



Risk factors of clinical mastitis and antimicrobial susceptibility test results of mastitis milk from dairy cattle in western Thailand: Bayesian network analysis

Wantida Horpiencharoen, Sukanya Thongratsakul, Chaithep Poolkhet*

Section of Epidemiology, Department of Veterinary Public Health, Faculty of Veterinary Medicine, Kasetsart University, Kamphaeng Saen, Nakhon Pathom, 73140, Thailand

ARTICLE INFO

Keywords:

Bayesian network
Clinical mastitis
Dairy cattle
Risk factors

ABSTRACT

Using Bayesian network analysis, this cross-sectional study aimed to identify the conditional probability among dairy farm practices, cow characteristics, bacteriological culture results, and antimicrobial susceptibility test results of milk from dairy cows with clinical mastitis in western Thailand. Data associated with risk factors and clinical signs were collected using a structured questionnaire that was administered to 34 small dairy holders. In total, 100 quarters of milk samples from 100 cows were used for Bayesian network analysis. Conditional probability results showed that the following variables had the highest probabilities relevant to the occurrence of clinical mastitis pathogens: parity, concrete and rubber floor, hand stripping after using machine milking, dry cow therapy, and routine cleaning of milking machines. These variables were associated with the first four highest posterior probabilities of the occurrence of *Streptococcus* spp. (16.68%; reachable range or the minimum and maximum posterior probability values for the occurrence of *Streptococcus* spp., 15.45%–17.91%), *Staphylococcus* spp. (11.87%; reachable range, 11.06%–12.67%), *Escherichia coli* (7.53%; reachable range, 6.95%–8.17%), and *Streptococcus dysgalactiae* (7.28%; reachable range, 6.73%–7.83%), which were the most frequently isolated pathogens. Conditional probability results indicated these pathogens were most sensitive to amoxicillin/clavulanic acid (80.58%) and cloxacillin (64.28%). Most pathogens were resistant to penicillin G (40.37%). In this study, Bayesian network analysis revealed several clinically significant risk factors of mastitis associated with various pathogens and farming characteristics. Simple statistics could not provide sufficient information for the successful control of mastitis. In contrast, through in-depth data analysis, Bayesian networks could identify risk factors in various situations, hence providing information that will be crucial to help farmers reduce the cost of farming.

1. Introduction

Clinical mastitis is a common problem in dairy farming that affects milk quality and causes economic losses. Important risk factors include inappropriate farm management such as cleaning the mammary glands using a single towel (Folosa et al., 2015); the implementation of dry cow therapy, which results in infection (Leelahapongsathon et al., 2016); cows with a high lactation number (Oliveira et al., 2015); and cows undergoing physiological change and stress (Burvenich et al., 2007; Morin, 2009). In Thailand, the conditions under which diseases occur are similar to those in other countries. Therefore, we utilized this knowledge to create or improve control measures to reduce the risk of mammary gland infection. A study of risk factors using ordinary

statistical techniques such as logistic regression or generalized linear modeling was also applied to the cattle population in Thailand. However, Bayesian networks can help to identify the probability of occurrence of causal pathogens and associated risk factors. This method can help farmers in making farm management decisions, rather than only identifying the type of pathogens (Steenefeld et al., 2009). In particular, Bayesian networks can aid in revealing hidden factors that cannot be detected by ordinary statistical techniques. This technique uses the concept of conditional probability to find the relationships between risk event and disease (Kjærulff and Madsen, 2005; Ward and Lewis, 2013). Bayesian networks are used in human medicine to calculate the probability of injury to help determine treatment decisions (Cypko et al., 2017; Luo et al., 2017). In veterinary sciences, Steeneveld et al. (2009)

* Corresponding author at: Section of Epidemiology, Department of Veterinary Public Health, Faculty of Veterinary Medicine, Kasetsart University, Kamphaengsaen Campus, Nakhon Pathom, 73140, Thailand.

E-mail address: wantida@pkku.ac.th (C. Poolkhet).

<https://doi.org/10.1016/j.prevetmed.2019.01.014>

Received 12 February 2018; Received in revised form 23 January 2019; Accepted 31 January 2019

0167-5877/© 2019 Elsevier B.V. All rights reserved.