

Cow-Level Bacterial Shedding Is a Dynamic and Herd-Specific Driver of High Bulk Tank Bacterial Counts

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Udder Health

Introduction

Traditionally, elevated bacterial counts in bulk tank milk (BTM) have been associated with issues related to milking equipment hygiene and insufficient milk cooling. Also, management factors such as pre milking sanitation and increased focus on stall management are associated with the BTM bacterial count (Piepers et al., 2014). While these factors remain important, evidence increasingly points towards bacterial shedding from the cows, particularly from cows infected with Streptococcus agalactiae (Group B Streptococci)—as a significant source of cross contamination in many herds (Katholm et al., 2012). Scientific research and field experience have shown that in herds with persistently high Individual Bacteria Counts (IBC), the primary source is often a subset of cows shedding high levels of bacteria, rather than systemic hygiene failures (Hayes et al., 2001; Zadoks et al., 2004).

Despite this, very little research has investigated what bacterial species pose the IBC problem and if they are mastitis pathogens at all. Furthermore, there is no knowledge about the dynamics of IBC, which may be fundamental in decision making.

To address this gap, we focused on herds with elevated BTM bacterial counts identified as infected with S. agalactiae where equipment hygiene and cooling was ruled out as the cause of that. In such cases, individual cows were suspected to be the source of BTM bacterial counts, and the project investigated their role in contaminating the milk.

Understanding the origin of bacterial contamination is essential to ensure milk quality and safety. However, identifying cow-level bacterial shedding is challenging due to variability between herds and variability over time within the same herd. To gain deeper insight into this variation, a pilot project was initiated. These results may contribute to the development of more targeted and effective strategies for reducing bacterial counts in situations where individual cows are the main source of contamination.

Material & methods

By convenience, a single herd was selected based on a history of fluctuating BTM bacterial counts and persistently variable IBC over a prolonged period. Typically, the IBC fluctuated around 60,000 IBC/mL, with occasionally higher values observed. The geometric mean of the BTM Somatic Cell Count (SCC) was 314,000 cells/mL. The study unit was the individual lactating cow. The herd consisted of 340 Holstein dairy cows, milked two or three times daily, depending on milk yield and stage of lactation. Prior to sampling, a milk quality advisor assessed the hygiene of the milking system and bulk tank, the dosing of cleaning chemicals, and the cooling system. During the study, all lactating cows had composite milk samples collected. The IBC was measured from these samples, and the procedure was repeated 13 days later. The cows were grouped into four categories according to the measured IBC: < 100.000 IBC/mL, 100.000 – 1. mio. IBC/mL, 1. mio. – 10 mio. IBC/mL, and last > 10 mio. IBC/mL. During sampling, cows were scored for udder hygiene.

All milk samples were cooled and transported to Eurofins® Milk Testing the following day for laboratory analysis.

Following the second sampling, aseptic quarter milk samples were collected from (N=25) cows with the highest IBC values. Microbiological examination was carried out following NMC standards and species identification with MALDI-TOF.

Results & Discussion

The analysis revealed substantial variation in bacterial shedding between individual cows (N=340), with IBC ranging from 3,000 IBC/mL to above 22 million IBC/mL. Most cows (N=312) had relatively low IBC (< 100,000 IBC/mL), but a notable number of cows (N=28) had values above 10 million IBC/m/L.

The repeated sampling showed that bacterial shedding was not consistent over time. Of the (N=28) cows above 10 million IBC/mL in the first sampling, only (N=6) cows remained above 10 million IBC/mL in the second sampling. Seven cows from the same high group dropped below 100,000 IBC/mL. Overall, (N=144) cows, remained in the same IBC/mL category across both test days. This indicates that while some cows are likely persistent high shedders, many cows fluctuate significantly over short periods or are occasionally not cleaned according to the farm protocols.

These findings suggest that elevated bacterial counts in BMT are not always driven by a fixed group of individual high-shedding cows. The variation observed within just 13 days implies that decisions—such as culling— based on a single high IBC may not effectively resolve the issue. Instead, repeated sampling and a more nuanced management approach are needed when addressing elevated IBC.

There was no clear correlation between SCC and IBC if the cow level SCC was below 400,000 cells/mL. Above this threshold, higher SCC often correlated with high IBC (>100.000 IBC/mL). Nearly all cows with high IBC also had high SCC, suggesting that cow level SCC could be used as an indicator of IBC and thereby a useful screening tool.

Another possible contributor to high IBC is udder contamination. However, no relationship was found between hygiene score and IBC, suggesting udder cleanliness was not a good indicator in this case.

Of the (N=25) cows selected for microbiological analysis on quarter level, three cows had all quarters culture negative. Among the culture positives, S. uberis was the most common isolate identified, followed by non-aureus staphylococci and mammaliicoccus (NASM), Corynebacterium spp., Enterococcus cecorum, and S. agalactiae.

These results align with previous findings confirming that Streptococcus spp. and similar pathogens can be associated with shedding in very high numbers. The study highlights the complexity of managing elevated IBC and underscores the need for herd-specific strategies based on repeated testing and pathogen identification.

Conclusion

- High bacterial counts in bulk tank milk can be caused by individual cows, but shedding patterns vary greatly over time. A single test is insufficient to identify persistent high shedders, as shedding appears to fluctuate.
- Cow level SCC may indicate high individual bacterial shedding but is only shown in a single herd.
- Udder hygiene scores did not correlate with individual bacterial shedding in this study.
- Pathogen analysis confirmed Streptococcus uberis and NASM as key contributors.

References

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