


REVIEW

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Prevalence, antimicrobial susceptibility and genotypic characteristics of *Staphylococcus aureus* in Tanzania: a systematic review

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Abstract

Background: Data on the prevalence, genotypes and antibiotic resistance patterns of colonizing and infection-associated *Staphylococcus aureus* (*S. aureus*) strains both in humans and animals in Tanzania are scarce. Given the wide range of infections caused by *S. aureus* and the rise of methicillin-resistant *S. aureus* (MRSA) globally, this review aims at collecting published data on *S. aureus* bacterium to improve our understanding of its epidemiology in Tanzania.

Main body: We carried out a systematic review of scientific studies reporting on prevalence, antibiotic resistance and genotyping data pertaining to *S. aureus* in human and animal infection and colonization. The literature extracted from electronic databases such as PubMed and Google Scholar was screened for eligibility and relevant articles were included. The review is limited to manuscripts published in English language between the years 2010 and 2020. A total of 45 studies conducted in 7 of the 9 administrative zones in Tanzania were reviewed to gather data on *S. aureus* prevalence in humans and animals. Prevalence in humans ranged from 1 to 60%. Antibiotic resistance patterns of *S. aureus* isolated from colonized humans showed high resistance rates against co-trimoxazole (46%) and erythromycin (41%) as compared to reports from studies conducted outside Africa. The review suggests an increased MRSA prevalence of up to 26% as compared to 6–16% reported in previous years. Genotypic data reviewed suggested that MRSA predominantly belonged to ST88. The prevalence of *S. aureus* in animal studies ranged from 33 to 49%, with 4 to 35% of MRSA isolates. Most studies reported low antibiotic resistance levels, with the exception of penicillin (85%) and ampicillin (73%).

Conclusion: The prevalence of *S. aureus* and MRSA in Tanzania is rising, although clear variations between different geographic areas could be observed. Non-susceptibility to commonly prescribed antibiotics in community-associated *S. aureus* is of concern. Research strategies to ameliorate our knowledge on *S. aureus* epidemiology should employ regular antibiotic resistance surveillance, antimicrobial stewardship as well as genotypic characterization.

Keywords: *Staphylococcus aureus*, Prevalence, Antimicrobial resistance, Genotyping, Infection, Colonization, Tanzania

Background

Antimicrobial resistance (AMR) is a global concern estimated to account for approximately 700,000 deaths each year (O'Neill 2016). If no appropriate measures are

taken to slowdown the progression of this epidemic it is estimated that by 2050 it will cost the world around 10 million lives per annum (O'Neill 2016). The lack of development of new antimicrobial agents in the pipeline further emphasizes the necessity to reduce dependency on antibiotics by implementing infection control strategies (O'Neill 2016; WHO 2014).

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According to the 2014 World Health Organization (WHO) report, most regions stated over 50% bacterial resistance against third-generation antibiotics, particularly methicillin-resistant *S. aureus* (MRSA) clones in hospitals (WHO 2014). Furthermore in 2017, the WHO listed antibiotic-resistant bacteria including *Staphylococcus aureus* (*S. aureus*) as a priority bacterium to guide research, discovery and development of new antibiotics (WHO 2017). The report further recommended special attention to be directed towards the identified resistant bacteria due to their ability to rapidly develop resistance against multiple antibiotic classes hence limiting therapeutic options (WHO 2017).

Staphylococcus aureus is an old bacterium discovered in the eighteenth century, antibiotic resistance in the bacterium against penicillin was described in the 1950's, the penicillin-resistant staphylococci inactivates penicillin function by an enzyme called penicillinase or beta-lactamase which degrades the β -lactam ring in penicillin, thus altering the shape of penicillin and preventing its binding to the penicillin binding proteins (Haddadin et al. 2002). Following penicillin failure in treating *S. aureus* infections, methicillin was introduced. Methicillin was particularly effective upon its introduction into clinical therapy due to its ability to resist the action of β -lactamase. However, methicillin resistance in *S. aureus* was also reported only a year after its introduction. Strains of *S. aureus* resistant to methicillin or oxacillin or other β -lactam compounds are still termed MRSA, only to honour the historic role of methicillin that used to effectively treat staphylococcal infections, and it is to methicillin that the resistance was first described (Jevons 1961). Several terms are used to describe different MRSA strains associated with outbreaks in different settings based on strains' genomic background and level of virulence (Zetola et al. 2005). MRSA strains associated with hospital-acquired infections are commonly abbreviated to HA-MRSA, while strains causing community-associated infection are abbreviated to CA-MRSA and those associated with livestock are abbreviated as LA-MRSA.

Staphylococcus aureus is both a commensal and potentially harmful pathogen in humans and animals. The bacterium can give rise to a variety of infections ranging from mild skin and soft tissue infections to more serious and complex diseases such as pneumonia, septicemia, infective endocarditis and other deep-seated infections (e.g. osteomyelitis) in humans as well as mastitis and necrotic infections in a variety of animal hosts. *Staphylococcus aureus* can also colonize the skin and approximately 30% of the human population is found to be transiently colonized if nasal swabs are examined microbiologically.

High levels of MRSA have been reported across Africa, ranging between 43 and 72%, as reported in Cameroon, South Africa and Ethiopia (Founou et al. 2017). The vast majority of clinical *S. aureus*/MRSA data in Africa is associated with hospital acquired infection (HAI) affecting individuals with healthcare-related risk such as hospitalization, surgery and underlying chronic diseases (David 2010). Information on community-acquired *S. aureus*/MRSA infections (CAI) causing diseases in people with no healthcare-associated risk is also available on the continent even though to a lesser extent. Moreover, very limited data on livestock acquired *S. aureus*/MRSA infections (LAI) whereby *S. aureus* clones of animal origins colonize or cause infections in humans have been published in Africa (Founou et al. 2017). Further information on the antibiotic-resistant clones occurring in both human and animal are very limited, hindering comprehensive understanding of the epidemiology of the bacterium (Lozano et al. 2016).

Tanzania, a developing country located along the East African coast, housing a population of about 57 million people, of which 36% is engaged in livestock keeping as the major source of livelihood. The potential for human-animal contact is very high, especially in tribes that cohabit with their animals such as Maasai people. The aim of this review is to summarize literature reporting on the prevalence, antibiotic resistance of *S. aureus* in Tanzania. Furthermore, reported genotypic characterization of *S. aureus* will be reviewed to provide a more nuanced profile of *S. aureus* genetic diversity in colonization and infections both in animal and human hosts as well as their possible relationship.

Main text

Methods

Eligibility criteria

A systematic review of Tanzanian scientific studies reporting on prevalence, antimicrobial resistance and genotypic characterization of *S. aureus* from human and animal sources published between 2010 and 2020 was performed. Information sought for in the publications included commensal and clinical *S. aureus* recovered from different infections including invasive and non-invasive. Animal studies reporting on *S. aureus* recovered from animals and their products were also considered. All studies that recovered less than five *S. aureus* isolates as well as publications that were written in a language other than English were excluded from this review.

Information sources and search strategies

PubMed database was researched in November 2018 and February 2021 by a librarian using Boolean operators "AND" and "OR" to identify studies fitting our inclusion

criteria. The following search terms were used “*Staphylococcus aureus* OR *S. aureus* AND antimicrobial susceptibility OR antibiotic resistance AND prevalence AND Tanzania.” Additionally search words such as “Molecular typing AND *S. aureus* AND antibiotic resistance AND Tanzania” and “*Staphylococcus aureus* OR *S. aureus* AND antimicrobial susceptibility OR antibiotic resistance AND prevalence AND Tanzania” were used in Google scholar to identify eligible articles. The bibliographies of all eligible documents were hand-searched for additional publications eligible for review.

Data extraction and appraisal process

The Joana Briggs Institute checklist was applied to appraise and review the quality of each study accessed by two independent reviewers. A data extraction form was designed to capture required information such as author, year of publication, study period, methodology, MRSA identification strategies, *S. aureus* and MRSA prevalence, antibiotic resistance patterns as well as genotypic information. Two reviewers were involved in the process whereby the first reviewer (TM) extracted the information and the second reviewer (TK) double checked the information to eliminate possible bias. All disagreement raised during the critical appraisal process were resolved through reviewers discussions. All extracted literature was analysed using reference manager ENDNOTE7. This study followed the standardized scientific writing format of the Preferred Reporting Items for systematic reviews and meta-analyses (PRISMA) guidelines. The study has not taken on any meta-analysis due to the heterogeneity of the studies under review; nevertheless, mean resistance rates and prevalence were calculated to help present the results better.

Scope of the study

This review is limited to prevalence, antibiotic resistance patterns and genetic typing information [i.e. specified resistance and virulence genes, Staphylococcus protein A (*spa*) typing and multi-locus sequence typing] of *S. aureus* retrieved from human and animal hosts.

Results

PubMed search resulted in 18 eligible articles followed by an additional 13 articles included from the Google scholar search. Rigorous reference list review supplemented another 14 eligible publications making a total of 45 (Fig. 1).

Data concerning *S. aureus* prevalence, antimicrobial resistance and genotyping were extracted from studies performed in 7 zones of the 9 administrative zones in Tanzania. Table 1 describes the distribution of the published articles review in their consecutive zones. The

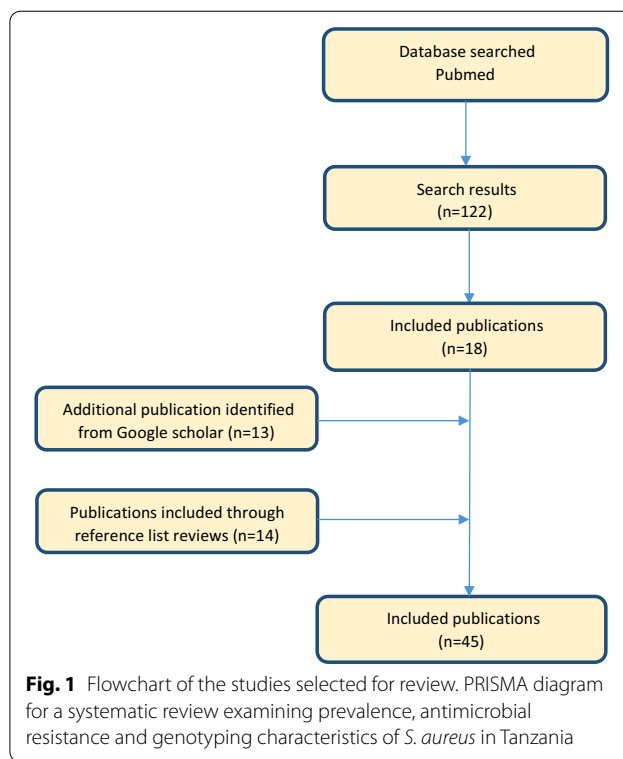


Table 1 Distribution of the reviewed *S. aureus* Studies by zone in Tanzania

| Zone | Human | Animal | Human and animal |
|-----------------------|-------|--------|------------------|
| Eastern Zone | 15 | 2 | 1 |
| Lake Zone | 15 | – | – |
| Northern Zone | 5 | 1 | – |
| Central | 1 | – | – |
| Zanzibar | 2 | 1 | – |
| East and lake Zone | 1 | – | – |
| Lake and Western Zone | 1 | – | – |
| Total | 40 | 4 | 1 |

majority of the publications reviewed were from regions in the eastern and lake zones (i.e. 40% and 33%, respectively), showing lack of *S. aureus* researched data in the other parts of the country.

The majority of the publications were reported in the Eastern and Lake Zones. *S. aureus* data of animal origin have been poorly represented throughout the country.

Prevalence, antibiotic resistance and genotyping of *S. aureus* isolated from humans

A total of 45 studies reported on prevalence, antimicrobial resistance and genetic characteristics of *S. aureus* in humans published between 2010 and 2020 in Tanzania as indicated in Table 1.

Prevalence of *S. aureus* in humans

Staphylococcus aureus prevalence was reported in 39 human-related studies, reporting a prevalence ranging from 6 to 69%. Higher infection rates were typically observed in SSTI's, nevertheless the bacterium was also implicated in other infections. Furthermore, it was notably observed that *S. aureus* colonization ranged around 10–60% in the three different zones that reported on colonization. The summary of *S. aureus* prevalence in colonization and different infections in human, as well as the geographic distributions reported in Tanzania between 2010 and 2020, is summarized in Table 2.

Antibiotic resistance in human *S. aureus* isolates

The primary method for establishing *S. aureus* antibiogram in the reviewed work was done phenotypically using the Kirby-Bauer disc diffusion test along with Clinical Laboratory Standard Institute (CLSI) guidelines. Kirby-Bauer is an antimicrobial susceptibility test based on the size of inhibition zones of microbial growth in a lawn culture around discs impregnated with the antimicrobial drug (Hudzicki 2009).

Twenty-four studies contributed information on antibiotic susceptibility of *S. aureus* bacteria. MRSA in most cases was identified by resistance against ceftazidime; however, one study used methicillin as their identification disc. As summarized in Table 3, extremely high resistance rates against β -lactams, i.e. penicillin (87–99%) and ampicillin (67–92%), were observed.

Apart from high resistance to the reported β -lactams, trimethoprim/sulphamethoxazole (co-trimoxazole) and erythromycin showed average resistance of 54% and 47%, respectively. Notably individual analysis of antibiotics susceptibility in isolates collected from colonization showed lower rates of resistance compared to *S. aureus* isolated from clinical infections, as summarized in Table 3.

Resistance rates of 50% (co-trimoxazole), 45% (clindamycin), 37% (erythromycin) and 32% (gentamicin) were observed in SSTI's. Unlike in commensal and SSTI-related isolates, blood born *S. aureus* showed higher resistance variation against most commonly used antibiotics (i.e. erythromycin, gentamicin, co-trimoxazole and clindamycin) ranging from 42 to 66%.

MRSA detection in all reported reviewed studies had an average prevalence of 21%, nevertheless 7 studies

reported on specific resistance patterns of MRSA isolates sighting higher rates against other antibiotics (clindamycin, erythromycin and co-trimoxazole) ranging from 50 to 100% (Joachim et al. 2018, 2017; Geoffrey et al. 2015; Moyo et al. 2014; Moremi et al. 2014) apart from the expected β -lactams antibiotic resistance.

Even though most articles reported 100% susceptibility to vancomycin, Geoffrey et al. 2015; Kayange et al. 2010; Seni et al. 2019a observed vancomycin resistance of above 10% in their respective studies (not demonstrated in Table 3).

Genotypic characterization of human *S. aureus* isolates

Five human-related studies were reviewed (summarized in Table 4). MSSA genotypic characterization by Staphylococcal protein A (*spa*) typing in one of the studies revealed 13 different *spa* types including one new *spa* type t10779. The most common *spa* types were t714 and t148 (associated with ST72) followed by t084 (ST15 and ST18) and t223 (ST 22). Furthermore, *spa* types t314 (ST121), t084 (ST15 and ST18) and t223 were reported to be shared by human and animal isolates in this study (Katakweba et al. 2016). In a more recent study whereby patients were swabbed for *S. aureus* carriage on admission, after their hospital stay as well as wound swabs for those who had SSTI's, the study further swabbed HCW attending the patients in question. Taking these groups into consideration 60 *S. aureus* were characterized by MLST, as in the other studies ST distribution was diverse. Eight STs were detected in the 17 isolates from admission of which ST8 (4/17) and ST5 (4/17) were dominant. Nine STs were detected among 13 acquired isolates typed of which ST152 (3/13) and ST5 (2/13) were predominant. Moreover in the 12 *S. aureus* SSTI isolates, eight STs were detected predominated by ST152 (3). Subsequently in a study which used the whole genome sequencing and multi-locus sequence typing (MLST) in their analysis reported 13 different sequence types predominated by ST8 (23%) followed by ST1 (13.3%) and ST152 (10%) (Kumburu et al. 2017). Unfortunately, the limited number of publications on genotypic MSSA data could not reveal dominance in any particular identified strain.

MRSA characterization was reported in three of the five publications (Moremi et al. 2019, 2012; Kumburu et al. 2017; Moremi et al. 2019) screened for the *mecA* resistance conferring gene as well as the Pantone–Valentine leukocidin (*pvl*) virulence gene by conventional PCR technique. All analysed 24 MRSA isolates harboured the *mecA* gene hence concordantly agreeing 100% with the phenotypic results. Of note 16.7% of the isolates also harboured the *pvl* gene. Further characterization of the isolates by MLST and *spa* typing was done. These typing methods categorized the isolates

Table 2 Human-related studies investigating *S. aureus* in different conditions and populations across Tanzania

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|--|---|---|-------------------------------------|---|-------------------------|
| 1 | 41.4% (157) | 37.6% (59) | Healthcare workers adults male and female from June 2016 to October 2016 | Nasal carriage | Dar es Salaam (Eastern zone) | Joachim et al. (2018) |
| 2 | NR | 11.8% in ICU patients and 2.1% in ICU HCW | ICU patients (male and female of all age groups) and ICU HCW from October 2012 to March 2013 | Nasal carriage | Dar es Salaam (Eastern zone) | Geoffrey et al. (2015) |
| 3 | 34.5% (89) in swabs collected on admission 20% (4) in swabs collected 48 h after admission | 24.7% (22) from samples on admission, and 50% (2) in samples collected after 48 h | Patients admitted to emergency or medical ward aged 5 and above | Nasal carriage | Dar es Salaam (Eastern zone) | Joachim et al. (2017) |
| 4 | 40% (114) | 8.3% (12) | Healthy children <5years From April 2010 to June 2010 | Nasal carriage | Dar es Salaam (Eastern zone) | Moyo et al. (2014) |
| 5 | Overall 23.2% (223), whereby 26.2% (95), detected in children with acute respiratory infection and 21.4% (128) were detected in children without acute respiratory infection | NR | Children 2–10 years old aged with axillary temperature of $\leq 38^{\circ}\text{C}$ Dar es Salaam from April to August 2008 (DSM) and June to December 2008 (Ifakara) | Nasal carriage | Dar es Salaam and Morogoro (Eastern zone) | Chochua et al. (2016) |
| 6 | 13.2% (138) | NR | Healthy children <5years born after mass distribution of Azithromycin for trachoma control. The study was conducted in 2014 | Nasal carriage | Kilosa, Morogoro (Eastern zone) | Bloch et al. (2017) |
| 7 | 2.2% (22) | 0% | 100 nasal swabs from healthy individuals with no epidemiological connection were collected within urban and peri-urban Morogoro Municipalities | Nasal carriage | Morogoro (Eastern zone) | Katakweba et al. (2016) |
| 8 | 13.2% (245) | 23.3% (57) | Male and female of all age groups who were subjected to microbiology testing between January 2005 and December 2009 (Retrospective study) | Bacteremia | Dar es Salaam (Eastern zone) | Moyo et al. (2010) |
| 9 | 28% (12) | NR | Male and female sickle cell anaemic patients of all age groups seeking healthcare at MNH from January 2006 to December 2008 | Bacteremia | Dar es Salaam (Eastern zone) | Makani et al. (2015) |

Table 2 (continued)

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|--|-----------------------|---|--|---|-------------------------------|
| 10 | In blood 36.5% (27), and in pus swabs 52.3% (132) | NR | Neonates aged 3–26 days suspected with neonatal sepsis. Study duration October 2009–January 2010 | Bacteremia and wound swabs | Dar es Salaam (Eastern zone) | Mhada et al. (2012) |
| 11 | 12.2% (18) | 44.4% (8) | 100 participants (male and female aged 18–80 years) with clinical evidence of Surgical site infection. Duration from September 2011 to February 2012 | Wound infections | Dar es Salaam (Eastern zone) | Manyahi et al. (2014) |
| 12 | 71.4% (132) | 0.8% (1) | Skin and soft tissue infections patients of all age groups | Wound infections | Bagamoyo (Eastern zone) | Kazimoto et al. (2018) |
| 13 | 48.3% (131) | NR | Asymptomatic otitis media (OM)-associated bacteria found in patients living with HIV | Ear colonization | Morogoro (Eastern zone) | Mwambete and Eulambius (2018) |
| 14 | Overall 28.4% (57/201) whereby the distribution was 56.3% (40/71) in blood samples, 20.4% (7/34) in pus samples, 23.1% (3/13) and 7.5% (6/80) in urine and sputum samples respectively | NR | Patients of all age groups presenting different infections. The study was conducted between July and November 2019. About 201 clinical samples were included in the study | Bacteremia, wound infection, urinary tract infection and pulmonary infection | Dar es Salaam (Eastern Zone) and Mwanza (Lake Zone) | Mikomangwa et al. (2020) |
| 15 | 22.7% (5) in Blood culture 9.3% (8) in endocervical culture | 53.8 (7/13) | 197 qualified woman aged between 20–35 years admitted in the maternity wards between Dec. 2017 and April 2018 for postnatal care with clinical diagnosis of puerperal sepsis at MNH | Blood samples and Endocervical swabs | Eastern Zone | Kiponza et al. (2019) |
| 16 | The overall carriage rate of <i>S. aureus</i> was 21.0% (66). 4.7% (31) were from preclinical students while 53% (35) from clinical students | 1.5% (1) | Healthy students (Clinical and Pre clinical) aged 18 years and above. Study duration February to June 2013 | Nasal carriage | Mwanza (Lake zone) | Okamo et al. (2016) |

Table 2 (continued)

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|--|--|---|-------------------------------------|--------------------|-----------------------|
| 17 | <ul style="list-style-type: none"> – 13.9% (129) in patients screened on admission – 9.6% (29/301) acquired SA after their hospital stay – 7.7% (11/143) in HCW – 21.1% (12/57) in patients who developed SSI during their hospital stay | <ul style="list-style-type: none"> – 5.4% (7/129) in patients screened on admission – 10.3% (3/29) acquired MRSA – 1.4% (2/143) in HCW – 3.5% (2/57) in SSI patients | 930 patients were enrolled between Dec.2014 and Sep.2015 from two healthcare centres in Mwanza, Nasal swabs were collected on admission ad discharge, additionally wound swabs were collected in patients who had developed SSI during their hospital stay. Subsequently nasal swabs from HCW attending the enrolled patients were collected for analysis | Nasal carriage and wound infections | Mwanza (Lake Zone) | Moremi et al. (2019) |
| 18 | 21.5% | 28% (9) | 300 neonates with clinical neonatal sepsis | Bacteremia | Mwanza (Lake zone) | Kayange et al. (2010) |
| 19 | 14.8% (8) | 50% (4) | 402 malnourished children aged < five years Study duration September 2012–January 2013 | Bacteremia | Mwanza (Lake zone) | Ahmed et al. (2017) |
| 20 | 17.0% (23) | 34.7% (8) | 950 children aged < 5 years with signs and symptoms of blood stream infections were enrolled from 4 Healthcare facilities including district, regional and referral hospitals with in Mwanza. Study was conducted between July 2016 and October 2017 | Bacteremia | Mwanza (Lake Zone) | Seni et al. (2019a) |
| 21 | 13.7% (29) | 79% (23) | Patients of all age groups and gender with lower limb ulcers seen at the surgical ward or outpatient department from November 2010 to April 2012 | Wound infection | Mwanza (Lake zone) | Mbunda et al. (2012) |
| 22 | 8.9%(18) | 44.4% (8) | Patients of all age groups with chronic lower limb ulcers seen at the surgical ward. 300 wound infection were swabbed between November 2011 and February 2012 | Wound infection | Mwanza (Lake zone) | Moremi et al. (2014) |

Table 2 (continued)

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|---|-----------------------|--|-------------------------------------|--------------------|-----------------------|
| 23 | 28.6% (18) | 1.9% (3) | 65 patients of all age groups who underwent major surgery at BMC between July 2009 and June 2010 | Surgical site wound infection | Mwanza (Lake zone) | Mawalla et al. (2011) |
| 24 | 27.3% (6) | 16.7% (1) | Woman aged 14–44 years who have developed surgical site infections after having undergone a caesarean Sections 345 women were swabbed between October 2011 and February 2012 | Surgical site wound infection | Mwanza (Lake zone) | Mpogoro et al. (2014) |
| 25 | 29.2% (7) | NR | 162 patients of all age group and gender who underwent major limb amputations at BMC between March 2008 and February 2010. 24 of the participants had surgical site infections out of which different bacteria were recovered as the cause of infection | Surgical wound infection | Mwanza (Lake zone) | Chalya et al. (2012) |
| 26 | 59.3% | NR | All patients of all age groups and gender presenting with animal-related injuries at the BMC between September 2007 and August 2011. Post-operative wound infection was the most commonest complication reported lead by <i>S. aureus</i> infections | Surgical site wound infections | Mwanza (Lake zone) | Gilyoma et al. (2013) |
| 27 | Overall prevalence 16.1 (25) out of which 28% (7) were isolated in HIV positive patients and 72%(18) in HIV negative patients | NR | The study was done to compare magnitude of bacterial resistance to co-trimoxazole/ other antimicrobials among isolates from HIV infected patients on co-trimoxazole prophylaxis and those not on prophylaxis and non-HIV patients attending BMC between January and October 2012 | Urine and wound swabs | Mwanza (Lake zone) | Marwa et al. (2015) |

Table 2 (continued)

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|--|--|---|--|--|----------------------|
| 28 | 18.2% (34) | 41.2% (14) | 301 patients aged > 1 year who presented with ear discharge for more than 6 weeks and tympanic membrane perforation at the ENT department between October 2013 and March 2014 were recruited into the study | Ear infection | Mwanza (Lake zone) | Mushi et al. (2016) |
| 29 | Overall 22.8% (100) Blood 80% (80) Pus swabs 18% (18) Other infections 2% (2) | Only 78 were subjected to AST.34.6% (27) were MRSA | A total of 3330 microbiological culture results scripts representing non-repetitive specimens reported between June 2013 and May 2015 were retrieved and analysed for pathogens and their susceptibility patterns using STATA-11 software | Bacteremia, wound infection, urinary tract infection and pulmonary infection | Mwanza (Lake zone) | Moremi et al. (2016) |
| 30 | 8.7% (28) | NR | 1828 pregnant woman with significant bacteriuria seeking healthcare at different healthcare facilities within the north-western part of the country. The woman were recruited from dispensaries, health centres, district and regional/referral Hospitals | Urinary infection | Mwanza, Shinyanga, Tabora (Lake and Western Zones) | Seni et al. (2019b) |
| 31 | 69.25 | 28.5% | 74 Patients aged between 8–20 years undergoing surgical treatment at BMC. Majority of the patients were male with history of abuse | Bone fragments collected during surgery | Mwanza (Lake Zone) | Silago et al. (2020) |
| 32 | 55.3% (68) | NR | Primary school children (aged 6–15 years) from 4 schools in Moshi municipality assessed/self-reported respiratory tract infection symptoms. The community-based study was conducted between January and March 2014 | Nasal and Throat swabs | Moshi (Northern zone) | Ngocho et al. (2015) |

Table 2 (continued)

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|---|---|--|---|---------------------------------|-----------------------|
| 33 | 66% (103) at 6 weeks, 36% (47) at 3 months and 24% (33) at 6 months. 38% (17) mothers were colonized by <i>S. aureus</i> parallel to their children | NR | Children born to HIV positive mothers attending RCH clinics to establish prevalence and influence of nasal pharyngeal bacterial colonization on children. Nasal swabs from children were taken at 6 weeks (n = 156), 3 (n = 136) and 6 (n = 130) months consecutively. Mothers (45) of the infants were also swabbed at 3- and 6-month visits (Study duration 2005–2009) | Nasal carriage | Moshi (Northern zone) | Kinabo et al. (2013) |
| 34 | 16% (23) | NR | Patients presenting with SSI, infected diabetic wounds, infected wounds due to trauma, and patients with other infected wounds admitted in surgical ward (study duration July 2013 to June 2014) | Wound infections | Moshi (Northern zone) | Kassam et al. (2017) |
| 35 | 9.3% (35) of which 82.9 (29) were from wound infections, 1.1% (4) from blood samples and 6% (2) from sputum samples | Only 22 isolates were subjected to AST. 27.3% (6) were MRSA | People admitted to the medical or surgical wards at KCMC between 2013 and 2015. The study collected stool, sputum, blood and wound/pus samples from patients of all age groups to describe causative agents of different infections | Wound infection Blood infection Bronchial infection | Moshi (Northern zone) | Kumburu et al. (2017) |
| 36 | 9.1% (6) | NR | A total of 867 patients aged between 2–5 years with fever above 37 °C were enrolled between January and October 2013. 373 urine samples were collected and 66 tested positive for UTI. All <i>S. aureus</i> isolates were recovered from UTI patients | Urinary tract infection | Tanga (Korogwe) (Northern zone) | Mahende et al. (2014) |

Table 2 (continued)

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|-----------------------------------|-----------------------|---|-------------------------------------|----------------------|------------------------|
| 37 | 17% (17) | NR | Children aged 0–12 years dismissed from the hospital with pneumonia diagnosis. 100 children were enrolled in the attempt to characterize aetiology of community-acquired pneumonia. (Study duration August 2014–April 2015) | Blood infection | Itigi (Central zone) | Caggiano et al. (2017) |
| 38 | 11.3% (9) | 0% | Febrile adults and children seeking care at the Mnazi mmoja hospital between March 2012– April 2013 | Blood infection | Zanzibar | Onken et al. (2015) |
| 39 | 6.3% (5) | 0% | Febrile patients seeking outpatient healthcare at 3 different district hospitals (Wete, Chake Chake, and Mkoani) on Pemba island between March 2009 to December 2010 | Blood infection | Zanzibar | Thriemer et al. (2012) |

NR Not reported

Table 3 Antimicrobial resistance rates of *S. aureus* in humans

| Antibiotic (N*) | (% range) | Mean resistance (n/N*) | (%) | References |
|--|-----------|------------------------|--------|---|
| Resistance rates in <i>S. aureus</i> isolates from human colonization | | | | |
| Penicillin(420) | (96–100) | (416/420) | (99%) | Joachim et al. (2018), Geoffrey et al. (2015), Joachim et al. (2017), Moremi et al. (2019) |
| Ampicillin (151) | (84–100) | (133/151) | (88%) | Katakweba et al. (2016), Okamo et al. (2016), Ngocho et al. (2015) |
| Tetracycline (381) | (9–95) | (103/381) | (27%) | Geoffrey et al. (2015), Moyo et al. (2014), Katakweba et al. (2016), Okamo et al. (2016), Moremi et al. (2019) |
| Erythromycin (402) | (19–100) | (163/402) | (41%) | Joachim et al. (2018), Geoffrey et al. (2015), Okamo et al. (2016), Moremi et al. (2019) |
| Gentamicin (540) | (9–34) | (105/540) | (21%) | Joachim et al. (2018), Joachim et al. (2017), Moyo et al. (2014), Katakweba et al. (2016), Moremi et al. (2019), Ngocho et al. (2015) |
| Co-trimoxazole (443) | (14–66) | (205/443) | (46%) | Joachim et al. (2018), Geoffrey et al. (2015), Moyo et al. (2014), Katakweba et al. (2016), Moremi et al. (2019) |
| Ciprofloxacin (233) | (4–11) | (15/233) | (6%) | Joachim et al. (2017), Moyo et al. (2014) |
| Clindamycin (336) | (9–76) | (33/336) | (9.8%) | Joachim et al. (2018), Geoffrey et al. (2015), Moremi et al. (2019) |
| Cefoxitin (546) | (2–100) | (103/546) | (19%) | Joachim et al. (2018), Geoffrey et al. (2015), Moyo et al. (2014), Okamo et al. (2016), Moremi et al. (2019) |
| Resistance rates in <i>S. aureus</i> isolates from invasive (blood-borne) infections | | | | |
| Penicillin (46) | (23–80) | (40/46) | (87%) | Kayange et al. (2010), Onken et al. (2015), Thriemer et al. (2012) |
| Ampicillin (50) | (85–100) | (46/50) | (92%) | Mhada et al. (2012), Seni et al. (2019a) |
| Erythromycin (60) | (20–66) | (38/60) | (63%) | Kayange et al. (2010), Seni et al. (2019a), Thriemer et al. (2012) |
| Gentamicin (50) | (26–56) | (21/50) | (42%) | Mhada et al. (2012), Seni et al. (2019a) |
| Co-trimoxazole (69) | (22–96) | (46/69) | (66%) | Kayange et al. (2010), Seni et al. (2019a), Onken et al. (2015), Thriemer et al. (2012) |
| Clindamycin (32) | (44) | (14/32) | (44%) | Kayange et al. (2010) |
| Methicillin (245) | (23) | (57/245) | (23%) | Moyo et al. (2010) |
| Cefoxitin (69) | (0–32) | (17/69) | (25%) | Kayange et al. (2010; Seni et al. (2019a), Onken et al. (2015), Thriemer et al. (2012) |
| Resistance rates in <i>S. aureus</i> isolates from non-invasive infections | | | | |
| Penicillin (202) | (30–100) | (183/202) | (91%) | Manyahi et al. (2014), Kazimoto et al. (2018), Moremi et al. (2014), Marwa et al. (2015), Moremi et al. (2012) |
| Ampicillin (263) | (47–88) | (177/263) | (67%) | Mhada et al. (2012), Mwambete and Eulambius (2018) |
| Tetracycline (67) | (6–45) | (14/67) | (21%) | Marwa et al. (2015), Mushi et al. (2016), Moremi et al. (2012) |
| Erythromycin (221) | (14–46) | (81/221) | (37%) | Moremi et al. (2014), Marwa et al. (2015), Mushi et al. (2016), Moremi et al. (2012) |
| Gentamicin (339) | (11–52) | (110/339) | (32%) | Mhada et al. (2012), Mwambete and Eulambius (2018), Moremi et al. (2014), Mushi et al. (2016), Moremi et al. (2012) |
| Co-trimoxazole (232) | (43–74) | (115/232) | (50%) | Mwambete and Eulambius (2018), Moremi et al. (2014), Marwa et al. (2015), Mushi et al. (2016) Seni et al. (2019b), Moremi et al. (2012) |
| Ciprofloxacin (187) | (4–25) | (20/187) | (17%) | Mwambete and Eulambius (2018), Marwa et al. (2015), Mushi et al. (2016) |
| Clindamycin (42) | (21–63) | (19/42) | (45%) | Moremi et al. (2014), Moremi et al. (2012) |
| Cefoxitin (226) | (1–100) | (55/226) | (24%) | Manyahi et al. (2014), Kazimoto et al. (2018), Moremi et al. (2014), Mushi et al. (2016), Moremi et al. (2012) |

Table 4 *S. aureus* genetic diversity as described by the reviewed publications

| Host | Sample type | Resistant gene | Virulence factor | spa Type | MLST | References |
|-------|---|---|--|---|--|-------------------------|
| Human | Wound, pus, nasal swabs (24 MRSA strains from previous studies) | <i>mecA</i> (100%) | <i>pvl</i> (16.7%) | t7231, t690, t064, t104, t1855, t7237, t186, t667 | ST88, ST1719, ST8, ST1820 | Moremi et al. (2012) |
| Human | Blood, sputum, wound/pus | <i>mecA</i> (33.3%) | <i>pvl</i> (16.7%), <i>tst</i> (6.7%) both in non <i>mecA</i> isolates | ND | ST8, ST1, ST152, ST1719, ST15, ST1847, ST188, ST22, ST239, ST30, ST5, ST580, ST6, ST97 | Kumburu et al. (2018) |
| Human | Nasal swabs | <i>mecA</i> and <i>mecC</i> (None detected) | NS | t714, t148, t084, t002, t223, t314, t311, t015, t451, t690, t1849, t2030, t10779* | ST15, ST18, ST72, ST22, ST5, ST121, ST231, ST45, ST8 | Katakweba et al. (2016) |
| Pig | Nasal swab | <i>mecA</i> and <i>mecC</i> (None detected) | NS | t131 | ST80 | Katakweba et al. (2016) |
| Dog | Nasal swabs | <i>mecA</i> and <i>mecC</i> (None detected) | NS | t084, t127, t223, t314, t267, t508, t1476 | ST15, ST18, ST1, ST22, ST121, | Katakweba et al. (2016) |
| Human | Nasal and SSTI swabs | <i>MecA</i> (exact information disclosed) | <i>pvl</i> (8.3%) | t148, t355, t002, t4353, t095, t223, t311, t690, t1257 | ST88, ST3118, ST152, ST5, ST72, ST508, ST22, ST4266*, ST612 | Moremi et al. (2019) |
| Human | Nasal, SSTI swabs | <i>dfrA</i> , <i>dfrG</i> and <i>dfrK</i> . <i>dfrG</i> detected by (37%) | NS | ND | ND | Nurjadi et al. (2014) |

ND Not done, NS not screened

in four sequence types. ST88 predominated by 52.2% ($n = 13$), followed by ST1719 at 29.2% ($n = 7$), ST8 and ST 1820 were assigned to 3 and 1 isolates, respectively. Of the 4 *pvl* positive isolates three belonged to ST88 and one to ST1820 (a single locus variant of ST 88). All isolates were ultimately divided into two clonal complexes, i.e. CC8 and CC88 (Moremi et al. 2012). In a subsequent study by Moremi et al. (2019) whereby conventional PCR methods were used so screen for *mecA* and *pvl* an account on the characterization of some of the MRSA analysed was given. The study reported that one MRSA from a healthcare worker nasal carriage belongs to ST88 and was *pvl* positive; furthermore, they reported that 2 SSTI-related MRSA were characterized to belong to ST612 (Moremi et al. 2019). Kumburu et al. (2018) on the other hand characterized MRSA using whole genome sequencing method. Of the 30 isolates analysed, 33.3% ($n = 10$) were confirmed to harbour the *mecA* resistance conferring gene. Among the identified 10 MRSA, 6 belonged to ST8 and 2 belonged to ST239, the remaining two had unknown sequence type. Furthermore, none of the MRSA strains harboured the *pvl* or toxin shock syndrome (*tst*) virulence genes (Moremi et al. 2016).

Nurjadi et al. 2014 while researching on trimethoprim resistance genes in *S. aureus* isolated from

Sub-Saharan Africa determined that 100% of the Tanzanian *S. aureus* in the study which were phenotypically trimethoprim resistant in fact harboured trimethoprim conferring resistance genes (Nurjadi et al. 2014).

Prevalence, antibiotic resistance and genotyping of *S. aureus* isolated from animals

As indicated in Table 5, few studies ($n = 5$) have reported on prevalence, antimicrobial resistance and genetic characteristics of *S. aureus* in animals published between 2010 and 2018 in Tanzania.

Prevalence of *S. aureus* in animals

Five publication reported on prevalence of *S. aureus* in animals whereby the most examined sample in animals was milk ($n = 4$). Prevalence of *S. aureus* varied in different geographic areas. Kashoma et al. (2018) and Mohammed et al. (2018) reported the highest prevalence at 49% and 41% in Morogoro, respectively. Suleiman and Mdegela (2018) did not fall far back when observing a prevalence of 37% describing subclinical mastitis in cows on Unguja Island. The lowest prevalence of 33% was recorded in a study aiming at assessing raw milk quality in Arusha and Meru District (Ngasala et al.

Table 5 *S. aureus* prevalence in animal-related samples

| S. no | Prevalence <i>S. aureus</i> % (n) | Prevalence MRSA % (n) | Population | Source of <i>S. aureus</i> isolates | Location | References |
|-------|--|--|---|-------------------------------------|---|-----------------------------|
| 1 | Milk: 49% (49) Cow nasal swabs: 28% (37) | Milk: 35% (17) Cow nasal swabs: 16% (6) | 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. All 3 farms carried out mixed animal farming | Milk samples and cow nasal swabs | Morogoro (Eastern zone) | Kashoma et al. (2018) |
| 2 | 41% (48) | 4% (3) | The study involved 18 of the 29 Wards within Morogoro Municipality. In each of the selected wards, sales points and local shops where raw milk is sold were randomly selected. A total of 117 milk samples. The study was conducted between January and June 2015 | Milk samples | Morogoro (Eastern zone) | Mohammed et al. (2018) |
| 3 | 37% (217) | NR | Study conducted between January and July 2014 on Unguja Island to establish prevalence of subclinical mastitis in smallholder dairy cows and pattern of antimicrobial susceptibility of major mastitis pathogens | Milk samples | Unguja (Zanzibar) | Suleiman and Mdegela (2018) |
| 4 | 33% (30) | NR | 105 milk samples from smallholder dairy farmers, milk vendors and retailers were taken within Arusha City and Meru District to assess the quality of raw milk and stakeholders' awareness on milk-borne health risks and factors for poor milk hygiene | Milk samples | Arusha city and Meru district (Northern zone) | Ngasala et al. (2015) |
| 5 | Pig nasal swabs 4% (4) Dog nasal swabs 11% (11) | Pig swabs: 0% Dog nasal swabs: 0% | 100 pigs and 100 dogs dwelling in urban and peri-urban Morogoro Municipality | Nasal swabs | Morogoro (Eastern zone) | Katakweba et al. (2016) |

NR Not reported

2015). Generally prevalence of *S. aureus* seemed to be much lower in swabs taken from nasal cavities. Kashoma et al. (2018) who took nasal swabs from cows observed a *S. aureus* prevalence of 28% whereas Katakweba et al. (2016) observed a prevalence of 4% and 11% in pig and dog nasal swabs, respectively.

MRSA detection in milk-associated studies varied tremendously ranging from 4 to 35% (Mohammed et al. 2018; Kashoma et al. 2018), even though both studies were conducted in Morogoro township. Furthermore, MRSA prevalence in isolates recovered from cow nasal cavities was repowered at 16% (Suleiman and Mdegela 2018), whereas no MRSA was detected in pigs and dogs nasal swabs (Kashoma et al. 2018).

Antibiotic resistance in animal originated *S. aureus* isolates

Four studies described antibiotic resistance in *S. aureus* using different antibiotic pallets which included cephalixin, gentamicin, kanamycin, neomycin, tetracycline, streptomycin, amoxicillin, cephalixin, clindamycin, vancomycin, ampicillin, co-trimoxazole, oxacillin and ceftiofur. This review, however, focused on the most reported antibiotics in this area as indicated in Table 6.

Most of the reviewed studies reported low antibiotic resistance levels with exception of penicillin and ampicillin which showed mean resistances rates of 85% and 73%, respectively. Suleiman and Mdegela (2018) also further

observed resistance against amoxicillin and cephalixin at a rate of 47% and 30%, which was unfortunately not reported by any of the other reviewed studies. Moreover, Tetracycline, co-trimoxazole and cephalixin were reported to have a resistance proportion of 30%, 32% and 30%, respectively.

MRSA detection in all studies was confirmed by resistance against ceftiofur and/or oxacillin, whereby mean resistance rates of 10% and 17% were observed, respectively. An average of 8% resistance against vancomycin was observed, reported in 3/5 studies as described in (Table 6).

Genotypic characterization of animal originated *S. aureus* isolates

Genotypic data retrieved from 2 of the 5 studies were reviewed. In both, real-time-PCR (qPCR) was used to confirm *S. aureus* as well as screening for *mecA* resistance conferring gene. Katakweba et al. (2016) additionally screened for *mecC*, a recently discovered *mecA* homologue said to have the potential to be mis-categorized as methicillin-sensitive *S. aureus* (MSSA). None of the two resistance conferring genes were detected in this study; however, *S. aureus* was confirmed in 4 pigs and 11 dog samples, respectively. Further *spa* typing of the pig originating MSSA characterized them

Table 6 Antimicrobial resistance rates of *S. aureus* in animals *

| Antibiotic (N*) | Range % | Mean resistance (n/N*) | (%) | References |
|--|----------|------------------------|-------|---|
| Resistance rates in different studies in animals | | | | |
| Penicillin(265) | (72–88) | (225/265) | (85%) | Mohammed et al. (2018), Suleiman and Mdegela (2018) |
| Ampicillin (99) | (62–100) | (72/99) | (73%) | Katakweba et al. (2016), Kashoma et al. (2018) |
| Tetracycline (364) | (16–73) | (110/364) | (30%) | Katakweba et al. (2016), Mohammed et al. (2018), Kashoma et al. (2018), Suleiman and Mdegela (2018) |
| Erythromycin (301) | (5–23) | (28/301) | (9%) | Kashoma et al. (2018), Suleiman and Mdegela (2018) |
| Gentamicin (99) | (6–25) | (4/99) | (4%) | Katakweba et al. (2016), Kashoma et al. (2018) |
| Co-trimoxazole (132) | (22–40) | (42/132) | (32%) | Mohammed et al. (2018), Kashoma et al. (2018) |
| Vancomycin (132) | (2–11) | (10/132) | (8%) | Katakweba et al. (2016), Mohammed et al. (2018), Kashoma et al. (2018) |
| Amoxicillin (217)* | (47) | (102/217) | (47%) | Suleiman and Mdegela (2018) |
| Cephalixin (217)* | (30) | (64/217) | (30%) | Suleiman and Mdegela (2018) |
| Oxacillin (147) | (0–34) | (25/147) | (17%) | Katakweba et al. (2016), Mohammed et al. (2018), Kashoma et al. (2018) |
| Ceftiofur (132) | (4–17) | (13/132) | (10%) | Mohammed et al. (2018), Kashoma et al. (2018) |

* Reported in only one study

as *spa* type t131 associated with ST80. Additionally isolates of dog origin were characterized as *spa* types t314 (ST121), t084 (ST15 and ST18) and t223 (ST22) all of which were also identified in human nasal isolates reported in the same study.

In the study by Mohammed et al. (2018), both coagulase positive ($n = 46$) and coagulase negative ($n = 2$) *S. aureus* were detected in their milk samples. *mecA* gene was detected in two coagulase positive and one coagulase negative *S. aureus* isolate making this study the first in Tanzania to report on coagulase negative *S. aureus* harbouring the *mecA* gene. Of the 3 MRSA isolates phenotypically detected in the study, one was genotypically coagulase negative *S. aureus* characterized as *spa* type t2603, whereas the other two MRSA's were *spa* un-typable.

Discussion

The publications under review showed that *S. aureus* was isolated in a number of infections including SSTI's, bloodstream, otitis media, respiratory tract and urinary tract infections staying true to characteristically causing a wide range of infections.

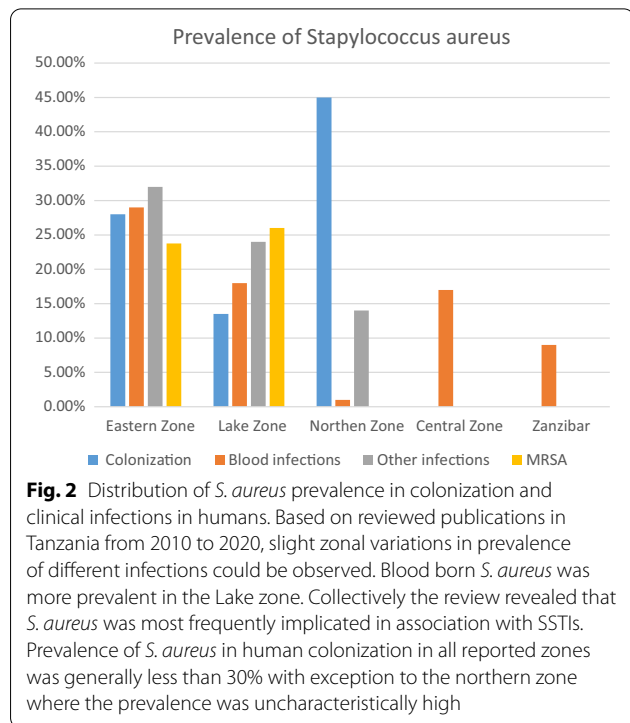
This review observed a *S. aureus* average prevalence ranging from 1 to 45% in human (Fig. 2). However, particularly higher infection rates were typically observed in SSTI's.

Furthermore, it was notably observed that *S. aureus* colonization ranged between 28 and 45% (Fig. 2) indicative of considerable circulation of both hospital- and community-associated *S. aureus* in the country. Considering the wide range of infections *S. aureus* can cause especially in various vulnerable populations such as children, elderly and the immune compromised individuals which was also observed in this review, there is need to emphasize the necessity to establish a reliable and sustainable surveillance system to monitor the *S. aureus* bacterium countrywide.

This review discovered that the antibiotic resistance patterns in colonization strains recorded uncharacteristically high proportions. Mean resistance rates of 41%, 27% and 46% against erythromycin, co-trimoxazole and tetracycline could be observed, respectively, whereas resistance rates of the same antibiotics reported in colonization strains in Europe and some parts of Asia did not exceed 20% (Heijer et al. 2013; Lestari et al. 2008). Contrary to resistance pattern in clinical *S. aureus* observed in this review were in accordance with other reports around Africa (Shittu and Lin 2006; Onwubiko and Sadiq 2011). As in many parts recorded resistance against β lactams was high. Resistance rates ranging from 30 to 65% against erythromycin, gentamicin, co-trimoxazole and clindamycin were also described in this review. The affected antibiotics are readily available in the community and also commonly used for empirical treatment of different cases of bacterial suspected infections. A notable presence of resistance against these antibiotics is an indication of their failure in treatment and a need for broader class antibiotics which are expensive and not accessible for most Tanzanians.

The two zones that reported on MRSA prevalence showed immense variation in their studies; however, on average prevalence was reported to be around 26% (Fig. 2). More than a third of the included studies reported prevalence above 25%. This shows that MRSA prevalence has risen in the last 10 years. Abdulgader's review on MRSA prevalence on the African continent categorized Tanzania as belonging to countries with low MRSA prevalence ranging from 6 to 16% between the years 2001 and 2009 (Abdulgader et al. 2015). This observed abrupt increase should be taken seriously by employing active antibiotic stewardship as well as directing more research efforts towards understanding and preventing the spread of these strains.

A wide spectrum of MSSA *spa* types and sequence types (ST) were identified in the reviewed studies. With the limited information gathered no dominance could be reported. Nevertheless, most *pvl* positive MSSA clones associate with skin infections identified in this review belonged to ST152 which concurs with the findings from



other African-based studies (Ruffing et al. 2017). Genetic characterization of MRSA strains has managed to categorize them into five predominant sequence types, i.e. ST8, ST1719, ST 1820, ST239, ST612 and ST88. Most characterized MRSA were *pvl* negative consistent with the findings by Abdulgader et al. (2015) who suggested that Africa is predominated by *pvl* negative MRSA belonging to ST88. Even though some important information was apparent in this review, data concerning MSSA and MRSA genotyping is still limited, Kumburu et al. (2018) was the only study that reported on other virulence factors apart from *pvl*, hence the scarcity of knowledge on *S. aureus* virulence factors circulating in our communities. Furthermore, genotypic characterization studies predominantly focused on screening for the *mecA* gene; the β -lactam-associated resistance gene, neglecting other resistant markers for other commonly used antibiotic in the country. Katakwebwa et al. (2016) was the only study that screened for *mecC* gene; a *mecA* homologue which has been identified in other studies to be associated with causing infection in humans with animal contact (Petersen et al. 2013). This homologue can easily be misdiagnosed as MSSA hence causing consequences on patient management as well as on antimicrobial resistance surveillance strategies. In order to make informed decisions about disease prevention and management, there is a need for extended surveillance as well as genotypic based research in Tanzania.

Studies reporting on prevalence, antimicrobial resistance and genetic characteristics of *S. aureus* in animals published between 2010 and 2020 in Tanzania were few; only 5 studies were included in this review, scantily representing a small area in the country. As in human, animal *S. aureus* isolates seem to harbour highly resistance rates against to penicillin and ampicillin antibiotics. Mean resistance rates against oxacillin (17%) and tetracycline (30%) were further able to describe the effects of over-using oxytetracycline previously stated as the most used antibiotic in the livestock keeping business in Tanzania (Caudell et al. 2017).

Staphylococcus aureus is one of the leading causes of bovine mastitis which explains the fact that the majority of publications included in this review concerning *S. aureus* in animals addressed the pathogen in clinical and sub-clinical mastitis or in regards to milk production quality. This has been instrumental in the reviews failure to make a link in describing either animals or humans acting as potential *S. aureus* reservoir for each other, as well as the effect of such in both public and animal health. Very few studies on genomic *S. aureus* characterization were available for review and did not suffice in showing such linkage. Even so one publication reported on the

genetic characteristics managed to confirm *S. aureus* strains belonging to the same *spa* type found to colonize both dogs and humans. Unfortunately, the humans and animals involved in this study were epidemiologically unrelated hence making it impossible to link the two. These findings nevertheless present a clear possibility for the *S. aureus* strain to infect across host species.

The primary method for establishing *S. aureus* anti-biogram in the reviewed work was done phenotypically by using the Kirby-Bauer disc diffusion test along with CLSI guidelines. This method has been reported to have inherent shortcomings such as being highly dependent on experimental conditions that may affect end results (Reller et al. 2009). With this fact in mind the Kirby Bauer antibiogram results would have to be confirmed by another test of a different principle to prevent over reporting of resistance, particularly in the confirmation of MRSA and Vancomycin resistant *S. aureus* strains. In this review, four studies had MRSA confirmed genotypically which showed 100% agreement with the phenotypic Kirby-Bauer disc diffusion test. This agreement between the methods should encourage the use of the Kirby-Bauer disc diffusion test as an antibiotic sensitivity monitoring strategy in the country, since it is the most available and affordable method in the Tanzanian setting.

Information about prevalence, antibiotic susceptibility and genotypic characteristics of *S. aureus* originating from different hosts and sources in Tanzania still remains scarce. It is evident that the majority of the publications included in this review are from research institutions or tertiary hospitals affiliated to universities with health-related focuses hence most information could be derived from three focal points MNH in Dar es Salaam, BMC Mwanza and, KCMC Moshi, respectively (i.e. Northern, Lake and Eastern zones). According to the Tanzania National Bureau of Statistics the focal regions represented in this review earn higher income per capital compared to the zones whereby no information could be gathered. This implies that most of the data obtained for review are based in relatively well to do regions (Tanzania National Bureau of Statistics 2018). No published data between 2010 and 2020 on the epidemiology of *S. aureus* were available for the southern and western parts of the country, which are home to some of the most impoverished regions in Tanzania (refer to Fig. 3). It is well known that poverty struck areas also face other challenges as poor health-care facilities and access, lack of basic needs such as food, proper housing and sanitation, which in turn leaves the population ridden by different infectious diseases (Alvarez-Uria et al. 2016). Furthermore, since the income gained by the poor is mainly for subsistence,



Fig. 3 Tanzania administrative zones. Modified map adopted from Suleiman 2018 (Suleiman 2018). Tanzania regions are classified into 9 zones: 1. Eastern Zone (Morogoro, Pwani and Dar es Salaam) 2. Northern Zone (Arusha, Kilimanjaro and Tanga); 3. Lake Zone (Kagera, Mwanza, and Mara); 4. Western Zone (Kigoma, Tabora and Shinyanga); 5. Central Zone (Dodoma, Manyara and Singida); 6. South West Highlands (Katavi, Mbeya and Rukwa); 7. Southern Highlands Zone (Iringa, Njombe and Ruvuma); 8. Southern Zone (Lindi and Mtwara) and 9. Zanzibar Zone

the tendency to resort to self-treatment and or consulting traditional healer is very high (Green et al. 2015) all of which are known indicators associated with driving antibiotic resistance (Byarugaba 2004).

Limitations

The data from this review cannot be generalized as true prevalence, antibiotic resistance patterns or genotypic

characterization of *S. aureus* bacterium in Tanzania, there is lack of *S. aureus* studies representation from other zones. High inter-study variations such as type of specimen analysed, objective of studies, time frame as well as methods employed including criteria set for resistance/MRSA confirmation may have influenced the outcome.

Methods used to genetically characterize *S. aureus* in this review were very divergent from simple PCR to whole genome sequencing. The data collected in these methods had different focuses which made comparing the results between studies difficult. Since the main objective in characterizing *S. aureus* or any other bacteria for that matter is understanding the genetic similarities and differences in conferring antibiotic resistance, strain type as well as virulence factors, it would therefore be useful to have a common guideline that allowing inter-laboratory comparability to gather more reliable and holistic data meant to guide treatment and infection prevention strategies in the country.

Conclusions

With the insight this review has given it is evident that prevalence of *S. aureus* and MRSA in Tanzania is rising, although clear variations between different geographic areas could be observed. Furthermore, non-susceptibility to commonly prescribed antibiotics in community-associated *S. aureus* is also of concern hence the need to emphasize further collection of inf epidemiology (susceptibility patterns and genotypic characterization) data of all bacteria of public health and animal health importance in Tanzania to gain a comprehensive description of the burden of the bacteria as well as enable proper strategies guiding empirical infections treatment and management in the country.

Abbreviations

AMR: Antimicrobial resistance; AST: Antibiotic susceptibility testing; BMC: Bugando medical centre; CAI: Community-acquired infection; CLSI: Clinical laboratory standard institute; CNS: Coagulase negative Staphylococcus; HAI: Hospital acquired infection; HCW: Healthcare workers; ICU: Intensive care unit; KCMC: Kilimanjaro Christian Medical Centre; LAI: Livestock acquired infections; MLST: Multi-locus sequence typing; MNH: Muhimbili National Hospital; MRSA: Methicillin-resistant *Staphylococcus aureus*; MSSA: Methicillin-sensitive *Staphylococcus aureus*; ND: Not done; NR: Not reported; NS: Not Screened; OM: Otitis media; RCH: Reproductive and child health; Spa: Staphylococcus protein A; SSI: Surgical site infection; SSTI's: Skin and soft tissue infections; ST: Sequence type; UTI: Urinary tract infection; WHO: World Health Organization.

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Authors' contributions

TM and TK were responsible for the concept, design, reviewing studies for the manuscript. JM contributed in literature search strategies and data extraction method. MB, RM and MM took part in revising important contents of the manuscript. TM drafted the manuscript. TK and SLB critically reviewed the manuscript for publication. All authors read and approved the final manuscript.

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Availability of data and materials

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Declarations

Ethics approval and consent to participate

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Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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