



UNIVERSITY OF LIFE SCIENCES
"KING MIHAI I" FROM Timisoara
**Multidisciplinary Conference on
Sustainable Development**
30-31 May 2024



Prevalence and Identification of Milk Pathogens in Clinical Mastitis: An On-Farm Culturing Approach

Andra-Sabina Neculai-Valeanu¹, Adina-Mirela Ariton¹, Ioana Porosnicu^{1,2}, Catalina Sanduleanu^{1,3}, Gabriela Amaritii³, Ciprian Radu¹

¹Research and Development Station for Cattle Breeding Dancu, 707252, Iasi, Iasi-Ungheni no. 9, Romania

²University of Life Sciences, Faculty of Veterinary Medicine, Iasi, 700489, Iasi, Aleea Mihail Sadoveanu 8, Romania

³University of Life Sciences, Faculty of Food and Animal Science, 700489, Iasi, Aleea Mihail Sadoveanu 8, Romania

Abstract

Mastitis, inflammation of the mammary gland, is a major economic burden in the dairy industry. It reduces milk production, quality, and cow fertility. Identifying the causative bacteria is crucial for effective treatment and control strategies. This study aimed to investigate the prevalence of bacteria associated with mastitis in dairy cows using an on-farm culturing system. A total number of 21 milk samples were collected from cows with clinical mastitis signs (visible abnormalities in milk) from farms across N-E Romania. A commercially available on-farm culturing system was used for rapid identification of common mastitis pathogens. The on-farm culturing system utilizes specific media and colony morphology to presumptively identify bacteria, including *Staphylococcus* spp., *Streptococcus* spp., *Escherichia coli*, yeast, algae, and other Gram-negative bacteria. The prevalence of each bacterial type isolated from the milk samples was calculated. The on-farm culturing system identified a variety of bacteria associated with mastitis. The most prevalent bacteria isolated were *Streptococcus dysgalactia* (33.33%) and *Streptococcus uberis* (26%). Additional bacterial isolated included *Staphylococcus aureus*, *Staphylococcus chromogens* and *Escherichia coli*. The findings of this study provide valuable insights into the bacterial profile associated with mastitis in dairy cows of N-E Romania. The on-farm culturing system proved to be a practical tool for rapid pathogen identification at the farm level.

Keywords: Mastitis; pathogens, on-farm culturing; milk quality

Introduction

Mastitis is the inflammation of the mammary gland and is the most common disease affecting dairy cows [1]. It results in significant economic losses due to reduced milk production, discarded milk, treatment costs, and cow replacement [2]. Mastitis can also negatively affect milk quality [3]. Identifying the causative bacteria involved in mastitis is essential for implementing effective treatment and control strategies. Traditionally, milk samples are sent to a diagnostic laboratory for bacterial culture. However, this method can be time-consuming, as it may take several days to receive results [4]. On-farm culturing systems offer a rapid alternative for identifying mastitis pathogens at the farm level. These systems utilize specific media and colony morphology to presumptively identify common mastitis pathogens.

Material and method

Sample collection

- ✓ A total of 21 milk samples were collected from cows with clinical mastitis signs (visible abnormalities in milk) from farms across N-E Romania.
- ✓ The samples were collected aseptically from individual quarters following standard procedures for teat disinfection.

On-farm culturing

- ✓ A commercially available on-farm culturing system (Clear Milk, Czech Republic) was used for bacterial identification. The system utilizes a variety of selective and differential media to target specific mastitis pathogens. These media allow for the growth and differentiation of bacteria based on colony morphology (size, color, shape, etc.).
- ✓ Following the manufacturer's instructions, milk samples were inoculated onto the appropriate media plates and incubated at the recommended temperature for a specified incubation time. After incubation, the plates were examined for bacterial growth.
- ✓ The presumptive identification of bacteria was based on colony morphology according to the manufacturer's guidelines.
- ✓ The on-farm culturing system allowed for the identification of the following bacteria: *Staphylococcus* spp., *Streptococcus* spp., *Escherichia coli*, Yeast, Algae, Other Gram-negative bacteria.

Prevalence determination

- ✓ The prevalence of each bacterial type isolated from the milk samples was calculated as the percentage of positive samples out of the total number of samples collected (n = 21).

Results and discussions

- The on-farm culturing system identified a variety of bacteria associated with mastitis.
- This study found that *Streptococcus dysgalactia* (33.33%) and *Streptococcus uberis* (26%) were the most prevalent bacteria isolated. Additional bacterial isolated included *Staphylococcus aureus*, *Staphylococcus chromogens* and *Escherichia coli* (Figure 1).

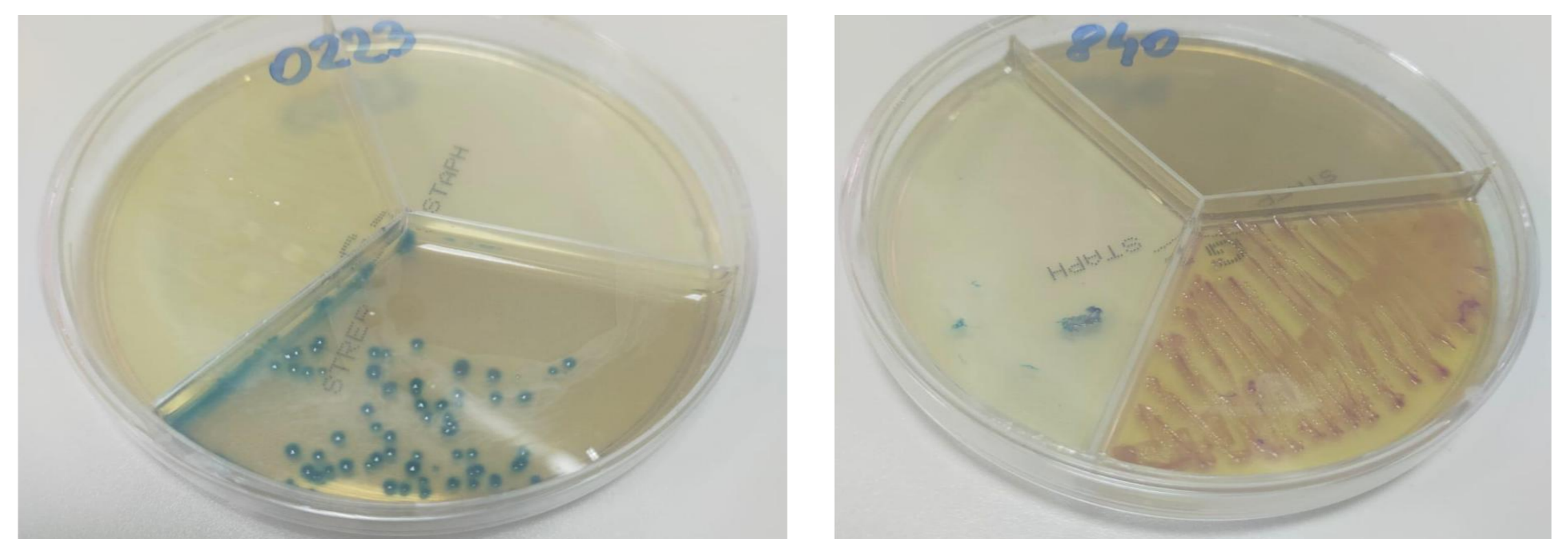


Figure 1. Pathogens identified in samples of mastitis milk using the Clear Milk Pathogen Atlas

- a) *Streptococcus dysgalactiae* Strep sector (streptococci), small turquoise colonies
- b) *E. coli = Escherichia coli* G- sector (gram-negative rods), pink, large bacterial colonies

Conclusions

- ✓ The use of an on-farm culturing system proved effective for the rapid identification of mastitis pathogens in dairy cows. This approach allows for timely and informed decision-making regarding treatment and management practices.
- ✓ The findings of this study highlight the prevalent bacterial pathogens in clinical mastitis cases in N-E Romania, providing valuable insights for dairy farmers and veterinarians in the region.
- ✓ The adoption of on-farm culturing systems can significantly enhance mastitis management by enabling prompt and accurate pathogen identification.

Selective References

1. Hameed, K.G.A., et al. (2018). "Economic Impact of Mastitis in Dairy Cows: A Review." *Veterinary World*, 11(4), 563-570.
2. Ruegg, P.L. (2020). "A 100-Year Review: Mastitis Detection, Management, and Prevention." *Journal of Dairy Science*, 103(9), 10481-10492.