

THE EFFECT OF ENVIRONMENTAL FACTORS ON THE MICROBIOLOGICAL QUALITY OF BULK TANK MILK

F. PELES – P. KERESZTÚRI – A. IGLÓI – A. SZABÓ

University of Debrecen Centre of Agricultural Sciences, Hungary
Department of Agricultural Microbiology

Introduction

Milk is widely recognized as a source of human pathogens. Several outbreaks of food borne illness involving contamination by microorganisms of both raw and pasteurized milk and dairy products have been reported (MacDonald et al. 1985; Bryant et al. 1988).

Bacterial contamination can originate from multiple sources, such as mastitic cows, dirty udders, and poorly cleaned milking equipment, which further complicate the issue (Hogan et al., 1989; Thomas et al., 1966).

Coliform bacteria and the *Escherichia coli* are good indicators of contamination; they are suitable for characterizing the hygienic condition of milk production (Deák, 1986). The *E. coli* are basically fecal bacteria and their presence in milk suggests that manure or manure contaminated material have somehow been allowed entry into the milk handling system. Seldom do *E. coli* infected cows cause the milk *E. coli* count to rise (Ingalls, 1998). Most *E. coli* are commensal intestinal organisms that do not cause disease, but a small percentage of *E. coli* is enteropathogenic. Infection with enteropathogenic *E. coli* usually results in mild illness; however, some serotypes are enterohemorrhagic *E. coli* and can lead to hemolytic-uremic syndrome (O'Brien and Kaper, 1998).

Staphylococcus aureus is shed in low numbers by infected quarters and generally does not cause high bacteria counts in bulk tank (Jones and Sumner, 1999). *Staphylococcus aureus* produce a toxin as a by-product of growth and multiplication in food and cause food intoxication (Kendall, 2004).

The aim of our research was to examine the connection between the microbiological quality of bulk tank milk and housing- and milking technologies of the dairy farms of different size.

Methods

The microbiological quality of the bulk tank milk of eighteen dairy farms in Hajdú-Bihar county (Hungary) were examined, from July 2005 to October 2005.

The bulk tank milk (BTM) samples from each farm were examined for standard plate count (SPC), coliforms count (CC), *Escherichia coli* count (ECC), *Staphylococcus aureus* count (SAC).

Plate count agar (PCA) was used for the enumeration of standard plate count (MSZ ISO 6610).

For the enumeration of coliforms count we used Violet Red Bile Lactose Agar (VRBLA) with subsequent biochemical identification of typical colonies using Brilliant Green Lactose Bile Broth (MSZ ISO 5541-1).

The *Escherichia coli* were counted by the standard Most Probable Number (MPN) method (ISO 11866-1:1997).

Staphylococcus aureus counts were estimated using Baird Parker's agar supplemented with egg's yolk tellurite emulsion (MSZ EN ISO 6888-1).

Six groups were formed by the farm size, housing- and milking methods (Table 1).

Table 1. The Grouping of the dairy farms

Groups	Farm size	Housing method	Milking method	Number of farms
1.	Large farm	Deep litter	Milking parlour	3
2.	Large farm	Loose cubicle	Milking parlour	4
3.	Middle farm	Deep litter	Milking parlour	1
4.	Middle farm	Tied stall	Bucket milking	1
5.	Middle farm	Tied stall	Milkpipe	1
6.	Small farm	Tied stall	Bucket milking	8

The categories of the microbiological quality of the bulk tank milk is shown in Table 2. The SPC, CC, ECC and SAC were categorized into 3 groups (low, medium and high).

Table 2. Categories of the microbiological quality of bulk tank milk

Groups	Standard plate count (CFU ml ⁻¹)	Coliform count (CFU ml ⁻¹)	<i>Escherichia coli</i> count (CFU ml ⁻¹)	<i>Staphylococcus aureus</i> count (CFU ml ⁻¹)
Low	$< 1.0 \times 10^4$	$< 1.0 \times 10^2$	$< 1.0 \times 10^1$	$< 5.0 \times 10^2$
Medium	1.0×10^4 - 1.0×10^5	1.0×10^2 - 1.0×10^3	1.0×10^1 - 1.0×10^2	5.0×10^2 - 2.0×10^3
High	$\geq 1.0 \times 10^5$	$\geq 1.0 \times 10^3$	$\geq 1.0 \times 10^2$	$\geq 2.0 \times 10^3$

All statistical analyses were performed using GraphPad Prism 3.02 (Motulsky, 1999).

Results and discussion

The results of the microbiological examinations of the bulk tank milk samples are shown in Table 3.

The **standard plate count** ranged from 1.2×10^3 – 1×10^6 CFU ml⁻¹. The mean SPCs were medium at the groups 1 – 5 and high at the group 6.

The **coliforms count** ranged from 0 – 2.1×10^5 CFU ml⁻¹. The mean CCs were low at the groups 3, 5; medium at group 1 and high at groups 2, 4, 6.

The ***Escherichia coli* count** ranged from 0 – 1.1×10^3 CFU ml⁻¹. The mean ECC values were low at groups 3, 4, 5; medium at groups 1, 2 and high at group 6.

The ***Staphylococcus aureus* count** ranged from 0 – 5.1×10^3 CFU ml⁻¹. The mean SACs were low at groups 2, 3, 4, 5 and medium at groups 1, 6.

After forming groups by the farm size, housing- and milking methods, we found that the mean SPC, CC, ECC and SAC values were medium at the large farms using deep litter housing stable and milking parlour (**group 1**).

The mean SPC, ECC values were medium, the mean CCs were high and the mean SACs were low at the large farms using loose cubicle housing stable and milking parlour (**group 2**).

The mean SPCs were medium or low (group 5), the mean CCs were low or high (group 4), the mean ECC and SAC values were low at the middle farms using various housing- and milking methods (**groups 3, 4, 5**).

The mean SPC, CC and ECC values were high, and the mean SACs were medium at the little farms using tied stall barns and bucket milking installation (**group 6**).

The group 6 significantly differed from the other groups ($P < 0.05$).

On the basis of standard plate, coliforms and *Escherichia coli* counts the hygienic conditions were appropriate at the large and middle farms, and inadequate at the little farms using tied

stall barns and bucket milking installation. The *Staphylococcus aureus* counts were low at the large and middle farms, and medium at the little farms.

Table 3. Results of the microbiological examinations of bulk tank milk

Groups	Standard plate count (CFU ml ⁻¹)	Coliforms count (CFU ml ⁻¹)	<i>Escherichia coli</i> count (CFU ml ⁻¹)	<i>Staphylococcus aureus</i> count (CFU ml ⁻¹)
1.	4.4×10^4	8.9×10^2	9.9×10^1	5.7×10^2
2.	7.6×10^4	5.4×10^3	7.5×10^1	2.2×10^1
3.	1.9×10^4	5.2×10^1	0.4×10^1	2.2×10^2
4.	5.4×10^4	1.9×10^3	0.6×10^1	1.5×10^2
5.	4.5×10^3	1.3×10^1	0.4×10^1	0
6.	5.2×10^5	5.2×10^4	2.8×10^2	1.2×10^3
Min	1.2×10^3	0	0	0
Max	1×10^6	2.1×10^5	1.1×10^3	5.1×10^3

Conclusion

Our results show that there is connection between the microbiological quality of bulk tank milk and housing- and milking technologies of the dairy farms of different size. Low bacterial counts were found at the middle farms, and high bacterial counts at the little farms. The majority of the bulk tank milk samples derived from the large and middle farms met the microbiological quality regulation. On the contrary, most of the bulk tank milk samples derived from the little farms did not meet the microbiological quality requirements.

On the basis of standard plate, coliforms and *Escherichia coli* counts the hygienic conditions were appropriate at the large and middle farms, and inadequate at the little farms using tied stall barns and bucket milking installation. The *Staphylococcus aureus* counts were adequate at all farms examined.

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