

Prevalence and antimicrobial susceptibility profiles of *Staphylococcus aureus* from cow's milk, nasal and environmental swabs in selected dairy farms in Morogoro, Tanzania

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SUMMARY

Staphylococcus aureus is a microorganism that is present as a commensal on the skin, the nose and mucous membranes of healthy humans and animals. However, it is also an opportunistic pathogen that can cause multiple infectious diseases of diverse severity. A cross-sectional study was carried out to determine the prevalence and antimicrobial resistance profiles of *S. aureus* from samples of cow's milk, farm environmental and cattle nasal swabs from three dairy farms in Morogoro. A total of 377 samples; raw milk (n = 100), nasal swabs (n=133) and environmental swabs (n = 144) were screened for the presence of *S. aureus*. California mastitis test (CMT) was used to establish the status of mastitis. Gram staining, oxidase, catalase, DNase, haemolysis and coagulase tests were employed for bacterial identification. Antimicrobial susceptibility testing was conducted using the Kirby- Bauer disk diffusion assay. Out of 200 cows (800 quarters milk) CMT screened for mastitis, (12.5%) quarters from 80 cows tested positive for subclinical mastitis, while twelve (1.5%) quarters from seven (3.5%) cows tested positive for clinical mastitis. Overall, 97 (25.7%) of 377 samples were positive for *S. aureus*, which were detected in 49.0%, 11.6%, and 40.0% of the milk, environment and nasal samples, respectively. Antimicrobial susceptibility testing revealed resistance to: Ampicillin (67.4%), Cefoxitin (14.8%), Erythromycin (21.1%), Gentamycin (3.2%), Oxacillin (37.9%), Tetracycline (55.8%), Trimethoprim-Sulfamethoxazole (29.5%) and Vancomycin (9.5%). 28.4% (n=27) of all isolates were resistant to Oxacillin and/or Cefoxitin, and therefore classified as Methicillin-Resistant *Staphylococcus aureus* (MRSA). 63% of the MRSA isolates originated from milk, 22.2% from nares and 14.8% from environmental samples. Over a half of all isolates were classified as multidrug resistant; of these 43.2% (n=41), 6.3% (n=6) and 1.1% (n=1) were simultaneously resistant to three, four and five antimicrobial agents, respectively. Taken together, this study revealed the prevalence of multidrug resistant *S. aureus* in cow's milk, nares and farm environment. Our findings also confirm the presence of livestock-associated MRSA, and thus underline the importance of applying biosecurity measures and good hygiene practices to prevent MRSA spread at the farm level and throughout the food production chain.

Key words: *Staphylococcus aureus*, Antimicrobial resistance, MRSA, Livestock environment

INTRODUCTION

Staphylococcus aureus, a non-spore forming and non-motile bacteria, is a microorganism that is present as a commensal on the skin, the nose and mucous membranes of healthy humans and animals. However, it is also an

opportunistic pathogen that can cause multiple infectious diseases of diverse severity both in animals and humans (Luzzago et al., 2014; Petonand Le Loir, 2014). Bovine mastitis is an infection of the mammary gland and is the major illness for dairy ruminants that leads to reduced milk production, and is often

associated with cattle disorders such as

related economic losses include the reduction in milk yield, increased treatment costs, discarded milk, increase in culling, pharmacologic costs, and increased labor costs (Cardozo *et al.*, 2014). In cattle, *S. aureus* cause variety diseases ranging from simple abscesses and mastitis to the more severe toxic shock syndrome (Mdegela *et al.*, 2005; Persson *et al.*, 2011; Sharma *et al.*, 2015). *S. aureus* is responsible for approximately one-third of cases of clinical and subclinical mastitis in cattle (Bradley, 2002; Mdegela *et al.*, 2005; Botrelet *et al.*, 2010).

Antibiotic use in the treatment of animal diseases including mastitis is frequent; however, there has been an increase in the bacterial resistance index. This fact reinforces the importance of adopting appropriate treatment protocols with effective medicines, which must be selected from phenotypic and genotypic testing. Treatment of mastitis is mainly dependent on antimicrobial therapy such as β -lactams, cephalosporin, aminoglycoside and macrolide (Kaliwa *et al.*, 2011; Awandkaret *et al.*, 2013; Chandrasekaran *et al.*, 2014). However, resistant *S. aureus* strains towards major classes of antibiotics have been reported, leaving veterinarians with limited options. The expression of the *mecA* gene in *S. aureus* confers resistance to most β -lactams, including methicillin resistance (MRSA), agents frequently used for treatment of mastitis (Sawant *et al.*, 2005). MRSA is an important human and animal pathogen that can be implicated in a wide diversity of infections, including bovine mastitis (Stefani *et al.*, 2012). Recently, a specific MRSA clone, CC398, has been found to be associated with pigs, veal calves, broiler chickens, companion animals and people in close contact with

fever and rumen motility. Other mastitis-

livestock (de Neeling *et al.*, 2007; Denis *et al.*, 2009; Graveland *et al.*, 2011), and this strain shows resistance against tetracycline, macrolides, lincosamides, aminoglycosides and fluoroquinolones (Witte *et al.*, 2007).

Methicillin resistant *Staphylococcus aureus* (MRSA) incriminated in bovine mastitis has been evidenced in many countries including Korea (Moon *et al.*, 2007), Switzerland (Huber *et al.*, 2010), Belgium (Vanderhaeghen *et al.*, 2010), South Africa (Ateba *et al.*, 2010), Turkey (Turkyilmaz *et al.*, 2010), Serbia (Zutic *et al.*, 2012), USA (Haran *et al.*, 2012), China (Pu *et al.*, 2014; Li *et al.*, 2015), Tanzania (Mohamed, 2015) and Italy (Locateli *et al.*, 2016). Similarly, *S. aureus* has been reported to colonize the nasal mucosa of different animal species, their owners, caretakers or veterinarians, and emphasized the importance of nasal MRSA carriage in terms of public and animal health (Faïres *et al.*, 2009; Gordoncillo *et al.*, 2012; Loeffler *et al.*, 2005; Van Duijkeren *et al.*, 2010).

Due to the intensive use of antibiotics in public health and animal husbandry, antibiotic resistance in pathogens has been an increasing medical problem over the last decades. In addition to the spread of resistant zoonotic foodborne pathogens, there is also a possibility that food-related commensal bacteria or opportunistic pathogens are carriers of resistance genes, and therefore a potential hazard to consumers (Sharma *et al.*, 2014). With regard to dairy production, the most relevant are resistant mastitis-causing bacteria, such as *Staphylococci*. The presence of resistant *S. aureus* in milk intended for human consumption or dairy products could be of public-health relevance. Hence, the aim of the present study was to determine the presence and

antimicrobial resistance profiles of *S. aureus* in mastitis cases in dairy cattle, cattle nares and farm environment at three farms belonging to Sokoine University of Agriculture, Morogoro, Tanzania.

MATERIALS AND METHODS

Study area

The study was carried out in Morogoro municipality, Tanzania. Geographically, the municipality extends between longitude 35.6 to 39.5° E and latitude 5.7 to 10° S at an elevation of 500 to 600 m above sea level and is about 200 km west of Dar es Salaam. The municipality has a mixture of warm and cool temperatures ranging between 27 to 33.7°C in the dry/warm season and 14.2 to 21.7°C in cool/wet season. Morogoro Municipality experiences a sub-humid tropical climate with a bimodal rainfall pattern characterized by two rainfall seasons in a year with a dry season separating the short rains (October to December) and long rains (which fall from March to May/June). There are about 6 months of dryness, the peak being September. The mean annual rainfall is about 870 mm and the total annual evapotranspiration is about 1300 mm.

Study animals

The study was carried out in 3 dairy farms (A, B and C) that belonged to Sokoine University of Agriculture. All farms were located within the same climatic zone. Farm A included dairy herds and goat flocks in close proximity, whereas, farm B had dairy cattle, goats, sheep, pigs and camels also kept in close proximity, but with different attendants. Farm C had both dairy and pig herds kept in close proximity but with different management systems. Dairy herds were grazing on pasture for about 8 hours

and fed with hay after returning to the housing pallor in the afternoon. Lactating cows were either hand-milked (farm B) or machinery-milked (Farm A and C) twice daily.

Study Design and sample collection

To investigate the prevalence of *S. aureus*, a cross-sectional study was conducted from January through April 2016. A total of 377 samples, including raw milk samples (n = 100), nasal swabs (n=133) and environmental swabs (n = 144), were collected from the three farms. The sample size was calculated according to Martin *et al.* (1987) to allow a detection level of 5% or with 95% certainty. From farm A, 140 samples (46 milk, 48 environmental swabs and 46 nasal swabs), 93 from farm B (20 milk, 48 environment and 25 nasal swabs), and 144 samples from farm C (34 milk, 48 environmental and 62 nasal swabs) were collected. For milk samples, 300 milking cows were first screened using California mastitis test (CMT) for the presence of clinical or subclinical mastitis as previously described by Karimuribo *et al.* (2015). The CMT positive mammary quarters of 54 cows were sampled for isolation of *S. aureus*. All samples were analyzed at Microbiology laboratory in the College of Veterinary and Medical Sciences, Sokoine University of Agriculture.

Milk samples

A single aseptic milk sample was collected from each of CMT-positive quarter after udder preparation by the farm personnel. The milk samples collection was done according to the procedure previously described by Mdegela *et al.* (2009). Briefly, the teat ends were first disinfected with 70% alcohol, and approximately 10 mL of individual quarter milk samples

were collected into sterile receptacles. Samples were stored in cool box with ice packs before shipped to the laboratory for further processing within a maximum of 12 hours or frozen at -20°C until bacteriological analyses.

Environmental swabs

During the visit to each farm, twelve environmental samples consisting of floor, door and wall swabs (representative of all parts of animal houses/barns), at monthly interval, were collected with sterile gauze. Each gauze pad was then placed in a sterile plastic bag (Ziploc®; SC Johnson), closed, labeled, and stored in a cool box with ice packs before transportation to the laboratory for further analyses within a maximum of 24 hours.

Nasal swabs

Nasal swab samples were taken from both nostrils (nares) of randomly selected healthy cows using cotton swabs. The cotton swabs were inserted into the anterior nares of both left and right nostrils and were gently rolled against the inner walls. Samples were then stored in a cool box with ice packs before transportation to the laboratory for further analyses within a maximum of 24 hours.

Isolation and identification of *S. aureus*

Nasal and environmental swabs were inoculated into tryptone soya broth (TSB, Oxoid Ltd., Basingstoke, Hampshire, UK), supplemented with 7% (w/v) sodium chloride, and incubated aerobically at 35°C for 24 hours. Then, 100 μL of the broth was inoculated onto Columbia blood agar (Oxoid Ltd., Basingstoke, Hampshire, UK), containing 7% sheep blood, and the plates were incubated under aerobic conditions incubated at $35\text{--}37^{\circ}\text{C}$ for 24

hours. Similarly, 10 μL of each milk sample was inoculated onto Columbia blood agar under the same condition as for broth. Presumptive colonies were provisionally identified based on Gram staining, morphology (presence of golden yellowish or creamy white colonies) and hemolytic pattern (with or without beta hemolysis). Identification *S. aureus* was achieved using standard conventional methods including, oxidase and catalase tests, slide and tube coagulase with rabbit plasma as well as DNase tests were used (Kateete *et al.*, 2010). In case of discrepancy between the coagulase and the DNase tests, a latex agglutination test (Slidex Staph Test, England) was carried out (Ridenour *et al.*, 2007). MRSA ATCC 33591 and MSSA ATCC 25923 were used as quality control strains. *Staphylococcus aureus* isolates were stored in TSB containing 15% glycerol at -20°C until needed.

Antimicrobial susceptibility test

The Kirby-Bauer Disk Diffusion Susceptibility test was used to obtain the antimicrobial resistance profile of the isolates. This was done following the protocol by CLSI, (2014). Samples were cultured in nutrient broth at 37°C for 18-24 hours. For phenotypic detection of MRSA antibiotic susceptibility testing, *S. aureus* isolates were tested against the antibiotics including oxacillin (1 μg) and ceftiofur (30 μg), whereas, Vancomycin (30 μg), Tetracycline (30 μg), Trimethoprim-sulfamethoxazole (25 μg), Ampicillin (10 μg), Erythromycin (15 μg) and Gentamycin (10 μg) for the routine drug susceptibility test. Methicillin was not included as a test antibiotic because it is no longer produced, and oxacillin remains a second option, though it was demonstrated that ceftiofur was more reliable than oxacillin for detecting MRSA (Zurita *et al.*,

2010). A suspension of the test organism were prepared in sterile saline equivalent to 0.5 McFarland using isolated colonies and were incubated at 37°C for 2 hour. Using a sterile cotton swab the organisms were inoculated on Mueller Hinton agar plate spread evenly over the entire surface. The antimicrobial-impregnated disks were placed on the surface of the agar plates and incubated at 37°C except oxacillin which was at 35°C for 24 hours. Following incubation, the diameter of the zone of inhibition was measured and the results interpreted according to the zone diameter interpretative standards (CLSI, 2014) for *Staphylococcus* spp. Determination of MRSA isolates was performed according to the results obtained in the evaluation of oxacillin and ceftiofur (Datta *et al.*, 2011). Any isolates that was resistant to ceftiofur and/or oxacillin were considered as MRSA (CLSI, 2014).

Statistical analysis

The prevalence and antimicrobial resistance of *Staphylococcus aureus* from milk samples, nasal and environmental swabs in all three farms were compared using the Chi-squared (χ^2) test. A value of

$P < 0.05$ was considered statistically significant.

RESULTS

Prevalence of *Staphylococcus* spp

The CMT screening for clinical or subclinical mastitis in 200 cows (800 samples of milk) revealed that 100 quarters of 80 out of 200 (40.0%) cows tested had subclinical mastitis in different number of quarters, while seven (3.5%) cows tested positive for clinical mastitis (Table 2). With regards to farm distribution, 46 out of 288 (16.0%) mammary quarters tested from farm A were CMT positive to mastitis. Twenty out of 140 mammary quarters (14.3%) and 8.2% (34 out of 416) mammary quarters tested positive to CMT on farm B and C, respectively.

Milk bacterial culture from the 100 mammary quarters yielded 49 *Staphylococcus aureus* intramammary infections (IMI) coming from the 80 cows. The overall prevalence of *S. aureus* was 25.7 % (97/377). Of these, 49 (49.0%) were from milk, 11 (7.9%) from environmental swabs, and 37 (27.8%) from nasal swabs (Table 1).

Table 1. The prevalence of *S. aureus* in cow milk, environment and nares from three dairy farms

Farm	Sources			
	Milk (No & %)	Environment (No & %)	Nares (No & %)	Total (%)
Farm A	22 (47.8)	8 (16.7)	10 (21.7)	40 (28.6)
Farm B	11 (55.0)	0	9 (36.0)	20 (2.5)
Farm C	16 (47.1)	3 (6.3)	18 (29.0)	37 (25.7)
Total	47 (49.0)	11 (7.6)	37 (27.8)	97 (25.7)

Table 2. Prevalence of *S. aureus* in cows with mastitis in three dairy farms

Source	No examined	No (%) of cows with subclinical mastitis	No (%) of cows with clinical mastitis	No (%) of cows with <i>S. aureus</i> mastitis	No (%) of mammary quarters affected with <i>S. aureus</i>
Farm A	72	25 (34.7)	2 (2.8)	17 (63.0)	22 (47.8)
Farm B	35	15 (42.9)	3 (8.6)	7 (38.8)	11 (55.0)
Farm C	104	40 (38.7)	2 (1.9)	17 (40.5)	16 (47.1)
Total	211	80 (37.9)	7 (3.3)	41 (51.3)	49 (49.0)

Antimicrobial susceptibility testing

To better assess the potential public health impact of *Staphylococcus* spp., a total of 95 of 97 (2 isolates from milk could not be retrieved from glycerol stocks) were assayed for their potential to resist eight antimicrobials. Analysis of the antimicrobial resistance profiles showed that 90 of the 95 isolates (94.7%) were resistant to one or more antimicrobials, whereas five (5.3%) isolates were pan-susceptible to all antimicrobials tested. Nineteen isolates (20.0%; 10 milk samples, 6 nasal and 3 environmental swabs) were resistant to a single antimicrobial and 23 isolates (24.2%; 9 milk samples, 13 nasal and 1 environmental swabs) showed resistance to two antimicrobials. Forty-

eight (50.5%) of all isolates (26 milk, 16 nasal and 6 environmental swabs) were resistant to three or more antimicrobials tested. Two *S. aureus* isolates recovered from milk were resistant to Gen, whereas 67.4% of all isolates were resistant to Amp (Table 3). Approximately 14.7% (6 from milk, 3 nasal and 3 from environmental swabs) and 37.9% (six 16 from milk, 6 nasal and 4 environmental swabs) of the isolates were resistant to Fox and Oxa, respectively (Tables 3). While resistance to Tet was significantly higher ($P < 0.05$) in isolates recovered from nares in comparison to those from milk, there were no significant differences ($P > 0.05$) in resistance associated with the remaining antimicrobials.

Table 3. Antimicrobial resistance profiles of *Staphylococcus aureus* isolated from dairy cow milk, environmental and nasal swabs

Source of isolates	Antimicrobial agent (%) ¹							
	Amp ¹	Fox	Ery	Gen	Oxa	Tet	CXT	Vac
Milk (n=47)	61.7	17.0	23.4	6.4	34.0	44.7	40.4	10.6
Nasal swabs (n=37)	75.7	8.1	16.2	0	16.2	73.0	21.6	10.8
Environmental swabs (n=11)	63.6	27.3	27.3	0	36.4	45.5	9.1	0
Total (n=95)	67.4	14.7	21.1	3.2	37.9	55.8	29.5	9.5

¹Amp,ampicillin; Fox,cefoxitin; Gen, gentamycin; Ery, erythromycin; Oxa, oxacillin; Tet, tetracycline; CXT, Trimethoprim-Sulfamethoxazole; Vac, vancomycin.

Multiple antibiotic resistance (MAR) phenotypes of *S. aureus*

The predominant MAR phenotypes for *S. aureus* isolated from this study were Amp-Tet-CXT, Amp-Ery-Tet and Amp-Fox-Oxa in 20.0%, 9.5% and 8.4% of the isolates, respectively (Table 4). Furthermore, the most commonly observed resistance pattern was between Amp-Tet (46.3%) followed by Amp-CXT (27.4%), Amp-Oxa (13.7%), Fox-Oxa (11.6%), Amp-Fox (11.6%), Ery-Oxa (5.3%), and Oxa-Vac (4.2%). Forty-one (43.2%) among of the isolates in this study revealed resistance with three types of antimicrobial agents in ten different combinations. Six (6.3%) of all isolates were resistant to four antimicrobial agents in four different

combinations, while resistance to five antimicrobial agents was observed once (Table 4).

Prevalence of Methicillin resistant *Staphylococcus aureus* (MRSA)

Twenty-seven (28.4%) of all isolates were resistant to oxacillin and/or cefoxitin, and therefore classified as MRSA. Of these, thirteen (56.5%) were resistant to both cefoxitin and oxacillin, one isolate showed resistant only to cefoxitin while 13 isolates were resistant only to oxacillin among of the two antibiotics. Majority of the MRSA isolates (63%) originated from milk with 22.2% and 14.8% isolated from nasal and environmental swabs, respectively.

Table 4. The predominant multiple antibiotic resistant phenotypes for *Staphylococcus aureus* isolated from cow's milk, environmental and nasal swabs

Phenotype ¹	Number observed	Percentage
Apm-Gen-Tet	1	1.1
Apm-Gen-CXT	1	1.1
Amp-Oxa-CXT	1	1.1
Amp-Fox-Gen	1	1.1
Fox-Oxa-Tet	1	1.1
Fox-Ery-Gen	1	1.1
Amp-Fox-Oxa	8	8.4
Amp-Ery-Tet	9	9.5
Amp-Tet-CXT	18	20.0
Amp-Tet-CXT-Vac	1	1.1
Amp-Fox-Oxa-Vac	1	1.1
Amp-Ery-Oxa-CXT	1	1.1
Amp-Fox-Oxa-CTX	1	1.1
Amp-Ery-Tet-CXT	2	1.1
Amp-Fox-Oxa-Tet-Vac	1	1.1

¹Amp, ampicillin; Fox, cefoxitin; Gen, gentamycin; Ery, erythromycin; Oxa, oxacillin; Tet, tetracycline; CXT, Trimethoprim-Sulfamethoxazole; Vac, vancomycin.

DISCUSSION

Mastitis in both clinical and subclinical forms is the main disease that affects milk

production. The present study revealed higher prevalence of subclinical mastitis compared to clinical mastitis. Similar findings have been observed from other studies conducted elsewhere (Kivaria *et al.*, 2004; Sori *et al.*, 2011; Zeryehun *et al.*, 2013). This observation could be attributed to the invisibility and silent nature of subclinical mastitis which is usually given little attention by farms when it comes to treatment unlike clinical mastitis towards which treatment and control efforts are concentrated (Karimuribo *et al.*, 2006; Girma, 2010).

Bovine mastitis is generally associated with the intensive farming system. For implementation of therapeutic and preventive measures, appropriate knowledge of the bacteriological population, antibiotic sensitivity pattern and epidemiological aspect holds key for the management of bovine mastitis in a dairy farm. The present study showed prevalence of 3.3% for clinical mastitis that is closer to the reports of 3.8% in smallholder dairy herds in the Dar es Salaam region (Kivaria *et al.*, 2004), 3.4% in Ethiopia (Abebe *et al.*, 2016), but lower than 11.5–14.8% in smallholder dairy herds in the urban and peri-urban areas of the Dodoma municipality in Central Tanzania (Mdegela *et al.*, 2005), and 10.0–22.4% reported in Ethiopia (Abera *et al.*, 2013; Zeryehun *et al.*, 2013). However, the present finding was much higher than the findings of 0.93% in Gondar, Ethiopia (Nibret *et al.*, 2011). Risk factors which influence the occurrence of clinical mastitis include animal, pathogen, and environment, which could contribute in the discrepancies of mastitis prevalence (Radostits *et al.*, 2007).

The present study also showed prevalence of 37.9% for subclinical mastitis that was closer to the reports of 33.3% in Kilosa

district (Karimuribo *et al.*, 2008), and 31.8% to 37.0% in Ethiopia (Sori *et al.*, 2005; Girma, 2010; Nibret *et al.*, 2011). However, the present results are lower than 51.6% (n = 91) reported in smallholder dairy farms in Tanzania (Mdegela *et al.*, 2009), 75.9% in dairy cattle kept by smallholders in Iringa and Tanga regions of Tanzania, 87.9% in Uganda (Kasozi *et al.*, 2014), and 61.2% in smallholder dairy of the Dodoma municipality (Mdegela *et al.*, 2005). The CMT results were found to be higher than the 13.5% to 22.0% reported in Kosovo (Sylejmani *et al.*, 2015), 10% in Ethiopia (Kerro and Tareke, 2003), and 8.33% from lactating cows in Peshawar district of Pakistan (Alam *et al.*, 2016). This variability in prevalence of subclinical mastitis in present and earlier studies may be attributable to various factors including climate, season, study methodology and farm management practices such as general hygiene, care of teat injuries, care and working of milking machine, and adoption of various mastitis control measures including teat dipping and dry cow therapy.

Staphylococcal mastitis accounts for single largest cause of economic losses in terms of depressed milk production, cost of treatment and culling of high genetic vigor animals (Le Mare'chalet *et al.*, 2011). The present study indicates that 49.0% of milk samples from mastitic cattle were positive for *S. aureus*. Similar studies conducted in Morocco, Brazil, Ethiopia and Kenya reported prevalence of *S. aureus* in milk to be 40%, 68%, 48.75% and 30.6% respectively (Bendahou *et al.*, 2008; de Oliveira *et al.*, 2011; Daka *et al.*, 2012; Shitandi and Sternesjö, 2004). The overall *S. aureus* nasal carriage (27.8%) observed in this study is relatively lower than the 43.7% reported in Saudi Arabia (Alzohairy, 2011), but higher than 5.06%

reported in Iran (Rahimi *et al.*, 2015), 16.0% in Norway (Mork *et al.*, 2012), and 19.8% in Belgium (Nemeghaire *et al.*, 2014). Environmental contamination with *S. aureus* was also observed in this study. Environmental prevalence of *S. aureus* (7.6%) observed in the present study was consistent to the findings observed elsewhere (Khan *et al.*, 2016; Locateli *et al.*, 2016). High prevalence of *S. aureus* observed in the nasal swabs of cattle and environment may be a predisposing factor for subsequent Intra-Mammary Infection (IMI), which needs additional comparative studies (Vautor *et al.*, 2005; Mork *et al.*, 2012). However, *S. aureus* prevalence can vary depending on many factors including geographical locations, sampling methods, laboratory testing methods, and age of the animals tested.

Antibiotic-resistant *S. aureus* isolates pose a severe challenge to both veterinary and health professions and dairy cattle producers because they have a negative impact on therapy (Brouillette and Malouin, 2005). The antimicrobial resistance level in our study was relatively high. Forty-eight out of 95 *Staphylococcal* isolates were resistant to 3 or more antimicrobial classes including most of the commonly used antimicrobials in the region. Multiple antibiotic resistant *S. aureus* strains have been isolated from milk obtained from cattle, beef and human samples in many parts of the world (Waage *et al.*, 2002; Shitandi and Sternesjö, 2004; Zhanelet *et al.*, 2005; Pesavento *et al.*, 2007; Atebaet *et al.*, 2010). The prevalence of antibiotic resistance between *S. aureus* usually varies between isolates from the different sampled stations and even between isolates from different herds and/or flocks of the same farm (Waage *et al.*, 2002). Furthermore, *S. aureus* has developed multidrug resistance in many

regions of the world (WHO, 2000) and the usage of antibiotics correlates with the emergence and maintenance of antibiotic-resistant traits within pathogenic strains (Shitandi and Sternesjö, 2004).

The highest resistance to the antimicrobials used was to ampicillin (67.4%). Ampicillin and oxacillin are beta-lactam antibiotics, and resistance to the beta-lactam antibiotics is most often due to a plasmid-encoded penicillinase/beta-lactamase (Lowy, 2003; Petinaki and Spiliopoulou, 2012). Beta-lactam antibiotics such as Penicillin is commonly used on dairy cattle farms in the study area, and this could be the reason for high Ampicillin resistance profiles of *S. aureus* observed in this study. Tetracyclines have been used extensively to treat animal infections because of their relative safety and broad-spectrum activity (Kuang *et al.*, 2009). Nevertheless, increasing tetracycline resistance rates in *S. aureus* strains from bovine mastitis have been reported (Kumar *et al.*, 2010; Wang *et al.*, 2012; Intorre *et al.*, 2013). Accordingly, a relatively high (55.8%) level of Tetracycline resistance was found in our study.

The antimicrobial susceptibility test for *S. aureus* revealed a relatively low resistance to ceftiofur (14.7%), vancomycin (9.5%), gentamycin (3.2%), and moderate resistance to oxacillin (37.9%), trimethoprim-sulfamethoxazole (29.5%) and erythromycin (21.1%). Similar observations have been reported from Ethiopia (Mekuria *et al.*, 2013) and China (Wang *et al.*, 2012). However, Daka *et al.* (2012) reported higher resistance in isolates from cow's milk to oxacillin (60.3%) and vancomycin (38.5%), whereas, a study reported in South Africa showed that 100% of isolates from commercial farms were susceptible to Vancomycin (Atebaet *et al.*, 2010). The

variations could be associated with the use of these antibiotics in dairy farms. Vancomycin is no longer used in veterinary medicine in many countries (Pace and Yang, 2006) including Tanzania, which may account for the results reported in this study.

The gold standard method for identifying MRSA is to detect the *mecA* gene or its product, PBP2a, by latex agglutination (Gosbell *et al.*, 2001). However, these tests are relatively expensive. Cefoxitin and oxacillin have been reported as surrogate markers for the detection of methicillin resistance (Fernandes *et al.*, 2005; Anand *et al.*, 2009; CLSI, 2014). In this study, 14.7%, 37.9% and 13.8% of isolates were phenotypically resistant to Cefoxitin, Oxacillin and co-resistance to both Cefoxitin and Oxacillin, respectively. This is an indicator of MRSA. MRSA strains in livestock including bovine milk samples have also been reported in China (Wang *et al.*, 2014), Pakistan (Alam *et al.*, 2016), USA (Smith, 2015), European countries (Johnson, 2011; Kock *et al.*, 2011), and African continent (Lozano *et al.*, 2016). Interestingly, variations in prevalence of MRSA have been reported in different Sub-Saharan Africa including 81.2 – 93.2% milk samples from communal farms versus 5.7% – 7.0% from commercial farms in South Africa (Ateba *et al.*, 2010), 60.3% in Ethiopia (Daka *et al.*, 2012), 28.57% in Nigeria (Maisiyama *et al.*, 2014), 15% in Morocco (Bendahou *et al.*, 2008), 7.8% in Kenya (Shitandi and Mwangi, 2004), and 2.38% to 4.17% in raw milk samples in Tanzania (Mohammed, 2015).

Based on the findings of this study, it is concluded that milk production is extremely vital to million households around the globe. In most developing countries, including Tanzania, milk is

produced by smallholders, and milk production contributes to household livelihoods, food security and nutrition. Milk provides relatively quick returns for small-scale producers and is an important source of cash income. Bovine mastitis is one of the most important diseases that have substantial consequences on the dairy industry and the public health as a whole. The detection of *S. aureus* in the milk samples indicates that the product is unwholesome for human consumption. A large proportion of the isolates obtained were resistant to three or more antibiotics, and a good number of these isolates were phenotypically confirmed as MRSA. Appropriate use of antimicrobials in animal husbandry could help to control the emergence of resistant strains and limit the acquisition of additional antimicrobial resistance genes in existing strains. A cost-effective policy in dairy cattle farms would consist of preventing MRSA colonization or intra-mammary infection by enforcing the same measures implemented for the *S. aureus* control, particularly focusing on the hygienic milking procedures and on the application of strict biosecurity measures.

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