Antimicrobial resistance and genomic analysis of staphylococci isolated from livestock and farm attendants in Northern Ghana

Beverly Egyir¹*, Esther Dsani², Christian Owusu-Nyantakyi¹, Grebstad Rabbi Amuasi¹, Felicia Amoa Owusu¹, Emmanuel Allegye-Cudjoe³ and Kennedy Kwasi Addo¹

Abstract

Background: The emergence of antimicrobial resistant bacteria in food producing animals is of growing concern to food safety and health. Staphylococci are common inhabitants of skin and mucous membranes in humans and animals. Infections involving antibiotic resistant staphylococci are associated with increased morbidity and mortality, with notable economic consequences. Livestock farms may enable cross-species transfer of antibiotic resistant staphylococci. The aim of the study was to investigate antimicrobial resistance patterns of staphylococci isolated from livestock and farm attendants in Northern Ghana using phenotypic and genotypic methods. Antimicrobial susceptibility testing was performed on staphylococci recovered from livestock and farm attendants and isolates resistant to cefoxitin were investigated using whole genome sequencing.

Results: One hundred and fifty-two staphylococci comprising S. sciuri (80%; n = 121), S. simulans (5%; n = 8), S. epidermidis (4%; n = 6), S. chromogens (3%; n = 4), S. aureus (2%; n = 3), S. haemolyticus (1%; n = 2), S. xylosus (1%; n = 2), S. cohnii (1%; n = 2), S. condimenti (1%; n = 2), S. hominis (1%; n = 1) and S. arlettae (1%; n = 1) were identified. The isolates showed resistance to penicillin (89%; n = 135), clindamycin (67%; n = 102), cefoxitin (19%; n = 29), tetracycline (15%; n = 22) and erythromycin (11%; n = 16) but showed high susceptibility to gentamicin (96%; n = 146), sulphamethoxazole/trimethoprim (98%; n = 149) and rifampicin (99%; n = 151). All staphylococci were susceptible to linezolid and amikacin. Carriage of multiple resistance genes was common among the staphylococcal isolates. Genome sequencing of methicillin (cefoxitin) resistant staphylococci (MRS) isolates revealed majority of S. sciuri (93%, n = 27) carrying mecA1 (which encodes for beta-lactam resistance) and the sal(A) gene, responsible for resistance to lincosamide and streptogramin. Most of the MRS isolates were recovered from livestock.

Conclusion: The study provides insights into the genomic content of MRS from farm attendants and livestock in Ghana and highlights the importance of using whole-genome sequencing to investigate such opportunistic pathogens. The finding of multi-drug resistant staphylococci such as S. sciuri carrying multiple resistant genes is of public health concern as they could pose a challenge for treatment of life-threatening infections that they may cause.

Keywords: Staphylococci, Antimicrobial resistance, Multi-drug resistance, WGS, Ghana

Background

Staphylococci are the most common bacteria found on the skin and mucous membranes of mammals [1]. Bacteria of this genus are usually commensal organisms and can be divided into two groups based on their ability to produce the enzyme coagulase [2]. Pathogenic infections...
may result from colonization with staphylococci if primary skin barriers are compromised due to trauma [3]. Among the species producing coagulase, *Staphylococcus aureus* is of primary importance to human and animal health. *S. aureus* is a notable cause of mastitis in livestock and has been associated with bacteremia, skin and soft tissue infections in humans [4, 5].

The less pathogenic group of coagulase negative staphylococci (CoNS) have garnered interest in recent times due to their increasing role in the occurrence of opportunistic infections [6]. CoNS-related infections in humans have been associated with the presence of foreign bodies and immunosuppressive states of patients [7]. *Staphylococcus epidermidis* falls within the category of CoNS and is the most common cause of foreign body related blood stream infections in humans [8]. *S. epidermidis* and *S. chromogens* have been isolated in subclinical and clinical mastitis cases in cattle [9]. CoNS are known carriers of transferable genetic elements that contribute to the survival of some strains of *S. aureus* and are often cited as reservoirs of resistance genes [10].

The emergence of antimicrobial resistance (AMR) in staphylococci, though partly dependent on innate microbial characteristics, is mainly driven by antimicrobial use [11, 12]. *S. aureus* are known to adapt and gain resistance to nearly all antibiotics used to treat it. Concurrent resistance to non-β-lactam agents such as quinolones, tetracyclines, aminoglycosides, macrolides and lincosamides are increasingly reported among methicillin resistant strains of staphylococci, further diminishing the treatment options available for infected humans or animals [13]. Methicillin resistance is attributed to the production of a transpeptidase (PBP2a), encoded by the mecA gene within the staphylococcal cassette chromosome [14]. Methicillin resistant *S. aureus* (MRSA) infections often result in increased morbidity and an increase in health care associated costs [15].

Mounting evidence suggests that the development of resistance in commensal pathogens of livestock origin contribute to the persistence of carriage of these resistant organisms in humans. Antimicrobials are used routinely in livestock production and its misuse in livestock farming often leads to emergence of resistance due to selective pressure on microbes like staphylococci exposed to antibiotics [16]. Colonized livestock may spread resistant strains directly to humans or indirectly through the food chain [17]. The detection of MRSA in humans that have been linked to animals has heightened concerns of its ability to be transferred among species [18]. Livestock farmers, veterinarians, wool sorters, meat hygiene inspectors and people who frequently visit livestock farms have been found to be at increased risk for MRSA colonization [19].

The presence of multidrug resistant strains of staphylococci in livestock have implications for food safety and contribute to the global challenge of AMR [20]. Knowledge on carriage rates of resistant strains of CoNS in livestock is scarce in Ghana; such information is necessary to inform antimicrobial policies and improve integrated surveillance on antimicrobial resistance. Findings from antimicrobial susceptibility testing of bacteria species such as CoNS offer vital information for surveillance but are limited when it comes detection of clones, resistance and virulence of bacteria pathogens. Genomic sequencing on the other hand, provides massive information for characterizing bacteria species [21] including staphylococci. This study therefore sought to characterize staphylococci recovered from livestock and farm attendants in the Northern part of Ghana using phenotypic and genotypic methods.

**Results**

**Farm attendant characteristics**

Majority of the farm attendants were male (89%). The age of farm attendants ranged from 14 to 58 years. Daily participation in livestock rearing activities such as feeding, grazing and handling was reported by all 19 respondents. Most of the livestock attendants worked primarily on only one type of livestock (84%). Three attendants worked with more than one livestock type. Most of the farm attendants lived on the farm (83%) and had been working on the farm for at least eight years (78%).

**Nasal carriage of staphylococci**

Of the 311 nasal swabs collected from livestock and 19 samples collected from farm attendants, 152 staphylococcal isolates were recovered. Staphylococci were obtained in close to half of livestock samples (45%; *n* = 149) and in most farm attendant samples (58%; *n* = 11). Most of the isolates (98%; *n* = 149) were CoNS, with three isolates (2%) identified as *S. aureus*. Ten different CoNS species were confirmed, with *S. sciuri* being the most prevalent (80%; *n* = 121). Others include *S. simulans* (5%; *n* = 8), *S. epidermidis* (4%; *n* = 6), *S. chromogens* (3%; *n* = 4), *S. haemolyticus* (1%; *n* = 2), *S. xylosus* (1%; *n* = 2) *S. cohnii* (1%; *n* = 2), *S. condimenti* (1%; *n* = 2), *S. hominis* (1%; *n* = 1) and *S. arlettae* (1%; *n* = 1).

*S. sciuri* was found in nasal swabs from all livestock types in this study. *S. epidermidis* was isolated only from nasal swabs obtained from farm attendants. *S. haemolyticus* was isolated from human and sheep samples. *S. condimenti* was found only in pigs, whilst *S. hominis* and *S. arlettae* were isolated only in sheep. Six different species of staphylococci were found in samples from goats and consisted of *S. sciuri*, *S. simulans*, *S. aureus*, *S. xylosus*, *S. chromogens* and *S. cohnii* (Table 1).
Antimicrobial resistance in staphylococcal isolates

Isolates from farm attendants were mainly resistant to penicillin (100%; n = 11), tetracycline (55%; n = 6), cefoxitin (27%; n = 3), clindamycin (36%; n = 4), sulphamethoxazole/trimethoprim (27%; n = 3), erythromycin (18%; n = 2) and gentamycin (18%; n = 2). All staphylococcal isolates from farm attendants were susceptible to linezolid, amikacin and rifampicin. Isolates obtained from livestock were mainly resistant to penicillin (88%; n = 124), clindamycin (70%; n = 98), cefoxitin (18%; n = 26), tetracycline (11%; n = 16) and erythromycin (10%; n = 14) (Table 2). Among isolates from livestock, resistance to gentamicin and rifampicin was less prevalent (3%; n = 4 and 1%; n = 1). All cefoxitin resistant isolates (19%; n = 29) were susceptible to vancomycin.

The predominant isolates detected, S. sciuri were resistant to 6 out of 10 antimicrobials agents tested in all: penicillin (94%; n = 114), clindamycin (80%; n = 97), cefoxitin (22%; n = 27), tetracycline (8%; n = 10), erythromycin (8%; n = 10) and gentamicin (2%; n = 3). S. epidermidis isolates were resistant to seven out of 10 antimicrobials with a single isolate exhibiting resistance to six antibiotic agents. Half (50%; n = 3) of S. epidermidis isolates were resistant to sulphamethoxazole/trimethoprim. Although low numbers of S. xylosus isolates were identified, resistance was detected to five out of 10 antibiotics (penicillin, clindamycin, tetracycline, erythromycin and rifampicin). S. aureus isolates recovered were resistant to penicillin, tetracycline and erythromycin. S. chromogens and S. cohnii were susceptible to all tested antibiotic agents except penicillin (Table 3).

Of the 152 staphylococci isolated, 49 (32%) were MDR. Overall, MDR rates were higher in farm attendants (45%; n = 5) than in livestock (31%; n = 44).

Genomic analysis of cefoxitin resistant staphylococci

Whole-genome sequencing of the cefoxitin-resistant isolates revealed that all S. sciuri possessed mecA1 gene, while S. epidermidis and S. haemolyticus harbored mecA gene. Tetracycline resistance genes

| Parameter | Humans | Cattle | Sheep | Goat | Pig | Total |
|-----------|--------|--------|-------|------|-----|-------|
| No. of isolates | 11 | 19 | 71 | 32 | 19 | 152 |
| Staphylococcal species | | | | | | |
| S. epidermidis | 6 | - | - | - | - | 6 |
| S. haemolyticus | 1 | - | 1 | - | - | 2 |
| S. xylosus | 1 | - | - | - | - | 2 |
| S. sciuri | 3 | 18 | 65 | 21 | 14 | 121 |
| S. aureus | - | - | 2 | 3 | 3 | 8 |
| S. simulans | - | - | 1 | 1 | 2 | 4 |
| S. chromogens | - | 1 | 1 | 2 | - | 4 |
| S. cohnii | - | - | - | - | - | 2 |
| S. hominis | - | - | 1 | - | - | 1 |
| S. arlettae | - | - | 1 | - | - | 1 |
| S. condimenti | - | - | - | - | 2 | 2 |

Table 2: Antimicrobial resistance of staphylococci isolated from livestock and farm attendants, 2018

| Antimicrobial resistance of staphylococci isolated from livestock and farm attendants, 2018 |
|---------------------------------|---------------------------------|---------------------------------|---------------------------------|
| Antimicrobial agent | Livestock n = 141 (%) | Farm attendants n = 11 (%) | Total N = 152(%) |
|---------------------|---------------------|---------------------|---------------------|
| Penicillin | 124 (88) | 11 (100) | 135 (89) |
| Clindamycin | 98 (70) | 4 (36) | 102 (67) |
| Cefoxitin | 26 (18) | 3 (27) | 29 (19) |
| Tetracycline | 16 (11) | 6 (53) | 22 (15) |
| Erythromycin | 14 (10) | 2 (18) | 16 (11) |
| Gentamicin | 4 (3) | 2 (18) | 6 (4) |
| Rifampicin | 1 (1) | 0 (0) | 1 (1) |
| Sulphamethoxazole-Trimethoprim | 0 (0) | 3 (27) | 3 (2) |
| Amikacin | 0 (0) | 0 (0) | 0 (0) |
| Linezolid | 0 (0) | 0 (0) | 0 (0) |
Table 3  Pattern of antimicrobial resistance of staphylococcal isolates, 2018

| S. sciuri | 121 | Pen | Clin | Cef  | Tet  | Ery  | Gen | Rif  | STX- |
|----------|-----|-----|------|------|------|------|-----|------|------|
| S. epidermidis | 6   | 114 (94) | 97 (80) | 27 (22) | 10 (8) | 10 (8) | 3 (2) | - | - |
| S. haemolyticus | 2   | 6 (100) | 1 (17) | 1 (17) | 5 (83) | 2 (33) | 1 (17) | - | 3 (50) |
| S. xylosus | 2   | 2 (100) | 1 (50) | 1 (50) | 1 (50) | 1 (50) | - | - | - |
| S. simulans | 8   | 1 (12.5) | - | - | - | 3 (38) | - | - | - |
| S. chromogens | 4   | 3 (75) | - | - | - | - | - | - | - |
| S. cohnii | 2   | 1 (100) | - | - | - | - | - | - | - |
| S. hominis | 1   | 1 (100) | - | - | - | - | - | 1 (100) | - |
| S. arlettae | 1   | 1 (100) | 1 (100) | - | 1 (50) | - | - | - | - |
| S. condimenti | 2   | - | - | - | 1 (50) | - | - | - | - |
| S. aureus | 3   | 3 (100) | - | - | - | 2 (67) | 1 (33) | - | - |
| Total (N, %) | 152 | 135 (89) | 102 (67) | 29 (19) | 22 (15) | 16 (11) | 6 (4) | 1 (0.7) | 3 (2) |

Discussion

The findings of this study show that multidrug-resistant staphylococci are prevalent in livestock and farm attendants on the farms sampled. The detection of S. sciuri, S. aureus, S. xylosus, S. simulans, S. chromogens, S. cohnii, S. hominis, S. arlettae and S. condimenti are consistent with previous reports on prevalence of CoNS in livestock [22, 23]. S. sciuri was the most prevalent staphylococci identified in this study (80%) and was isolated in both livestock and farm attendants. Primarily considered a livestock-associated bacterium, S. sciuri can be found in large numbers in the farm environment [22]. Though the colonizing population may be low outside the farm environment, they are found to readily adapt and persist in health care settings and thus may pose a threat to human health [23]. S. sciuri has been associated with pneumonia and septicemic shock in Grasscutter (Thryonomys swinderianus) in Ghana [24]. This pathogen was detected in China as the causative organism for endocarditis [25] and in Thailand, as the agent in a food poisoning outbreak investigation [26].

S. aureus was detected in samples from three goats and none contained the mecA gene (MRSA). This is in sharp contrast with reports from other geographic areas [9]. Of note, the CoNS that were resistant to cefoxitin and also positive for mecA1 in this study originated from livestock. Previous studies in Ghana however, found MRSA among farm attendants and none from livestock [27]. MRSA may be more prevalent in intensive farming systems where antimicrobials are used in the production chain more frequently, and in hospital settings due to selective pressure of bacteria in these environments and their presence in colonized inpatients [28].
and *S. xylosus* were frequently detected in samples from farm attendants. This concurs with previous reports that identified *S. epidermidis* as the most frequently occurring CoNS found on skin and mucosae in humans [1]. *S. epidermidis* and *S. haemolyticus* have increasingly been associated with nosocomial infections and are described to be highly adaptable to medical devices hence the need to monitor carriage rates in humans [29].

The level of resistance of staphylococci to critically needed antimicrobial agents is a growing public health concern. The overall prevalence of MDR was 32%, with higher rates observed for farm attendants. The high rate of resistance to penicillin observed in this study is consistent with previous reports on staphylococci from both clinical and non-clinical samples in Ghana [27, 30–34] and elsewhere [35, 36] thus, was expected.

The proportion of isolates resistant to tetracycline was higher in isolates from farm attendants (55%) as compared to livestock (11%), and this is in concordance with the rates of tetracycline resistance in staphylococci. More than half of CoNS from livestock attendants (*S. epidermidis, S. haemolyticus*) were tetracycline resistant. Tetracycline resistance in all livestock in this study was lower (11%) than was reported in *S. aureus* isolates recovered from livestock (47%) in a previous study in Ghana [27] and from chicken droppings (74%) elsewhere [37]. This observation can be attributed to the frequency of its use in the various farming systems.

Tetracycline and its derivatives are often used as part of feed for growth promotion and prophylaxis in intensive poultry farming. Though its use in livestock is widespread, oral preparations are not common.

Resistance to sulphamethoxazole/trimethoprim (STX) was found in *S. epidermidis*, from three farm attendants. STX has been used in the treatment of infections caused by community-acquired *S. aureus*; resistance to this agent among methicillin resistance strains may point to a reduction in its efficacy due to exposure [38]. High susceptibility of isolates to vancomycin, linezolid, amikacin, rifampicin and gentamicin is crucial for the treatment of severe infections in humans. A notable example is the use of vancomycin for the treatment of MRSA infections [39].

Phylogenetic analysis of MRS isolates showed close genetic relatedness between isolates recovered from humans and livestock, suggesting that these pathogens may not be host-specific. The observation could also reflect possible transmission between the different hosts.

The *mec* variants (*mecA* and *mecA1*) found in the MRS have been linked to resistance to beta-lactam antibiotics in staphylococci [40]. Several studies have pointed to *mecA1* detected in *S. sciuri* as an evolutionary ancestor of the *mecA* gene found in MRSA [40–42]. *mecA1* gene is naturally adapted to *S. sciuri* resistance to beta-lactams due to changes in the promoter region of this gene have been reported [40, 43].
The high levels of resistance to clindamycin among the isolates can be linked to the sal(A) gene detected in majority of the S. sciuri (93%) isolates. sal(A) is located between two housekeeping genes of the core genome of S. sciuri subspecies; it encodes for resistance to lincosamide and streptogramin antibiotics [44].

The plasmids detected in this study harbored antibiotic resistance genes. Many resistance determinants are plasmid-mediated, and this has been demonstrated in previous studies on staphylococci [45]. Horizontal transfer of plasmids can occur among staphylococcal strains of different species although data on plasmid distribution in staphylococci are scarce [10, 46]. In this study, seven different plasmid sequences were detected based on the sequences of their rep genes. The most prevalent sequence was rep7a, which is similar to studies conducted on the sequences of their rep genes. The most dominant rep genes in S. aureus isolates [47].

Co-occurrence of rep7a plasmid with tet(K) gene was observed in three isolates. Similarly, the occurrence of rep7a plasmid with cat(pC221) was observed in one isolate. This is consistent with reports of strong association between this plasmid, tetracycline and chloramphenicol resistance [48, 49]. Tetracycline resistance genes: tet(K), (M) and (L) have been reported among staphylococci recovered from clinical and non-clinical samples in African countries including Ghana [27, 33, 35, 50] suggesting that these genes are widely disseminated in these regions.

The potential risks of transfer of plasmid-borne AMR genes from S. sciuri to other Staphylococcus species was previously reported by Li et al., [51] pointing to the need to routinely monitor AMR gene carriage on plasmids in coagulase negative staphylococci. The presence of AMR genes borne on plasmids in CoNS isolated supports the evidence that CoNS may serve as reservoirs for the spread of AMR [10]. Dissemination of plasmids carrying multiple resistance genes will substantially limit the efficacy of antibiotic agents and urgently warrants surveillance of staphylococci from animal and human sources. Previous studies have shown that plasmid sequence associated with rep16 and rep20 was prevalent in clinical S. aureus and S. haemolyticus isolates [52]. rep13, rep16, rep19, rep22 and rep20 have also been detected in S. aureus isolates from different geographic regions with rep16 carrying multiple resistance genes [53, 54]. To the best of our knowledge, the co-occurrence of erm(B), dfrK, aadD resistance genes and replicon plasmids rep16, rep22, repP767 in ST 226 S. epidermidis has not been reported from farm attendants in previous studies in Ghana. Interestingly, ST 226 S. epidermidis was detected in a blood sample of a neonate in Ghana and from hospital and community settings in China [55, 56]; on the other hand, ST30 S. haemolyticus found in this study, has also been detected in blood stream and catheter related infections from India, often showing vancomycin heteroresistance [57, 58] thus, confirming invasive characteristics of these CoNS clones.

**Conclusion**

The study provides insights into the genomic content of MRS from farm attendants and livestock in Ghana and therefore highlights the importance of using whole-genome sequencing to investigate such opportunistic pathogens. CoNS may serve as reservoirs for transmission of resistant genes to S. aureus at the farm level among livestock and farm attendants. The finding of multi-drug resistant CoNS including S. sciuri carrying multiple resistant genes is of public health concern as they could pose a challenge for treatment of life-threatening infections that they may cause.

**Materials and methods**

**Study sites and sample collection**

The Northern region is a major hub for livestock production in Ghana, consisting of numerous smallholder and pastoral farming systems [59]. Samples were collected in July 2018 from one multi-species livestock breeding station and four livestock farms in the Northern region of Ghana (Fig. 2). The Livestock breeding station was selected purposively due to its role in the livestock supply chain in the Northern region. The four farms were selected randomly from 2 districts in the region which were integrated with households in four communities. Nasal swabs were obtained from three hundred and eleven (311) livestock and nineteen (19) farm attendants. Livestock on selected farms were selected randomly within their pens or sheds making sure to collect samples from at least five pens on farms with more than five pens. On farms with very few pens (≤5) samples were collected from at least three pens.

All nasal swabs were placed in 10 ml of Mueller–Hinton broth (Oxoid Ltd., Basingstoke, UK), supplemented with 6.5% NaCl in sterile tubes and labeled. Samples were immediately transported on ice to the laboratory for testing. Data on demographic characteristics for each livestock attendant was collected using a semi-structured questionnaire.

**Identification of S. aureus and Coagulase Negative Staphylococci**

Pre-enrichment was carried out by incubating samples in Mueller–Hinton broth with 6.5% NaCl for 48 h at 37 °C. A volume of 10 µl of each sample was then plated on Mannitol salt agar and incubated for 48 h at 37 °C. Based on the colony morphology and ability to ferment
mannitol, presumptive colonies were streaked on 5% sheep blood agar (Oxoid Ltd., Basingstoke, UK), and incubated for 24 h at 37 °C. Identification of staphylococci was achieved by using the matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) instrument. Briefly, the procedure for MALDI-TOF MS involved spreading well isolated colonies from overnight cultures on a steel target plate. This film is then overlaid with 1 µl of formic acid and allowed to dry for 15 min. 1 µl of matrix preparation containing cyan-4-hydroxy-cinnamic acid in 50% acetonitrile with 2.5% trifluoroacetic acid was placed on each sample and left to dry for a further 15 min. MALDI-TOF MS was then conducted and ionization peaks generated were matched against the integrated reference library for speciation of the bacteria [60, 61].

Antimicrobial susceptibility testing of staphylococci

Antimicrobial susceptibility testing was performed using Kirby Bauer’s disk diffusion method with 10 antimicrobial agents: (cefoxitin (30 µg), amikacin (30 µg), penicillin (1 unit), rifampicin (5 µg), clindamycin (2 µg), erythromycin (15 µg), gentamycin (10 µg), sulphamethoxazole/trimethoprim (25 µg), tetracycline (30 µg), linezolid (10 µg). The measured diameters of the zones of inhibition were interpreted according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines [62]. The minimum inhibitory concentration of cefoxitin-resistant isolate was done using vancomycin using E-test strips (bioMerieux) and interpreted based on EUCAST guidelines. Multidrug resistance was defined as resistance to three or more antimicrobial agents [63].

Whole-genome sequencing and Analysis

Whole-genome sequencing was performed on all cefoxitin-resistant isolates using the illumina Miseq platform. DNA of freshly cultured isolates was extracted using Qiagen DNA MiniAmp kit following the manufacturer’s instructions. Extracted DNA was quantified using Qubit 4.0 Fluorometer assay kit (Thermo Fisher Scientific, MA), followed by library preparation with illumina DNA prep following the manufacturer’s instructions. The quality and concentration of fragmented DNA were assessed with the 2100 bioanalyzer system (Agilent) and qPCR (Kapa Sybr Fast qPCR kit) respectively. Libraries were then pooled and loaded on illumina 2 × 300 cycle cartridge for sequencing on Miseq platform (Illumina Inc., San Diego, CA).

Raw sequenced reads were quality filtered and trimmed using FASTQC (http://www.bioinformaticsb abraham.ac. uk/ projects/fastqc/) and Trimmomatic (http://www.usadellab.org/cms/index.php?page=trimmomatic) respectively with a minimum quality set at Q20 [64, 65]. Trimmed reads were
de-novo assembled with Unicycler V0.4.9 from which only contigs greater than 200 bp were used for further analysis.

Assembled files were uploaded to Resfinder (https://cge.cbs.dtu.dk/services/ResFinder/), a tool available on Center for Genomic Epidemiology platform to detect resistance genes present in the sequenced isolates using an identity threshold of 90% and a minimum length of 60%. Plasmids and mobile genetic elements were predicted using PlasmidFinder (https://cge.cbs.dtu.dk/services/PlasmidFinder/) and MGEfinder (https://cge.cbs.dtu.dk/services/MobileElementFinder/) respectively. The sequence types of the isolates were predicted using MLSTFinder (https://cge.cbs.dtu.dk/services/MLST/).

Assembled sequences were mapped to a reference genome (GenBank accession number LS483305.1) and a core maximum likelihood phylogenetic tree was constructed using CSI phylogeny tool on Center for Genomic Epidemiology (CGE). Analysis was performed with default parameters. The resultant tree was annotated in the Interactive Tree of Life (iTOL) [66].

Acknowledgements
The research team is thankful to farm attendants and farm owners of selected farms for their participation in the study.

Authors' contributions
BE was involved in the design of this study and supervision of all aspects of the study. BE, ED, CON, GRA, and FO were involved in sample and data collection, laboratory testing, interpretation of data and drafting of the manuscript. EAC and KKA contributed to the writing of the manuscript. All authors contributed to the writing of the manuscript and approved the final manuscript.

Funding
This study was supported by the University of Ghana Research Fund [URF/9/ILG-067/2015–2016] and The DELTAS Africa Initiative [Africa One – ASPIRE/DEI-15–008]. Africa One – ASPIRE is funded by a consortium of donors including the African Academy of Sciences (AAS), Alliance for Accelerating Excellence in Science in Africa (AESA), the New Partnership for Africa’s Development Planning and Coordinating (NEPAD) Agency, the Wellcome Trust [107753/A/15/Z] and the UK government. Sequencing of cefoxitin positive faecal samples and sequencing of cefoxitin negative faecal samples was supported by the Fleming fund/SEQAFRICA project.

Availability of data and materials
The data sets used during the current study are available from the corresponding author on reasonable request.

Declarations
Ethics approval and consent to participate
Ethical clearance for this study was obtained from the institutional review board (IRB) (FWA00001824) and Animal Care and Use Committee at Noguchi Memorial Institute for Medical Research (2016–01–3 N) for human and animal research activities respectively. All methods were performed in accordance with the relevant guidelines and regulations for field studies and research on animals. Informed consent to participate in the study was obtained from farm owners and farm attendants. In the case of farm attendants who were minors, informed consent was also obtained from legal guardians. Samples collected were coded, and any information obtained was used for the study and remains confidential.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

Author details
1 Department of Bacteriology, Noguchi Memorial Institute for Medical Research, University of Ghana, Accra, Ghana. 2 Regional Veterinary Laboratory, Ho, Volta Region, Ghana. 3 Central Veterinary Laboratory, Pong-Tamale, Northern Region, Ghana.

Received: 2 August 2021 Accepted: 1 July 2022
Published online: 21 July 2022

References
1. Otto M. Staphylococcus colonization of the skin and antimicrobial peptides. Expert Review of Dermatology. 2010;5:183–95.
2. Winn W, Allen S, Janda W, Koneman E, Procop G, Schreckenberger P, et al. Isolation of Pathogenic Gram-Negative Bacteria from Urinary Tract Infected Patients [Internet]. 2006 [cited 2022 Mar 15]. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1922007/
3. Cunha MLRS, Calsolari RA. Toxicity of Staphylococcus aureus and coagulase-negative staphylococci: epidemiological and molecular aspects. Microbiol Insights. 2008;1:MBI–S796.
4. Tong SYC, Davis JS, Eichenberger E, Holland TL, Fowler VG. Staphylococcus aureus infections: Epidemiology, pathophysiology, clinical manifestations, and management. Clin Microbiol Rev. 2015;28(3):603–61.
5. Flu C. Live associations and Coagulase-negative Staphylococcus aureus. Clin Microbiol Infect. 2012;18:735–44.
6. Heilmann C, Ziebuhr W, Becker K. Are coagulase-negative staphylococci virulent? Clin Microbiol Infect. 2019;25:1071–80.
7. Von Eiff C, Arciola CR, Montanaro L, Becker K, Campoccia D. Emerging Staphylococcus aureus species as new pathogens in implant infections. 2006.
8. Sievert DM, Ricks P, Edwards JR, Schneider A, Patel J, Srinivasan A, et al. Antimicrobial-Resistant Pathogens Associated with Healthcare-Associated Infections Summary of Data Reported to the National Healthcare Safety Network at the Centers for Disease Control and Prevention, 2009–2010. Infection Control & Hospital Epidemiology. 2013;34(1):1–14. Available from: https://www.cambridge.org/core/core/product/identifier/501959417000131921?type=journal_article.
9. Klimešová M, Wanja I, Nejeschlebová L, Horáček J, Ponižil A, Vondrušková E. Occurrence of Staphylococcus aureus in cattle, sheep, goat, and pig rearing in the Czech Republic. Acta Vet Brno. 2017;86(1):3–10.
10. Otto M. Coagulase-negative staphylococci as reservoirs of genes facilitating MRSA infection: Staphylococcal commensal species such as Staphylococcus aureus epidermids are being recognized as important sources of genes promoting MRSA colonization and virulence. BioEssays. 2013;35(1):4–11.
11. Founou RC, Founou LL, Essack SY. Clinical and economic impact of antibiotic resistance in developing countries: A systematic review and meta-analysis, vol. 12. PLoS ONE: Public Library of Science; 2017.
12. WHO. Global Strategy for Containment of Antimicrobial Resistance. 2001.
13. Gilani M, Usman J, Latif M, Munir T, Gill MM, Anjum R. Methicillin resistant coagulase negative Staphylococcus from colonizer to a pathogen. 2016.
14. Stryjewski ME, Corey GR. Methicillin-resistant staphylococcus aureus: An evolving pathogen. Clin Infect Dis. 2014;58(suppl_1):S10–9.
15. Goetchebeur M, Landry PA, Han D, Vicente C. Methicillin-resistant Staphylococcus aureus: A public health issue with economic consequences. 2006.
16. Catry B, Laevens H, Devriese LA, Opsomer G, de Kruif A. Antimicrobial resistance in livestock. 2003.
as Causes of Human Infection and Colonization in Germany. PLoS ONE. 2013;8(2):e55040.

18. Cömblé F, Argudín MA, Vanderhaeghen W, Hermans K, Haesebrouck F, Butaye P. Transmission dynamics of methicillin-resistant Staphylococcus aureus in pigs. Front Microbiol. 2013;4:57.

19. Morgan M. Methicillin-resistant Staphylococcus aureus and animals: Zoonosis or humanosis? J Antimicrob Chemother. 2008;62:1181–7.

20. Kadazi J, Smith TC, Thapalya D. Staphylococcus aureus and Staphylococcal Food-Borne Disease: An Ongoing Challenge in Public Health, vol. 2014. BioMed Research International: Hindawi Publishing Corporation; 2014.

21. WHO. GLASS Whole-genome sequencing for surveillance of antimicrobial resistance Global Antimicrobial Resistance and Use Surveillance System (GLASS). 2020.

22. Piessens V, van Coillie E, Verbeist B, Supré K, Braem G, van Nuffel A, et al. Distribution of coagulase-negative Staphylococcus species from milk and environment of dairy cows differs between herds. J Dairy Sci. 2011;94(6):2933–44.

23. Dąkic I, Morrison D, Vuković M, Szewczyk EM. Staphylococcus haemolyticus An emerging threat in the twilight of the antibiotics age. Microbiology. 2006;14:5.

24. Enyetornye B, Kwamena Ab R, Kodua E, Sop Foka EI, Narh Ahia K, Habibur R, et al. Whole genome Sequencing for food-borne outbreaks in Thailand. 2021 [cited 2022 Feb 12]. Available from: https://www.ncbi.nlm.nih.gov/nuccore/CP070060.1/.

25. Hu X, Zheng B, Jiang H, Kang Y, Cao Q, Ning H, et al. Draft genome sequence of Staphylococcus sciuri subspp. sciuri strain 28, isolated from human skin. Genome Announc. 2015;3(4):e00714-15.

26. Buahpong R, Joyinda Y, Rodpan A, Yornrat S, Pomprnt T, Ampoot W, et al. Whole genome Sequencing for food-borne outbreaks in . 2021. Available from: http://www.biomedcentral.com/1471-2180/12/104.

27. Egyir B, Hadjirin NF, Gupta S, Owusu F, Agbodzi B, Adogla-Bessa T, et al. Characterization of methicillin-resistant Staphylococcus sciuri isolates from industrially raised pigs, cattle and broiler chickens. J Antimicrob Chemother. 2014;69(1):2928–34.

28. Gómez-Sanz E, Haro-Moreno JM, Jansen SD, Roda-Garcia JJ, López-Pérez M. The Resistome and Mobilome of Multidrug-Resistant Staphylococcus sciuri C29865 Unveil a Transferable Trimethoprim Resistance Gene. Designated dfrE, Spread Unnoticed. 2021. Available from: https://journals.asm.org/journal/msystems.

29. Couto I, Wu SW, Tomas A, de Lencastre H. Development of methicillin resistance in clinical isolates of Staphylococcus sciuri by transcriptional activation of the mecA homologue native to the species. J Bacteriol. 2011;193(18):5645–53.

30. Czekaj T, Ciszewski M, Szewczyk EM. Staphylococcus aureus USA300. Journal of Global Antimicrobial Resistance. 2015;3(1):26–30.

31. Egyir B, Oteng AA, Owusu E, Newman MJ, Addo KK, Larsen AR. Characterization of metmethicillin-resistant Staphylococcus aureus isolates from livestock and farm attendants in Ghana. J Clin Microbiol. 2005;43(4):2782–5.

32. Egyir B, Guardabassi L, Sørum M, Nielsen SS, Kolekang A, Frimpong E, et al. Molecular epidemiology and antimicrobial susceptibility of clinical and food samples in Algeria. BMC Res Notes. 2018;11(1):663.

33. Dakić I, Morrison D, Vuković D, Savić B, Shittu A, Ježek P, et al. Isolation and molecular characterization of Staphylococcus sciuri in the hospital environment. J Clin Microbiol. 2005;43(6):2933–44.

34. Egyir B, Guardabassi L, Nielsen SS, Larsen AJ, Ali A, Khan MA, Rizwan M, et al. Molecular epidemiology of clinical and carrier strains of methicillin resistant Staphylococcus aureus (MRSA) in the hospital settings of north India. Ann Clin Microbiol Antimicrob. 2006;14:5.

35. Czekaj T, Crzewski M, Szewczyk EM. Staphylococcus haemolyticus An emerging threat in the twilight of the antibiotics age. Microbiology. 2015;161:2061–8.

36. Egyir B, Oteng AA, Owusu E, Newman MJ, Addo KK, Larsen AR. Characterization of staphylococcus aureus from human immunodeficiency virus (HIV) patients in Accra, Ghana. J Infect Dev Ctries. 2010;4(5):453–6.

37. Egyir B, Guardabassi L, Esson J, Nielsen SS, Newman MJ, Addo KK, et al. Insights into nasal carriage of Staphylococcus aureus in an urban and a rural community in Ghana. PLoS ONE. 2014;9(2):e89716.

38. Egyir B, Guardabassi L, Monecke S, Addo KK, Newman MJ, Larsen AR. Methicillin-resistant Staphylococcus aureus strains from Ghana include USA300. Journal of Global Antimicrobial Resistance. 2015;3(1):26–30.

39. Egyir B, Guardabassi L, Nielsen SS, Larsen AJ, Addo KK, Newman MJ, et al. Prevalence of nasal carriage and diversity of Staphylococcus aureus among inpatients and hospital staff at Korle Bu Teaching Hospital. Ghana Journal of Global Antimicrobial Resistance. 2013;3(4):189–93.

40. Rolo J, Worning P, Boye Nielsen J, Sobral R, Bowden R, Bouchami O, et al. Novel sequence types among staphylococcus haemolyticus isolated from neonatal blood samples. Microbiol Resour Announc. 2021;10(3):e00710–21.

41. Nemeghaire S, Vanderhaeghen W, Angeles Argudín M, Haesebrouck F, Butaye P. Characterization of methicillin-resistant Staphylococcus sciuri isolates from poultry farms in. 2010. Available from: https://www.researchgate.net/publication/284028206.

42. Wool JB, Smith DB, Baker EH, Brecher SM, Gupta K. Has the emergence of community-associated methicillin-resistant Staphylococcus aureus increased trimethoprim-sulfamethoxazole use and resistance? A 10-year time series analysis. Antimicrob Agents Chemother. 2012;56(1):5655–60.

43. Monophor P. Vancomycin hydrochloride for injection. Tokyo: USP, Fresenius Kabi Canada Inc.; 2017. Control. (204448).

44. Butaye P. Transmission dynamics of methicillin-resistant Staphylococcus sciuri. 2014. Available from: https://www.researchgate.net/publication/284028206.

45. Olayinka B, Bala Lis H, Olojey B, Onalopajo LA. Multidrug resistant Staphylococcus aureus isolates from poultry farms in Zaria, Nigeria. Antimicrobial resistance profile and enterotoxigenicity of S. aureus isolated from dry fish View project Mercy Aboh View project Multidrug resistant Staphylococcus aureus isolates from poultry farms in. 2010. Available from: https://www.researchgate.net/publication/284028206.

46. Morgan M. Methicillin-resistant Staphylococcus aureus and animals: Zoonosis or humanosis? J Antimicrob Chemother. 2008;62:1181–7.

47. Rolo J, Worning P, Boye Nielsen J, Sobral R, Bowden R, Bouchami O, et al. Evidence for the evolutionary steps leading to mecA-mediated B-lactam resistance in staphylococci. PLoS Genet. 2017;13(4):e1006674.

48. Piessens V, van Coillie E, Verbeist B, Supré K, Braem G, van Nuffel A, et al. Distribution of coagulase-negative Staphylococcus species from milk and environment of dairy cows differs between herds. J Dairy Sci. 2011;94(6):2933–44.
59. DAI. DFID Market Development (MADE) in Northern Ghana Programme [Internet]. 2014. Available from: www.dai.com.

60. Wolters M, Rohde H, Maier T, Belmar-Campos C, Franke G, Scherpe S, et al. MALDI-TOF MS fingerprinting allows for discrimination of major methicillin-resistant Staphylococcus aureus lineages. Int J Med Microbiol. 2011;301(1):64–8.

61. Christner M, Rohde H, Wolters M, Sobottka I, Wegscheider K, Aepfelbacher M. Rapid Identification of Bacteria from Positive Blood Culture Bottles by Use of Matrix-Assisted Laser Desorption-Ionization Time of Flight Mass Spectrometry Fingerprinting. J Clin Microbiol. 2010;48(5):1584–91.

62. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. 2019.

63. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18(3):268–81.

64. Bolger AM, Lohse M, Usadel B. Trimmomatic: A flexible trimmer for Illumina sequence data. 2014;30(15):2114–20.

65. Andrews S. FastQC: a quality control tool for high throughput sequence data. 2010 [cited 2022 Mar 20]. Available from: https://www.bioinformatics.babraham.ac.uk/projects/fastqc/.

66. Letunic I, Bork P. Interactive Tree of Life (iTOL) v4: Recent updates and new developments. Nucleic Acids Res. 2019;47(W1):W256–9.

**Publisher’s Note**
Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.