of pathogenic microorganisms in tank milk from dairy farms nationwide. Of 135 samples examined, some bacteria were present in 14 % of cases, while others were present in 20 % of cases, exceeding the limit value. With this study, we aim to draw attention to the need to improve hygiene practices and highlight the importance of more accurate identification and exclusion of clinically or subclinically sick cows on dairy farms to prevent contaminated milk from entering the distribution tank, thereby avoiding deterioration in milk quality. Additionally, strict attention should be paid to transport conditions, as suboptimal environments can promote the rapid growth of bacteria and fungi. Our results also highlight the need for consumers to heat-treat raw milk before consumption.

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ÖSSZEFOGLALÁS

Tanulmányunk célja az ország különböző részein található tejgazdaságok tartálytejének kórokozó mikroorganizmusokkal kapcsolatos állapotának felmérése volt. Magyarországon a nyerstej árkonzisztens tanúsítása során a szabványoknak megfelelően határozzák meg az összcsíraszámot, a szomatikus sejtszámot és az inhibitor jelenlétét. Sajnálatos, hogy más kórokozó baktériumokat nem vizsgálnak, bár köztudott, hogy a tej kiváló táptalaj ezeknek a mikroorganizmusoknak. A nyerstejfogyasztás növekvő tendenciája növeli a kórokozók és az antibiotikum-rezisztens kórokozók élelmiszer eredetű terjedését. Ezért szerettünk volna átfogó képet kapni a nagyobb hazai szarvasmarha-tenyésztő gazdaságok mikrobiológiai hátteréről. Az ország 16 helyszínéről gyűjtöttünk nyerstejmintákat, és a hat hónapos vizsgálat során *Listeria, Salmonella, Coliform, E. coli, Staphylococcus aureus, Clostridium* és *Enterococcus faecalis* jelenlétét vizsgáltuk 4/1998. (XI.11) EüM rendelet alapján. A minták 91,9 %-a megfelelő összcsíraszámmal rendelkezett, azonban a *Listeria, Coliform* és *E. faecalis* 14,0 %, 15,5 % és 20,0 %-ban előfordult a határértéket meghaladó mennyiségben. *E. coli* az esetek 13,3 %-ában, míg *Listeria spp*. a minták harmadában fordult elő. A tanulmány kimutatta, hogy fontos lenne a minták időnkénti ellenőrzése, mielőtt a nyerstej fogyasztása komoly közegészségügyi kockázatot jelentene. Az összes csíraszám mindössze négy megyében haladta meg a küszöbértéket. Ezek a megállapítások rávilágítanak a lehetséges egészségügyi kockázatokra (élelmiszer eredetű betegségek).

Kulcsszavak: kórokozók, monitorozás, emberi egészség, tartálytej

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REFERENCES

Adams, V., Han, X., Lyras, D., & Rood, J. I. (2018). Antibiotic resistance plasmid and mobile genetic elements of *Clostridium perfringens.* Plasmid*, 99*, 32-39. https://doi.org/10.1016/j.plasmid.2018.07.002

Addis, M. F., Tanca, A., Uzzau, S., Oikonomou, G., Bicalho, R. C., & Moroni, P. (2016). The bovine milk microbiota: Insights and perspectives from -omics studies. *Molecular BioSystems, 12*(8), 2359-2372. https://doi.org/10.1039/C6MB00217J

Bencardino, D., Amagliani, G., & Brandi, G. (2021). Carriage of *Staphylococcus aureus* among food handlers: An ongoing challenge in public health. *Food Control*, *130*, 108362. https://doi.org/10.1016/j.foodcont.2021.108362

Berhanu, L., Gume, B., Kassa, T., Dadi, L.S., Tegegne, D., Getnet, M., Bediru, H., Getaneh, A., Suleman, S., Mereta, S.T. (2021) Microbial quality of raw cow milk and its predictors along the dairy value chain in Southwest Ethiopia. *International Journal of Food Microbiology*. *350*, https://doi.org/10.1016/j.ijfoodmicro.2021.109228

Bi, R., Qin, T., Fan, W., Ma, P., & Gu, B. (2018). The emerging problem of linezolid-resistant enterococci. *Journal of Global Antimicrobial Resistance, 13*, 11-19. https://doi.org/10.1016/j.jgar.2017.10.018

Claeys, W. L., Cardoen, S., Daube, G., De Block, J., Dewettinck, K., Dierick, K., De Zutter, L., Huyghebaert, A., Imberechts, H., Thiange, P., Vandenplas, Y., & Herman, L. (2013). Raw or heated cow milk consumption: Review of risks and benefits. *New Zealand Science Review, 70*(3), 70. https://doi.org/10.26686/nzsr.v70.8727

Dalzini, E., Bernini, V., Bertasi, B., Daminelli, P., Losio, M-N., Varisco, G. (2016). Survey of prevalence and seasonal variability of Listeria monocytogenes in raw cow milk from Northern Italy. *Food Control, 60*, 466-470. https://doi.org/10.1016/j.foodcont.2015.08.019

Disson, O., Moura, A., & Lecuit, M. (2021). Making sense of the biodiversity and virulence of Listeria monocytogenes. Trends in *Microbiology,* 29(9), 811-822. https://doi.org/10.1016/j.tim.2021.01.008

Dunn, S. J., Connor, C., & McNally, A. (2019). The evolution and transmission of multidrug-resistant Escherichia coli and Klebsiella pneumoniae: The complexity of clones and plasmids. *Current Opinion in Microbiology, 51*, 51-56. https://doi.org/10.1016/j.mib.2019.06.004

Eng, S. K., Pusparaja, P., Ab Mutalib, N. S., Ser, H. L., Chan, K. G., & Lee, L. H. (2015). Salmonella: A review on pathogenesis, epidemiology and antibiotic resistance. *Frontiers in Life Science, 8*(3), 284-293. https://doi.org/10.1080/21553769.2015.1051243

Godziszewska, J., Pogorzelska-Nowicka, E., Brodowska, M., Jagura-Burdzy, G., & Wierzbicka, A. (2018). Detection in raw cow's milk of coliform bacteria: Reservoir of antibiotic resistance. *LWT, 93*, 634–640. https://doi.org/10.1016/j.lwt.2018.04.019

Hill, B., Smythe, B., Lindsay, D., Shepherd, J. (2012). Microbiology of raw cow milk in New Zealand. *International Journal of Food Microbiology*, *157*(2), 305-308. https://doi.org/10.1016/j.ijfoodmicro.2012.03.031

Jancsó, A. (2015). *A termelői nyers tehéntej közvetlen értékesítésének gyakorlata és a minőség értékelése* [Doktori disszertáció, Nyugat-Magyarországi Egyetem]. Mosonmagyaróvár.

Kao, P. H. N., & Kline, K. A. (2019). Dr Jekyll and Mr Hide: How Enterococcus faecalis subverts the host immune response to cause infection. *Journal of Molecular Biology*, *431*(16), 2932-2945. https://doi.org/10.1016/j.jmb.2019.05.030

 DOI: 10.17108/ActAgrOvar.2025.66.2.17

Khalid, L., Fatima, A., Nawaz, S., Khurram, A., Hussain, Z., & Sajid, I. (2024). Quality, safety, and microbiological assessment of loose market milk and antibiotic resistance analysis of Escherichia coli isolates in different areas of Faisalabad, Pakistan. *International Dairy Journal, 154*, 105936. https://doi.org/10.1016/j.idairyj.2024.105936

Antonio Lourenco, A., Maria Fraga-Corral, M., Lorenzo De Colli, L., Mary Moloney, M., Martin Danaher, M., Kieran Jordan, K. (2020). Determination of the presence of pathogens and anthelmintic drugs in raw milk and raw milk cheeses from small scale producers in Ireland. *LWT*, *130*. https://doi.org/10.1016/j.lwt.2020.109347

Li, N., Wang, Y., You, C., Ren, J., Chen, W., Zheng, H., & Liu, Z. (2018). Variation in raw milk microbiota throughout 12 months and the impact of weather conditions. *Scientific Reports, 8*(1), 2371. https://doi.org/10.1038/s41598-018-20862-8

Liu, G. Y., Essex, A., Buchanan, J. T., Datta, V., Hoffman, H. M., Bastian, J. F., Fierer, J., & Nizet, V. (2005). *Staphylococcus aureus* golden pigment impairs neutrophil killing and promotes virulence through its antioxidant activity. *Journal of Experimental Medicine, 202*(2), 209-215. https://doi.org/10.1084/jem.20050846

Loss, G., Apprich, S., Waser, M., Kneifel, W., Genuneit, J., Büchele, G., Weber, J., Sozanka, B., Danielewicz, H., Horak, E., van Neerven, R. J. J., Heederik, D., Lorenzen, P. C., von Mutius, E., Braun-Fahrlander, C., & GABRIELA Study Group. (2011). The protective effect of farm milk consumption on childhood asthma and atopy: The GABRIELA study. *Journal of Allergy and Clinical Immunology, 128*(4), 766-773. https://doi.org/10.1016/j.jaci.2011.07.048

Luo, Q., Wang, Y., & Xiao, Y. (2020). Prevalence and transmission of mobilised colistin resistance (mcr) gene in bacteria common to animals and humans. *Biosafety and Health, 2*(2), 71-78. https://doi.org/10.1016/j.bsheal.2020.05.001

Martin, N. H., Evanowski, R. L., & Wiedmann, M. (2023). Invited review: Redefining raw milk quality – Evaluation of raw milk microbiological parameters to ensure high-quality processed dairy products. *Journal of Dairy Science, 106*(3), 1502-1517. https://doi.org/10.3168/jds.2022-22416

Miller, W. R., Murray, B. E., Rice, L. B., & Arias, C. A. (2020). Resistance in vancomycin-resistant enterococci. *Infectious Disease Clinics of North America, 34*(4), 751-771. https://doi.org/10.1016/j.idc.2020.08.004

Moor, J., Aebi, S., Rickli, S., Mostacci, N., Overesch, G., Oppliger, A., & Hilty, M. (2021). Dynamics of extended-spectrum cephalosporin-resistant Escherichia coli in pig farms: A longitudinal study. *International Journal of Antimicrobial Agents, 58*(3), 106382. https://doi.org/10.1016/j.ijantimicag.2021.106382

Nagy, Á., Székelyhidi, R., Hanczné Lakatos, E., & Kapcsándi, V. (2021). Review on the occurrence of the mcr-1 gene causing colistin resistance in cow's milk and dairy products. *Heliyon, 7*(4), e06800. https://doi.org/10.1016/j.heliyon.2021.e06800

Ndahetuye, J. B., Artursson, K., Båge, R., Ingabire, A., Karege, C., Djangwani, J., Nyman, A.-K., Ongol, M. P., Tukei, M., & Persson, S. (2020). MILK symposium review: Microbiological quality and safety of milk from farm to milk collection centres in Rwanda. *Journal of Dairy Science, 103*(11), 9730-9739. https://doi.org/10.3168/jds.2020-18302

Oliver, S. P., Jayarao, B. M., & Almeida, R. A. (2005). Foodborne pathogens in milk and the dairy farm environment: Food safety and public health implications. *Foodborne Pathogens and Disease, 2*(2), 115-129. https://doi.org/10.1089/fpd.2005.2.115

Oikonomou, G., Addis, M. F., Chassard, C., Nader-Macias, M. E. F., Grant, I., Delbès, C., Bogni, C. I., Le Loir, Y., & Even, S. (2020). Milk microbiota: What are we exactly talking about? *Frontiers in Microbiology, 11*, 60. https://doi.org/10.3389/fmicb.2020.00060

Quigley, L., O'Sullivan, O., Stanton, C., Beresford, T. P., Ross, R. P., Fitzgerald, G. F., & Cotter, P. D. (2013). The complex microbiota of raw milk. *FEMS Microbiology Reviews, 37*(5), 664-698. https://doi.org/10.1111/1574-6976.12030

Peles, F., Máthéné Szigeti, Zs., Béri, B., & Szabó, A. (2008). The effect of keeping technology on the microbiological status of raw milk. Acta Agraria Debreceniensis, 31, 49-54. https://doi.org/10.34101/actaagrar/31/3009

Peles, F., Wagner, M., Varga, L., Hein, I., Rieck, P., Gutser, K., Keresztúri, P., Kardos, G., Turcsányi, I., Béri, B., & Szabó, A. (2007). Characterisation of *Staphylococcus aureus* strains isolated from bovine milk in Hungary. *International Journal of Food Microbiology, 118*(2), 186-193. https://doi.org/10.1016/j.ijfoodmicro.2007.07.010

Rood, J. I., Adams, V., Lacey, J. A., Lyras, D., McClane, B. A., Melville, S. B., Moore, R. J., Popoff, M. R., Sarker, M. R., Songer, J. G., Uzal, F. A., & Van Immerseel, F. (2018). Expansion of the *Clostridium perfringens* toxin-based typing scheme. *Anaerobe, 53*, 5-10. https://doi.org/10.1016/j.anaerobe.2018.04.011

Singh, G. M., Micha, R., Khatibzadeh, S., Shi, P., Lim, S., Andrews, K. G., Engell, R. E., Ezzati, M., Mozaffarian, D., & Global Burden of Diseases Nutrition and Chronic Diseases Expert Group. (2015). Global, regional, and national consumption of sugar-sweetened beverages, fruit juices, and milk: A systematic assessment of beverage intake in 187 countries. *PLoS ONE, 10*(8), e0124845. https://doi.org/10.1371/journal.pone.0124845

Sozańska, B., Pearce, N., Dudek, K., & Cullinan, P. (2013). Consumption of unpasteurised milk and its effects on atopy and asthma in children and adult inhabitants in rural Poland. *Allergy, 68*(5), 644-650. https://doi.org/10.1111/all.12147

Stulova, I., Adamberg, S., Krisciunaite, T., Kampura, M., Blank, L., Laht, T-M. (2010). Microbiological quality of raw milk produced is Estonia. *Letters In Applied Microbiology. 51*(6), 683-690. https://doi.org/10.1111/j.1472-765X.2010.02951.x

Szakály, S. (Ed.). (2001). *Tejgazdaságtan*. Dinasztia Kiadó.

Tong, S. Y., Davis, J. S., Eichenberger, E., Holland, T. E., & Fowler, V. G., Jr. (2015). *Staphylococcus aureus* infections: Epidemiology, pathophysiology, clinical manifestations, and management. *Clinical Microbiology Reviews, 28*(3), 603-661. https://doi.org/10.1128/CMR.00134-14

Varga, L. (2016). *Nyers tejek és funkcionális savanyú tejtermékek bakteriológiája, higiéniája* [Doctoral dissertation, Széchenyi István Egyetem]. Mosonmagyaróvár.

Willis, C., Jørgensen, F., Aird, H., Elviss, N., Fox, A., Jenkins, C., Fenelon, D., Sadler-Reeves, L., & McLauchlin, J. (2018). An assessment of the microbiological quality and safety of raw drinking milk on retail sale in England. *Journal of Applied Microbiology, 124*(2), 535-546. https://doi.org/10.1111/jam.13660

 DOI: 10.17108/ActAgrOvar.2025.66.2.17