



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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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.

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

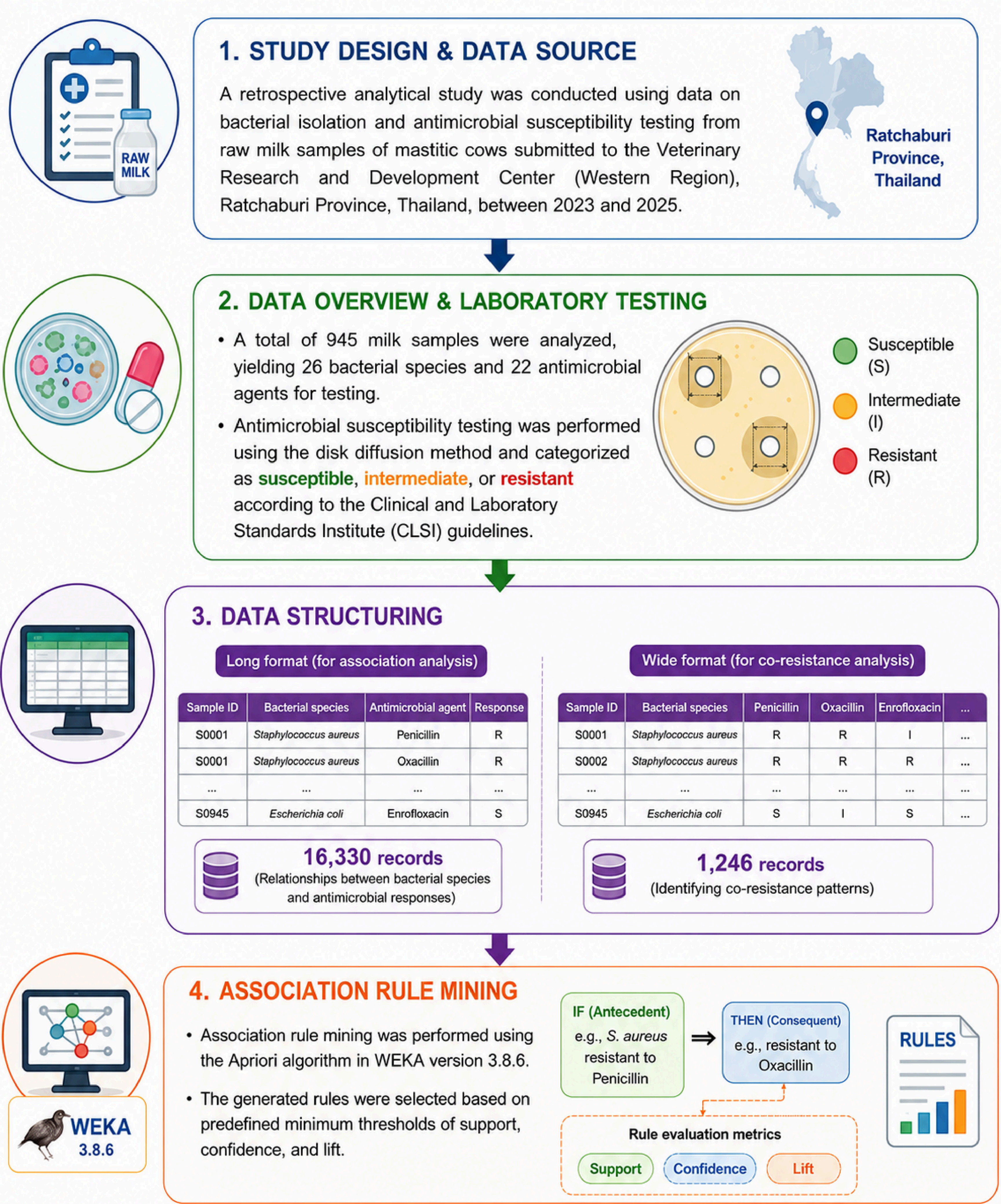


Figure 1. Workflow of the study, illustrating the study design, laboratory testing, data structuring, and association rule mining for antimicrobial resistance pattern analysis

Results and Discussion

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. (Table 1)

Table 1. Association rules between bacterial species and antimicrobial susceptibility identified using the Apriori algorithm

No.	Antecedent	Consequent	Support	Confidence	Lift
1	<i>Escherichia coli</i> + Penicillin G	Resistant	0.01	1	2.9
2	<i>Streptococcus uberis</i> + Amoxicillin-Clavulanic acid	Susceptible	0.01	0.98	1.73
3	coagulase-negative staphylococci (CNS) + Amoxicillin-Clavulanic acid	Susceptible	0.01	0.97	1.71
4	<i>Streptococcus uberis</i> + Cephalothin	Susceptible	0.01	0.96	1.7
5	<i>Streptococcus uberis</i> + Amoxicillin	Susceptible	0.02	0.89	1.58
6	<i>Streptococcus uberis</i> + Sulfamethoxazole/Trimethoprim	Resistant	0.02	0.88	2.56
7	<i>Streptococcus uberis</i> + Ceftiofur	Susceptible	0.01	0.88	1.56
8	<i>Streptococcus uberis</i> + Penicillin G	Susceptible	0.02	0.88	1.55
9	<i>Streptococcus uberis</i> + Ampicillin	Susceptible	0.02	0.86	1.53

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. (Figure 2)

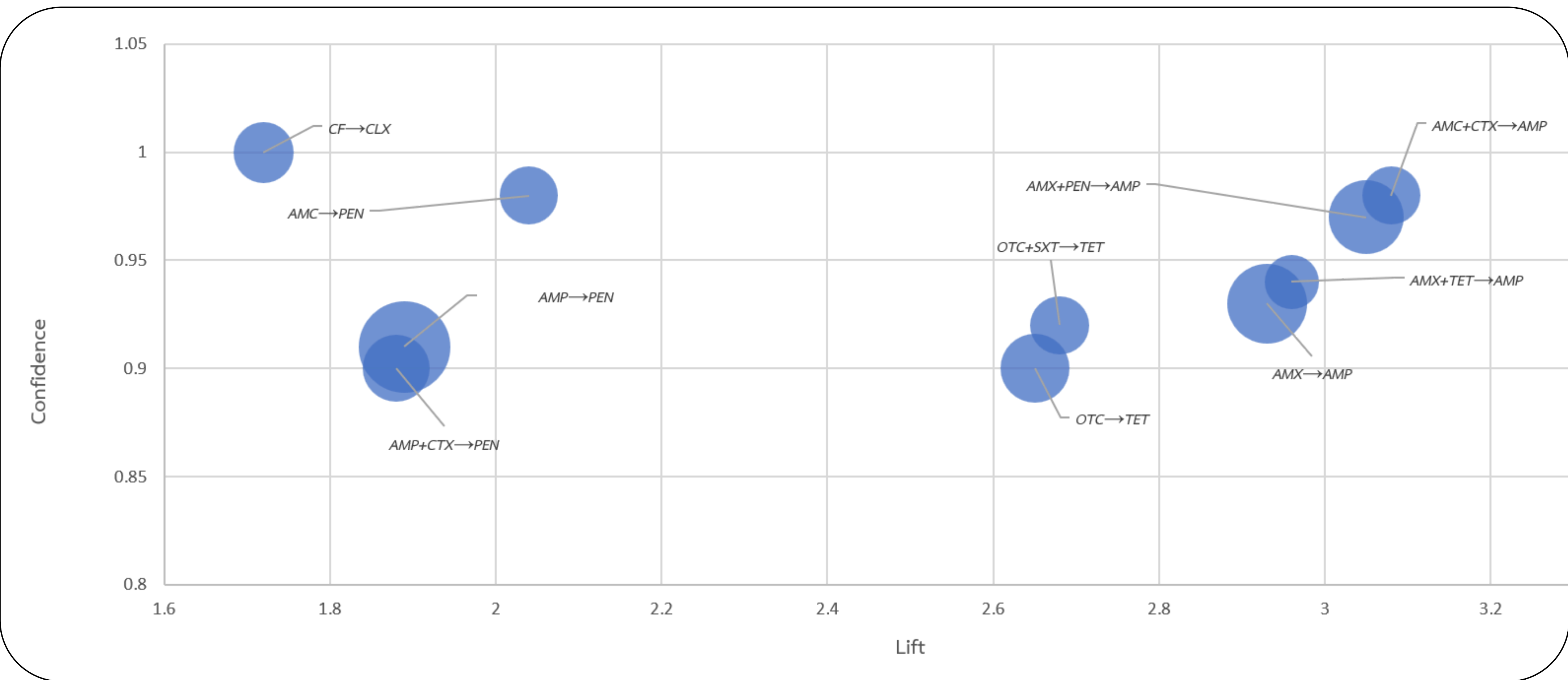


Figure 2. Bubble plot showing confidence and lift values of association rules of co-occurring antimicrobial resistance patterns derived from the Apriori algorithm

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References

- Agrawal, R., & Srikant, R. (1994). Fast algorithms for mining association rules. In J. B. Bocca, M. Jarke, & C. Zaniolo (Eds.), Proceedings of the 20th International Conference on Very Large Data Bases (VLDB '94) (pp. 487–499). Morgan Kaufmann. <https://www.vldb.org/conf/1994/P487.PD>
- Camsing, A., Phetburorn, N., Chopjitt, P., Pumhirunroj, B., Patikae, P., Watwiengkam, N., & Kerdsin, A. (2024). Occurrence of antimicrobial-resistant bovine mastitis bacteria in Sakon Nakhon, Thailand. Veterinary World, 17(6), 1202–1209.
- Han, J., Kamber, M., & Pei, J. (2012). Data mining: Concepts and techniques (3rd ed.). Morgan Kaufmann.

Conclusions

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.

