Estimation of *Brucella* and *Mycobacterium bovis* contamination in bovine milk in Africa

Nozyechi Ngulube Chidumayo

Department of Clinical Studies, University of Zambia, School of Veterinary Medicine, P. O. Box 32379, Lusaka, Zambia. **Corresponding author:** Nozyechi Ngulube Chidumayo, e-mail: nozyechic@yahoo.com **Received:** 06-10-2020, **Accepted:** 19-01-2021, **Published online:** 26-02-2021

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Abstract

Background and Aim: Bovine brucellosis and tuberculosis are zoonotic bacterial diseases transmitted through the consumption of raw milk and dairy products. Many developed countries have eliminated bovine brucellosis and tuberculosis in their cattle herds, however, the diseases are still endemic in Africa. Despite the public health risk of these pathogens, the sale and consumption of unpasteurized milk are still common in some African countries. This study aimed to estimate the prevalence of *Brucella* and *Mycobacterium bovis* in bovine milk.

Materials and Methods: A conceptual model for milk contamination was constructed and 1 million simulations were performed using data from published articles.

Results: *Brucella* milk contamination was estimated at a median of 8.68% (interquartile range [IQR]: 5.95-11.97%; range: 2.41-25.16%). The median prevalence of *M. bovis* was estimated at 6.86% (IQR: 4.25-9.40%; range: 0.01-15.16%).

Conclusion: These results indicate that there is a risk of *Brucella* and *M. bovis* transmission through the consumption of unpasteurized milk. The findings of this study highlight the need to improve the safety and quality of informally marketed milk in the region.

Keywords: Africa, Brucella, cattle, milk, Mycobacterium bovis, zoonoses.

Introduction

Bovine milk is an important source of dietary protein; however, unpasteurized milk may contain zoonotic pathogens such as *Brucella* and *Mycobacterium* [1]. Despite the risk of zoonotic disease transmission, the consumption of raw milk and unpasteurized milk products is still common in some African countries [2-8]. Milk in Africa is marketed through formal and informal milk value chains [5]. The final product in the formal value chain is packed pasteurized milk [5]; however, the safety of milk in the informal value chain is not regulated and consumers are often sold unpasteurized milk [5,7,9]. The consumption of raw milk, therefore, poses a health risk in bovine brucellosis and tuberculosis endemic areas.

Brucellosis is a disease caused by intracellular bacteria belonging to the genus *Brucella* [10]. The disease has public health and economic importance due to its zoonotic nature [11] and negative impact on livestock production [12]. The genus *Brucella* consists of several species capable of infecting preferred terrestrial and aquatic mammalian hosts [10]. *Brucella abortus* is associated with brucellosis in cattle [13,14]; however, outbreaks of bovine brucellosis

due to *Brucella melitensis* have been reported [15,16]. Serological tests such as the Rose Bengal plate test (RBPT) and complement fixation test are commonly used for screening and monitoring brucellosis in cattle [17], although, not all seropositive animals have active infections [18]. The bacteria have also been isolated from the milk of seronegative cows [17-19].

Bovine tuberculosis is a zoonotic bacterial disease caused by *Mycobacterium bovis*, a member of *Mycobacterium tuberculosis* complex [4]. Bovine tuberculosis is of economic importance due to post-slaughter carcasses condemnation [20,21]. The bacteria are transmitted to humans through the consumption of raw milk, but not all infected cows shed the bacteria in milk [22-24]. The single intradermal comparative cervical tuberculin (SICCT) test is commonly used to identify cattle infected with *M. bovis;* however, not all infected cattle are detected using this test [25,26].

This study aimed to estimate the prevalence of *Brucella* and *M. bovis* in milk in Africa. This was the secondary study and all the data used for the analysis were based on published articles. The findings of this study highlight the public health significance of raw milk consumption and the need to improve the safety and quality of milk in Africa.

Materials and Methods

Ethical approval

Ethical approval was not required for this study.

Conceptual model

The prevalence of bacterial milk contamination was calculated based on six parameters: The prevalence

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of test positive females (P1); the proportion of lactating cows among the test positive females (P2); the probability of a test positive lactating cow shedding the bacteria in the milk (P3); the prevalence of test negative females (P4=1–P1); the proportion of lactating cows among the test negative females (P5); and the probability of a test negative lactating cow shedding the bacteria in the milk (P6). The probability of contaminated milk from a seropositive and seronegative female is P7 (P7=P1×P2×P3) and P8 (P8=P4×P5×P6), respectively. The prevalence of contaminated milk is the sum of P7 and P8; divided by the probability of lactating females ([P1×P2]+[P4×P5]).

The parameter values for the estimation of *Brucella* milk contamination are shown in Table-1[3,18,27-38]. The secretion probability was based on bacteria culture results of milk collected from RBPT seropositive and seronegative cattle [18]. The female prevalence was based on RBPT results from five African countries; Egypt [27], Ethiopia [28,29], Nigeria [30,31], Tanzania [32], and Sudan [33,34]. One million probability values for P1, P2, and P5 were randomly generated based on uniform distributions of the values in Table-1. Ersatz version 1.35 (EpiGear International, www.epigear.com) was used to randomly generate the parameter values. All the calculations were performed in Microsoft Excel. The results were reported as median, interquartile range (IQR), and range.

The parameter values for the estimation of *M. bovis* milk contamination are shown in Table-2. The secretion probability was based on bacteria culture results of milk from SICCT test negative and positive cows. The female prevalence was based on SICCT test results from five African countries; Nigeria [39], Mozambique [40], Uganda [41], Tanzania [42], and Ethiopia [43,44]. One million values for each parameter were randomly generated based on uniform distributions of the values in Table-2 [22-24,39-46].

Results

Brucella milk contamination was estimated at a median of 8.68% (IQR: 5.95-11.97%; range:

Table-1: Model parameter values for the estimation of *Brucella* milk contamination.

Parameter	Values	References
P1	0.042-0.307	[27-34]
P2	0.196-0.545	[3,35-38]
Р3	0.458	[18]
Р5	0.212-0.588	[3,35-38]
P6	0.018	[18]

Table-2: Model parameter values for the estimation of *Mycobacterium bovis* milk contamination.

Parameter	Values	References
P1	0.004-0.335	[39-44]
P2	0.333-0.620	[42,43,45]
Р3	0-0.188	[22-24]
P5	0.362-0.542	[42,43,45]
P6	0-0.125	[22,46]

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2.41-25.16%). Milk contamination of <5% prevalence occurred in 7.12% of the simulations. Only 2.13% of the simulations had $\ge 20\%$ prevalence.

The median prevalence of *M. bovis* was estimated at 6.86% (IQR: 4.25-9.40%; range: 0.01-15.16%). Only 4.24% of the simulations had \geq 12% prevalence.

Discussion

One million simulations were performed to estimate the prevalence of *Brucella* and *M. bovis* in individual cow milk samples. The results indicate that *Brucella* milk contamination in Africa is unlikely to exceed 20%. The estimated *Brucella* prevalence corresponds with the 4.7% and 5.3% prevalence reported in Bangladesh [18] and Uganda [47], respectively. Other studies in Africa have reported higher prevalences of 38.1% in Nigeria [48] and 29% in Uganda [49]; however, the milk contamination in these studies was based on the detection of *Brucella* antibodies and not the isolation of the bacteria, which may overestimate the prevalence [50].

M. bovis milk contamination was estimated at 0.01-15.16% but the results indicate that the prevalence is unlikely to exceed 12%. Several authors have reported the prevalence of M. bovis in milk in Africa; however, their results were based on the isolation of the bacteria from tuberculin reactors [51-53]. The reported bacterial contamination may have been underestimated since positive milk from false-negative cows was excluded. There are limited studies investigating the prevalence of *M. bovis* in the milk of tuberculin negative cows in Africa; however, a study conducted in Tanzania detected M. bovis genetic material from non-reactor lactating cows [54]. Falsenegative cows may, therefore, play an important role in the epidemiology of bovine tuberculosis in the region.

Although this study focused on the estimation of *M. bovis* milk contamination, other members of the genus *Mycobacterium* such as *M. tuberculosis*, *Mycobacterium africanum*, and non-tuberculosis mycobacteria (NTM) have been isolated from bovine milk [55-58]. *M. tuberculosis* and *M. africanum* are both members of *M. tuberculosis* complex and cause infections in humans [59,60]. The presence of these bacteria in bovine milk poses a potential public health risk. The public health significance of NTM in milk is not well defined but the bacteria are considered emerging causes of infections in humans [61-63].

A limitation of this study is that it only considers the possibility of milk contamination from individual cows which may underestimate the risk of human exposure through milk consumption. One shedding cow may contaminate the farm bulk milk when the milk from several cows is pooled [64]. The risk of bulk milk contamination at farm level has been reported for several milk-borne pathogens including *M. bovis* [64] and *Listeria monocytogenes* [65,66].

Conclusion

The findings of this study highlight the public health significance of bovine brucellosis and tuberculosis in Africa. The quality and safety of milk, particularly in the informal value chain, needs to be improved to reduce the risk of zoonotic disease transmission. Further studies are required to investigate the role of false-negative cattle in the epidemiology of these diseases.

Author's Contributions

NNC designed the study, analyzed the data, drafted, reviewed and approved the manuscript.

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Competing Interests

The author declares that she has no competing interests.

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