

Association Rule Mining of Bacterial Species and Antimicrobial Susceptibility in Milk from Cows with Mastitis: A Case Study of Livestock Region 7, Thailand, 2023–2025

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Abstract

Background: Bovine mastitis is a major problem in the dairy industry and is one of the primary causes of antimicrobial use in dairy production systems, which may contribute to the development of antimicrobial resistance. However, conventional data analysis methods have limitations in detecting complex relationships, particularly co-occurring resistance patterns among multiple antimicrobial agents in bacterial isolates.

Objectives: This study aimed to apply association rule mining techniques to analyze the relationships between bacterial species and antimicrobial susceptibility, as well as to identify co-resistance patterns among antimicrobial agents from raw milk samples of mastitic dairy cows within the jurisdiction of Regional Livestock Office 7, Department of Livestock Development, Thailand.

Methods: A retrospective analytical study was conducted using data on bacterial isolation and antimicrobial susceptibility testing from raw milk samples of mastitic cows submitted to the Veterinary Research and Development Center (Western Region), Ratchaburi Province, Thailand, between 2023 and 2025. A total of 945 milk samples were analyzed, yielding 26 bacterial species and 22 antimicrobial agents for testing. Antimicrobial susceptibility testing was performed using the disk diffusion method and categorized as susceptible, intermediate, or resistant according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. The dataset was structured into a long format for analyzing the relationships between bacterial species and antimicrobial responses (16,330 records) and into a wide format for identifying co-resistance patterns (1,246 records). Association rule mining was performed using the Apriori algorithm in WEKA version 3.8.6, and the generated rules were selected based on predefined minimum thresholds of support, confidence, and lift.

Results: A total of 9 strong association rules were identified between bacterial species and antimicrobial susceptibility test results (support 0.01–0.02, confidence 0.86–1.00, lift 1.53–2.90). *Escherichia coli* showed a strong association with resistance to penicillin G, whereas *Streptococcus uberis* was associated with susceptibility to β -lactam antibiotics. Resistance to sulfamethoxazole/ trimethoprim was also observed in some rules. In addition, ten co-resistance patterns were identified (support 0.11–0.32, confidence 0.90–1.00, lift 1.72–3.08), indicating frequent co-occurrence of resistance to multiple antimicrobial agents, particularly within the β -lactam group. Notably, clear co-resistance patterns were observed within the tetracycline group.

Conclusion: Association rule mining enabled the identification of complex, multi-dimensional relationships among bacterial species, antimicrobial susceptibility, and co-resistance patterns that are difficult to capture using conventional analytical methods. This approach provides added value for antimicrobial resistance surveillance and offers a promising tool for supporting evidence-based and rational antimicrobial use in dairy production systems.

Keywords: association rule mining, antimicrobial resistance, bovine mastitis, raw milk, Apriori algorithm

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