



Prevalence of mastitis in dairy cows from smallholder farms in Zimbabwe

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A cross-sectional study was conducted to determine the prevalence of sub-clinical and clinical mastitis and the associated factors in cows from selected smallholder dairy farms in Zimbabwe. Physical examinations were conducted on all lactating cows for evidence of signs of clinical mastitis. Composite milk samples were collected from all lactating cows for bacterial culture and somatic cell counting. Cows were categorised as clinical if they exhibited clinical features of mastitis, or sub-clinical if no apparent signs were present but they had a positive bacterial isolation and a somatic cell count of at least 300×10^3 cells/mL. Farm-level factors were obtained through a structured questionnaire. The association of mastitis and animal- and herd-level factors were analysed using logistic regression. A total of 584 animals from 73 farms were tested. Overall, 21.1% (123/584) had mastitis, 16.3% (95/584) had sub-clinical mastitis and 4.8% (28/584) had clinical mastitis. Herd-level prevalence was 49.3%. Coagulase-negative staphylococci (27.6%), *Escherichia coli* (25.2%), *Staphylococcus aureus* (16.3%), *Klebsiella* spp. (15.5%) and *Streptococcus* spp. (1.6%) were the most common isolates. In individual cows, pure dairy herds (OR = 6.3) and dairy crosses (OR = 3.1) were more likely to have mastitis compared to Mashona cows. Farms that used pre-milking teat dipping were associated with reduced mastitis prevalence. Further research is needed on the prevalence of mastitis and a comparison of data for both smallholder and commercial dairy farms in all regions of Zimbabwe should be undertaken.

Introduction

In Zimbabwe, smallholder dairy farming developmental programmes were initiated in 1983 (Ngongoni *et al.* 2006; Muchenje *et al.* 2007). Their contribution to national-marketed milk increased gradually from 2% in 1998 and to an estimated 5% in 2002 (Ngongoni *et al.* 2006). Smallholder dairy farming has the potential to increase the milk production base of the country, improve household nutrition and empower rural communities with income-generating ventures. It can assist farmers to diversify, lessen farming risks and create an opportunity for use of idle forage (Ngongoni *et al.* 2006).

Shortage of and poor quality fodder have been reported to be two of the major limiting factors to smallholder dairy farming in the country (Ngongoni *et al.* 2007). Mastitis is another major limiting factor; it is a disease of dairy cattle that causes low milk production and high economic losses (Ericsson-Unnerstad *et al.* 2009; Tesfaye, Regasa & Kelay 2009). Mastitis is an inflammation of the mammary gland that is mostly caused by infectious agents, especially bacteria, but it can also be due to physical or chemical agents. Somatic cell counts (SCC) in milk are commonly used as indicators of mastitis, on the basis that an increase reflects an immune response to the presence of infection in the mammary gland (Green *et al.* 2008). Mastitis is associated with high SCC; this is mostly due to increased leukocyte levels, as they are involved in the removal of the infectious agents, and also exfoliated epithelial cells (Bagnicka *et al.* 2011). Leukocytes are responsible for destroying bacteria, and the enzymes left behind during the phagocytic process significantly reduce the shelf life of milk and milk products (Ingalls 2009). However, animals with low SCC can also have the mastitis pathogen present. Demands by consumers and processors for safe, high-quality dairy products are major factors in motivating the need for additional improvements in mastitis control in dairy herds. Mastitis could be reduced by improving milking procedures and hygiene in the herd (Karimuribo *et al.* 2008; Kivaria, Noordhuizen & Msami 2007). Dry cow treatment, milking technique, post-milking teat dipping and antimicrobial treatment of clinical mastitis are examples of management factors that have a significant effect on the reduction of mastitis cases and bulk tank milk SCC (Lievaart, Barkema, Hogeveen & Kremer 2009; Lievaart *et al.* 2009).

In Zimbabwe, there is little current information about the prevalence of mastitis, factors associated with mastitis and the bacteria mainly responsible for intra-mammary infections in the smallholder dairy sector. The only data that is available is from studies that were conducted more than a



decade ago (Perry *et al* 1987; Makaya, Aarestrup & Olsen 1996; Kudinha & Simango 2002). Therefore, the objectives of this study were to determine (1) the individual animal- and herd-level prevalence and factors associated with mastitis and (2) the most common bacteria associated with sub-clinical and clinical mastitis in cows from smallholder dairy farms in Zimbabwe.

Materials and methods

Study sites and selection of study sites

A convenient sample of smallholder dairy farms ($n = 73$) in Zimbabwe was selected. Selection was based on the presence of farms that were producing and selling milk to milk-collecting centres when the study commenced, and on agro-ecological regions and locations of the areas.

The four selected smallholder dairy centers were: Dowa (18°32'S, 32°07'E) in agro-ecological region IIA; Guruve (16°20'S, 30°35'E) and Marirangwe (18°06'S, 30°48'E) both in agro-ecological region IIB; and Nharira (19°15'S, 31°15'E) in agro-ecological region III.

Study animals

Animal ownership by the smallholder dairy farmers and the demographics of cows sampled are presented in Table 1. All smallholder dairy farms in the respective study areas with at least a single lactating cow were recruited to the study. A total of 73 smallholder farmers were still operational when the study commenced. The average herd size per farm ranged from 10 to 16, with a median of 13 animals. The breeds kept by these farmers included the local indigenous Sanga type (*Bos indicus*) commonly known as 'Mashona', exotic dairy breeds (*Bos taurus*), such as Red Dane and Jersey, dairy crosses, such as Friesian, Jersey and Red Dane crosses, and beef crosses, such as Brahman, Hereford and Mashona crosses. All of the lactating cows ($n = 584$) on the selected farms were eligible for milk sample collection. A total of 584 lactating cows were sampled with most being the local indigenous Mashona breed (44%) and dairy crosses (43.7%), whilst a few were pure dairy (2.4%) and beef crosses (9.9%). Due to the unavailability of records, the exact ages and milk production levels of the sampled cows was not determined. However, the parity of the cow was recorded.

Assessment of milking practices

A pre-tested structured questionnaire with close-ended questions was used to collect data on milking practices and

other farm management variables thought to influence the prevalence of mastitis in smallholder dairy cows. These factors included milking procedures, milking place and frequency of milking, cleaning and drying methods of teats, source of water (open or closed source), pre- and post-milking teat dipping and milking practices for suspected mastitic cows. The questionnaire was administered through a face-to-face interview. The pre-testing of the questionnaire was carried out on a few selected farmers who farmed in one of the study areas; clarity of questions and its user friendliness was checked and later revised. The survey was carried out between November 2009 and March 2010.

Milk sample collection and clinical examination

The collection of milk samples for bacterial culture and somatic cell counting was carried out during the same period as the questionnaire survey. Teats were washed using clean running water, wiped dry with disposable paper towels and disinfected using 70% ethyl alcohol. To minimise contamination with bacteria from the skin around the teat canal, the first streams of milk were discarded. Composite quarter milk samples were collected aseptically from all lactating cows and were transported to the laboratory in cooler boxes on ice (approximately 4 °C) where milk samples were plated out and preparations for microscopic cell count commenced on the day of sampling. A thorough physical examination for evidence of clinical mastitis was conducted on all lactating cows that were sampled in this study. Clinical findings such as secretions, abnormalities of size and shape of the udder, its consistency and temperature were assessed by visual inspection and palpation. A cow was considered to have clinical mastitis if it fulfilled at least two of the clinical findings, (1) pain reaction upon palpation, (2) changes in colour and consistency of milk (blood tinged milk, watery secretions, clots, pus) and (3) change in consistency of the udder (Lakew, Tolosa & Tigre 2009). Cows that did not have clinical mastitis were tested further for sub-clinical mastitis based on culture and somatic cell counting. A cow showing no apparent clinical signs of mastitis and whose milk was macroscopically normal, but had a positive bacterial culture and SCC of at least 300×10^3 cells/mL (International Dairy Federation 1987), was regarded as positive for sub-clinical mastitis.

Laboratory tests

All the tests for bacterial culture and isolation were performed at the Central Veterinary Laboratory in Harare. Milk samples were cultured for bacteria as described by Haltia *et al.* (2006). All samples were plated on blood agar

TABLE 1: Smallholder farmers' cattle ownership and demographics of sampled cows.

Study area	Number of farmers	Herd size			Number of lactating cows sampled				Total
		Total Number Cattle	Median	Range	Mashona (%)	Dairy (%)	Dairy crosses (%)	Beef crosses (%)	
Marirangwe	23	269	10	4–21	39	12	106	13	170
Nharira	14	163	13	7–18	51	0	42	9	102
Guruve	23	356	14	4–33	132	2	86	26	246
Dowa	13	210	16	4–24	35	0	21	10	66
Total	73	998	13	4–33	257 (44.0)	14 (2.4)	255 (43.7)	58 (9.9)	584



(Oxoid, Basingstoke, Hampshire, UK), MacConkey agar (Oxoid) and Edward's agar (Oxoid) to detect most aerobic pathogens, enteric bacteria and streptococci respectively. The plates were incubated aerobically at 37 °C for up to 48 h. A milk sample was considered positive for mastitis pathogen(s) if at least a single colony of a potential pathogen was detected and positively identified by biochemical tests. Plates showing mixed and confluent growths, with no evidence of single discernible colonies, were not investigated further. Primary identification of staphylococci was based on colony morphology, catalase test, Gram-staining morphology and differentiated from micrococci on the basis of the oxidative-fermentative (OF) test carried out on semi-solid OF medium (Difco, Becton, Dickinson and Company, Franklin Lakes, NJ, USA). The staphylococci were also tested for production of coagulase enzyme by the tube method as described by Quinn *et al.* (1994). Isolates that produced Gram-positive cocci in clusters, and were catalase positive, glucose-fermentative, resistant to bacitracin and did not produce coagulase were identified as coagulase-negative staphylococci (CNS). *Staphylococcus aureus* isolates were differentiated from other coagulase-positive staphylococci (*Staphylococcus intermedius* and some strains of *Staphylococcus hyicus*) on the basis of mannitol fermentation on mannitol salt agar (Oxoid), susceptibility to 5 µg novobiocin and 300 units of polymixin B as reported by Kudinha and Simango (2002). The enteric bacteria were identified using colony morphology, oxidase test, lactose fermentation on MacConkey agar (Oxoid), indole production test, citrate utilisation, and other standard biochemical tests as described by Quinn *et al.* (1994).

Somatic cell counts (SCC) were carried out in the Bacteriology Laboratory of the Central Veterinary Laboratory in Harare. The SCC were determined by using the Breed's direct smear method; spreading 0.1 mL of milk to cover about 1 cm² of a glass slide, drying and staining with methylene blue (Quinn *et al.* 1994). The somatic cells were counted microscopically over approximately 50 fields under oil immersion for each sample, and the total number of cells was recorded using a counter. The counts were converted to the total number of somatic cells per mL using the formula suggested by Quinn *et al.* (1994).

Data analysis

The proportion of mastitis-positive cows was calculated against the total number of animals investigated; this was based on the clinical features of mastitis (clinical mastitis), the pathogen isolated and a SCC of at least 300 × 10³/mL (sub-clinical mastitis). The prevalence of mastitis in individual cows was calculated according to the study area, breed, parity and history of mastitis. A herd was denoted as positive for mastitis if at least a single animal with mastitis (either clinical or sub-clinical) was detected. The farm-level prevalence of mastitis was calculated according to the study area and milking management practices, such as the use of pre- and post-milking teat dipping, milking frequency, cleaning of teats prior to milking, use of disposable paper towels, and source of water (open or closed

source) for milking. The association between mastitis (0 = negative and 1 = positive) and categorical animal- and farm-level variables was assessed in univariable analyses using Fisher's exact X² test. All the variables having $P < 0.25$ were further investigated using multivariable logistic regression analysis (Tables 3 and 4) for an association with mastitis. Due to the low numbers of mastitis-positive animals per farm (low clustering effect), an adjustment for clustering per herd was not considered critical as the logistic regression was unlikely to result in artificially low coefficients (Matope *et al.* 2011).

Two multivariable logistic regression models were built; one for individual animals (Table 3) and another for farm level variables (Table 4) using STATA version SE 10.0 (Stata Corp., Texas, USA). In both models, the outcome variable was the mastitis status (0 = negative and 1 = positive). The models were manually constructed by forward-selection, applying the maximum likelihood estimation procedure and statistical significance contribution of individual predictors (or group of predictors) using the likelihood ratio test (Matope *et al.* 2010; Dohoo, Martin & Stryhn 2003). The presence of interaction between variables was checked by constructing a two-product term and forcing it into the model and examining the changes in the coefficients and P -values of the main effects (Matope *et al.* 2010). Evidence of confounding was checked by dropping one of the variables and assessing changes of the coefficients (Matope *et al.* 2010). Goodness-of-fit of the logistic regression models was assessed using the Hosmer-Lemeshow test, whilst predictive ability was determined using the receiver operating characteristic (ROC) curve (Dohoo *et al.* 2003; Matope *et al.* 2010).

Ethical considerations

The Ethical and the Higher Degrees Committees of the Faculty of Veterinary Science and the Department of Animal Science, Faculty of Agriculture, approved the use of animals and all protocols or procedures in this study. The objectives of this study were well explained to all participating smallholder dairy farmers who all expressed their consent to participating in the study. Questionnaire responses were given on a voluntary basis and respondents were permitted to withdraw their consent up to seven days before data submission. Standard operating procedures were used for the collection of milk samples and the dairy cows were supplied with adequate food and clean drinking water.

Results

Descriptive statistics

A total of 584 animals from 73 farms were tested. Of these, 21.1% (123/584) had mastitis, with 16.3% (95/584) and 4.8% (28/584) having sub-clinical and clinical mastitis respectively. Only one cow (0.8%) with signs of clinical mastitis was negative on bacterial culture, but had a SCC > 300 × 10³ cells/mL. The farm-level prevalence of mastitis was 49.3% (36/73). From the mastitis-positive cows, coagulase-



negative staphylococci (CNS) (27.7%), *Escherichia coli* (25.2%), *S. aureus* (16.3%), *Klebsiella* spp. (15.4%) and *Streptococcus* spp. (1.6%) were the most predominant isolates obtained. It was found that 3.2% had mixed pathogens (various combinations of pairs of *E. coli*, *Klebsiella* spp., CNS and *Streptococcus* spp.) and 9.0% had contaminated growths (Table 2). Cows with clinical mastitis were associated with *E. coli* (32.1%), *S. aureus* (21.4%), CNS (14.3%), *Klebsiella* spp. (10.7%), mixed *E. coli* and *Klebsiella* spp. (3.6%), contaminated growths (unidentified pathogens) (14.3%) and no bacterial isolates (3.6%).

Individual animal logistic regression model

On univariable analysis, study area, breed, parity and history of mastitis were found to have significant associations with mastitis. However, the final logistic regression model revealed that study area and breed (Mashona, pure dairy, dairy crosses and beef crosses) were independently associated with mastitis in individual cows (Table 3).

Farm level logistic regression model

Cleaning of the teats was not included in the regression model since all farmers practiced it. On univariable analysis;

post-milking teat dipping, frequency of milking, fore-milk testing, cloth use and water source were found not to be significantly associated with mastitis in herds. The final logistic regression model revealed that study areas and pre-milking teat dipping were independently associated with mastitis in herds (Table 4).

Discussion

The results of the present study show that utilisation of recognised pure exotic dairy breeds, such as the Holstein, Jersey or Red Dane, in the selected smallholder dairy farms is uncommon. Instead, farmers predominantly use crosses of these dairy cattle and beef breeds (mainly Mashona) for their dairy farming. This may be reflective of either the absence of a sound breeding policy for pure exotic dairy breeds by resource-limited smallholder farmers, or preference of the local beef breeds, which are better adapted to the harsh environments and offer more resistance to diseases prevalent in these areas.

In individual cows, the prevalence of sub-clinical mastitis recorded during the present study is comparable to that reported from other smallholder farming sectors

TABLE 2: Summary of the bacterial isolates from smallholder dairy cows with mastitis.

Pathogen	Subclinical		Clinical		Total	
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%
Coagulase negative staphylococci (CNS)	30	24.4	4	3.3	34	27.7
<i>Escherichia coli</i>	22	17.9	9	7.3	31	25.2
<i>Staphylococcus aureus</i>	14	11.4	6	4.9	20	16.3
<i>Klebsiella</i> spp.	16	13.0	3	2.4	19	15.4
<i>Streptococcus</i> spp.	2	1.6	0	-	2	1.6
<i>Citrobacter</i> spp.	1	0.8	0	-	1	0.8
<i>Klebsiella</i> spp. and <i>Escherichia coli</i>	0	-	1	0.8	1	0.8
<i>Escherichia coli</i> and CNS	1	0.8	0	-	1	0.8
<i>Klebsiella</i> spp. and NS	1	0.8	0	-	1	0.8
<i>Streptococcus</i> spp. and CNS	1	0.8	0	-	1	0.8
Contaminated	7	5.7	4	3.3	11	9.0
No isolates	0	-	1	0.8	1	0.8
Total isolates	95	77.2	28	22.8	123	100

CNS, Coagulase negative staphylococci; *n*, number of isolates.

TABLE 3: Summary of univariable and multivariable logistic regression analysis of associations between mastitis and potential risk factors for individual animals.

Factor	Level	<i>N</i>	Prevalence (%)	<i>P</i>	Multivariable logistic regression†				
					<i>b</i>	SE (<i>b</i>)	<i>P</i>	OR	95% CI
Constant	-	-	-	-	-1.8	0.3	0.00	-	-
Area	1: Marirangwe	170	31.2	0.00	-	-	-	1.0	-
	2: Nharira	102	19.6		-0.3	0.3	0.34	0.7	0.4–1.4
	3: Guruve	246	15.9		-0.6	0.3	0.04	0.6	0.4–1.0
	4: Dowa	66	16.7		-0.5	0.4	0.24	0.6	0.3–1.4
Breed‡	1: Mashona	257	10.5	0.00	-	-	-	1.0	-
	2: Dairy	14	50.0		1.8	0.6	0.00	6.3	2.0–20.1
	3: Dairy cross	255	29.4		1.1	0.3	0.00	3.1	1.9–5.1
	4: Beef cross	58	24.1		1.0	0.4	0.01	2.6	1.3–5.4

N, used as number; *P*, probability value; *b*, logistic regression coefficient; SE (*b*), standard error for the logistic regression coefficient; OR, Odds Ratio; CI, Confidence Interval.

†, Overall data of the model: Log likelihood = -280.4, LR χ^2 (6d.f) = 40.6, *P* = 0.00, Number of observations = 584.

‡, Breeds of cattle used in this study: Mashona, a local Sanga (*Bos indicus*) beef breed; Dairy breed, Jersey, Friesian or Red Dane; Dairy Cross, A crossed breed between Mashona and dairy breed; Beef cross, a crossed breed between Mashona and other unspecified beef breeds.

Hosmer-Lemeshow χ^2 = 4.4, d.f.8, *p* = 0.62; Area under the ROC curve = 0.7.

**TABLE 4:** Summary of univariable and multivariable logistic regression analysis of associations between mastitis and potential herd-level risk factors.

Factor	Level	N	Prevalence (%)	P	Multivariable logistic regression [†]				
					b	SE (b)	P	OR	95% CI
Constant	-	-	-	-	-2.1	1.0	0.03	-	-
Area	1: Marirangwe	23	65.2	0.162	-	-	-	1.0	-
	2: Nharira	14	57.1	-	-0.8	0.8	0.3	0.4	0.1 – 2.0
	3: Guruve	23	34.8	-	-1.5	0.7	0.04	0.2	0.1 – 0.9
	4: Dowa	13	38.4	-	-1.9	0.8	0.02	0.1	0.01 – 0.7
Pre-milking teat dipping not done	0: No	29	27.6	0.004	-	-	-	1.0	-
	1: Yes	44	63.6	-	1.9	0.6	0.002	6.7	2.1 – 22.0

N, used as number; P, probability value; b, logistic regression coefficient; SE (b), standard error for the logistic regression coefficient; OR, Odds Ratio; CI, Confidence Interval.

[†], Overall data of the model: Log likelihood = -42.1, LR chi² (4d.f) = 16.9, P = 0.002, Number of observations = 73. Hosmer-Lemeshow X² = 2.5, d.f.7, p = 0.8; Area under the ROC curve = 0.8.

(Harouna *et al.* 2009; Karimuribo *et al.* 2008; Kivaria, Noordhuizen & Kapaga 2004). Compared to individual milk samples, composite milk samples may be less effective for the isolation of micro-organisms due to the dilution factor from uninfected quarters. The prevalence of clinical mastitis in our study (4.8%) is within the range of other reports from smallholder dairy farms in some countries in Sub-Saharan Africa (Abera *et al.* 2011; Getahun *et al.* 2008; Kivaria *et al.* 2004). This provides further support of other studies in the region, which have concluded that sub-clinical mastitis is more prevalent than clinical mastitis (Almaw, Zerihun & Asfaw 2008; Lakew, Tolosa & Tigre 2009). This is likely to be partly influenced by virulence of the circulating bacterial strains and the levels of immunity of the cows to these pathogens. The relatively high prevalence of sub-clinical mastitis recorded in this study could possibly indicate a substantial financial loss through decreased milk production due to progressive destruction of the alveolar epithelial cells in the mammary gland (Zhao & Lacasse 2008). Mungube *et al.* (2005) reported a substantial loss due to subclinical mastitis; the overall financial loss for each cow per lactation was estimated to be US \$78.65 (Tesfaye *et al.* 2009). However, most smallholder farmers are not well informed about the invisible losses from sub-clinical mastitis and do not normally recognise the condition (Mungube *et al.* 2004).

All of the smallholder farmers clean the teats of dairy cows with running water prior to milking, but, as observed earlier (Millogo *et al.* 2008), the implementation of mastitis preventive measures such as using separate drying cloths for each cow, and practicing pre- and post-milking teat dipping are noted to be infrequent amongst the farmers. A lower prevalence of both clinical and sub-clinical mastitis has been reported on farms where separate towels for teat cleaning and post-milking teat dipping were routinely practiced (Kivaria *et al.* 2007). Despite the fact that some of these risk factors are not found to be statistically significant in the final logistic regression model, presumably due to low sample sizes, the need to implement mastitis preventive measures such as the use of pre-milking and post-milking teat dipping cannot be overemphasised.

The isolation of CNS, *S. aureus*, *E. coli*, *Klebsiella* spp. and *Streptococcus* spp. from mastitic cows in this study supports

findings from previous studies conducted in both commercial and smallholder dairy farms in Zimbabwe (Perry *et al.* 1987; Makaya *et al.* 1996; Kudinha & Simango 2002), South Africa (Swartz, Jooste & Novello 1984) and smallholder dairy farms in other regions of Africa (Getahun *et al.* 2008; Lakew *et al.* 2009). As observed in other studies in Zimbabwe and elsewhere (Makaya *et al.* 1996; Kudinha & Simango 2002; Petzer *et al.* 2009), sub-clinical mastitis is most commonly associated with CNS. This highlights the importance of the role of CNS in sub-clinical mastitis and that some of them are more pathogenic than is generally assumed. Therefore, the general mastitis-control programmes, such as dry cow-therapy, that take these pathogens into consideration will be more beneficial. In this study, environmental bacteria *E. coli* and *Klebsiella* spp. predominate over *S. aureus* in both sub-clinical and clinical mastitis; this is contrary to other reports where *S. aureus* was the most common isolate (Swartz *et al.* 1984; Tesfaye *et al.* 2009). Inadequate hygiene in the dairies in our study, especially during the rainy season when cow udders are mainly soiled due to animals lying in muddy overnight cow pens, is likely to increase the risk to infection with environmental pathogens.

Pure exotic dairy cows (OR = 6.3), cows of dairy crosses (OR = 3.1) and beef crosses (OR = 2.6) are more likely to be positive for mastitis compared to the local indigenous Mashona breed. The difference in mastitis prevalence might reflect a number of general resistance characteristic attributes of the breeds, such as udder and teat morphology. Since cows in the same study area are all under similar conditions, management factors such as grazing, kraaling, milking procedures, et cetera are unlikely to influence this breed difference. Hence, it is likely that the indigenous breeds have over the years become better adapted to regional stressors than the exotic breeds. Similarly, as in previous studies (Green *et al.* 2008; Harouna *et al.* 2009), indigenous breeds (in this instance Mashona) are found to have significantly lower SCC than exotic dairy breeds and their crosses (data not shown). Therefore, due to these breed differences in levels of SCC, the diagnosis of sub-clinical mastitis, especially in indigenous cows like Mashona, may be improved by lowering the cut-off points for SCC rather than adopting the universal criteria that were designed for high-milk producing cows.



In support of previous observations (Byarugaba *et al.* 2008; Getahun *et al.* 2008), the present study shows a progressive increase in the prevalence of mastitis with increased parity. This apparent increase in the risk of mastitis in older cows, especially after the fourth parity, could be attributed to chronic sub-clinical mastitis especially caused by host-adapted pathogens such as *S. aureus* (Bradley 2002). However, studies in other regions have reported higher prevalence in heifers compared to older cows; this could possibly be due to differences in management practices (McDougall *et al.* 2009).

Although, based on the available data, the differences in farm-level prevalence of mastitis in this study cannot be explained fully, it is likely that this can be attributed to animal husbandry practices. For instance, Marirangwe farms that keep the highest proportions of dairy crosses are associated with a higher prevalence compared to Dowa, which keep very few dairy crosses and predominantly the Mashona breed. Since the selection of the study areas was influenced by the availability of operational farms, the inclusion of more study areas across the country could have revealed differences in prevalence of mastitis according to the different agro-ecological regions. Nevertheless, considering that sub-clinical mastitis is quite prevalent and that common mastitis pathogens such as CNS, *E. coli*, *Klebsiella* spp. and *S. aureus* were isolated from all the study areas, the wide-spread of mastitis in smallholder dairy farms in Zimbabwe cannot be ruled out.

In conclusion, this study established an overall mean cow-level mastitis prevalence of 21.1%, where subclinical (16.3%) is more prevalent than clinical (4.8%) mastitis. Mastitis is found to be prevalent in all of the study areas, with a mean of 49.3%. Pure exotic dairy cows, cows of dairy crosses and beef crosses have greater odds of mastitis compared to the Mashona breed. The bacteria most commonly associated with mastitis include CNS, *E. coli* and *Klebsiella* spp. and *S. aureus*. At farm-level, the differences in mastitis prevalence can be related to management factors like the use of pre-milking teat dipping. Further research is needed on mastitis prevalence in all regions of Zimbabwe in both smallholder and commercial dairy farms. A comparison of data between these distinct dairy farming practices is an area of further research.

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Competing interests

The authors declare that they have no financial or personal relationship(s) that may have inappropriately influenced them in writing this article.

Authors' contributions

D.M.P. (University of Zimbabwe) was the project leader responsible for study design and data analysis, G.M. (University of Zimbabwe) and M.N. (University of Zimbabwe) were co-leaders responsible for conceptual contributions and writing of the manuscript and S.K. (University of Zimbabwe) collected data and performed most of the experiments.

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