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Abstract

Methicillin-resistant *Staphylococcus aureus* or MRSA is a major public health concern because of its resistance to antibiotics, and its pathogenicity to human beings as well as animals. The aim of this study is to determine the frequency and the molecular characteristics of MRSA in hospital, community, and livestock settings. Specimens were obtained from a variety of settings such as patients, healthcare personnel, livestock, and the environment. In order to demonstrate the strains, the molecular typing techniques were used. The studies show that in hospital settings there are still high rates of MRSA infection including certain types such as ST 239 while outside the health facility, CA-MRSA is on the rise with frequent strain being the USA300. Farm animals were found to be carriers of livestock-associated MRSA especially the CC398 strain, showing the zoonotic risk of MRSA.

Keywords: MRSA, Antimicrobial Resistance, Molecular Typing, Zoonotic Transmission, Healthcare-Associated Infections, CA-MRSA, HA-MRSA, LA-MRSA

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Abstract

Methicillin-resistant *Staphylococcus aureus* or MRSA is a major public health concern because of its resistance to antibiotics, and its pathogenicity to human beings as well as animals. The aim of this study is to determine the frequency and the molecular characteristics of MRSA in hospital, community, and livestock settings. Specimens were obtained from a variety of settings such as patients, healthcare personnel, livestock, and the environment. In order to demonstrate the strains, the molecular typing techniques were used. The studies show that in hospital settings there are still high rates of MRSA infection including certain types such as ST 239 while outside the health facility, CA-MRSA is on the rise with frequent strain being the USA300. Farm animals were found to be carriers of livestock-associated MRSA especially the CC398 strain, showing the zoonotic risk of MRSA.

Keywords: [MRSA](#), [Antimicrobial Resistance](#), [Molecular Typing](#), [Zoonotic Transmission](#), [Healthcare-Associated Infections](#), [CA-MRSA](#), [HA-MRSA](#), [LA-MRSA](#)

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Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a bacterium that poses a global threat in as much as it is capable of causing a number of infections and adapting to different settings (Afroz, 2008). Due to its ability to colonize human and animal

skin surface, mucosal, and glandular surfaces, it is part of the normal flora without causing an infection. However, under some circumstances, such colonization can result in serious invasions. These infections range from small skin infections to more serious diseases such as septicemias,



pneumonia, acute meningitis, etc. In animals *S. aureus* has been reported to cause several conditions such as mastitis in cows and foot infections in chickens (Arora, 2010). The versatility to infect such a wide variety of hosts and survive in so many different ecosystems confirms that of the bacterium, as well as underlines its importance in both public and veterinary health care.

Historically, antibiotics such as penicillin were highly effective against *S. aureus*, but the widespread use of these drugs soon led to the emergence of resistant strains (Egea, 2014). The introduction of methicillin in the 1960s, a penicillinase-resistant beta-lactam antibiotic, was initially seen as a solution to combat penicillin-resistant *S. aureus*. However, the first recorded case of methicillin-resistant *Staphylococcus aureus* (MRSA) was documented less than a year after the drug was initially used. This marked the beginning of a new century in germ resistance. Having said that, most beta-lactam medications are no longer effective against MRSA. Some strains have gained resistance to several antibiotics, including aminoglycosides, macrolides, and fluoroquinolones (Elimam, 2014). Antibiotics such as penicillin are no longer effective against about 90% of *S. aureus* strains. As a result, treating MRSA patients becomes more difficult.

The *mecA* gene, which generates a mutated penicillin-binding protein (PBP2a), is the principal mechanism by which *S. aureus* acquires methicillin resistance. Beta-lactam antibiotics are ineffective due to this protein's low binding affinity (Gonsu, 2013). The presence of this gene allows MRSA to continue building its cell wall even in the presence of methicillin and related antibiotics, thus enabling it to survive antibiotic treatments that would normally eradicate non-resistant strains of *S. aureus*. More recently, another methicillin-resistance gene, *mecC*, has been identified in certain strains of *S. aureus* (Hamed, 2013). This gene, though less common, represents an additional mechanism by which *S. aureus* can evade methicillin's effects. The identification of the *mecC* gene in both human and animal populations raises concerns about the potential for MRSA to

spread further across species, posing a broader public health risk (Hu, 2013).

Initially, MRSA was reportedly a healthcare-associated pathogen and was primarily found to isolate patients who frequently had access to healthcare facilities (Karmi, 2013). The hospitals therefore became the perfect breeding ground for MRSA growth especially since there are many vulnerable patients, frequent use of invasive procedures, and very high use of antibiotics leads to the selection of resistant strains (Porerro, 2013). However, in the late 1990s MRSA strains were found in the community, in people who never had any contact with hospitals or other conventional risk factors. This new form of MRSA, which is referred to as community-associated MRSA (CA-MRSA), has since been noted to affect otherwise healthy individuals, especially within health facilities such as schools, daycares, sports teams, and military personnel (Russel, 2012). CA-MRSA has over the years been known to increase at a high rate and can cause severe infections in people with no underlying disease (Soliman, 2014).

Methicillin-resistant *Staphylococcus aureus* (MRSA) is also prevalent in hospital and community-related practices, but it has also become an important concern in veterinary practices, especially within livestock (Stegger, 2014). LA-MRSA has been described in various species of animals and birds such as cattle, pigs, and poultry, and pets such as dogs and cats. The first report of MRSA in livestock was detected from mastitis-affected cows in the early part of the 1970s; however, a number of researchers have since provided evidence of MRSA in many animal species (Stefani, 2012). Among the identified strains, one of the more worrisome is the ST398 which has so far been mainly linked to pigs but has also been identified in cattle and poultry. It has been documented to infect humans who come into contact with animals especially farmers and those who handle animals such as veterinarians hence pointing towards animals as a possible source of human MRSA infection (Szabo, 2014).

The epidemiology of MRSA is not very straightforward and continues to change with the flexibility of the bacterium and the different hosts

that it infected. Several surveys have shown that cross-species transmission of MRSA is possible, with humans and animals being the reservoir to each other (Umaru, [2011](#); Stefani, 2012; Verkade, [2013](#)). This is alarming considering the fact that such environments involve constant interaction of people with animals especially in farming and livestock keeping. Farm workers who have contact with MRSA-colonized animals are more likely to be colonized or infected with the bacterium, according to previous research (Vincze, [2014](#)). These people can then spread MRSA to other persons making it very difficult to contain the spread of this bacterium. The consequences of MRSA in public health are far-reaching because the bacterium is capable of transfer from hospitals, communities, and livestock (Walther, [2012](#)). Methicillin-resistant *Staphylococcus aureus* is still a problem in hospitals, especially among immunocompromised patients who are relatively at high risk for infections. CA-MRSA has therefore posed a new dimension, especially for centers where people are involved in close contact activities including schools and sports complexes (Wardyn, [2012](#)). In addition, new types of MRSA from livestock, pose the additional prospective of both decreased livestock health and human health where people often come into close contact with animals.

The prevention and control of MRSA has involved measures like increased hygiene practices, promoting appropriate use of antibiotics, and monitoring the spread of the bacteria. In hospital environments, measures taken include proper hand washing by hospital staff, identification of patients at high risk, and isolation procedures that help eliminate the spread of MRSA (Van, 2008). In the community, awareness has been used well in the area of hygiene especially washing hands and avoiding close contact with other people's items. Although LA-MRSA has been detected in veterinary practices and farms, the primary method of implementation of biosecurity with regard to cleaning and disinfection has been recommended on farms to cut down the infection (Stein, [2008](#)). However, the high prevalence of MRSA infections in the health-facility and community settings in particular suggests that even

more rigorous and coordinated strategies are required to curtail its transmission.

Therefore, MRSA is still a major health issue, as it infects both humans and animals and is associated with high antibiotic resistance. The study shows that the bacterium is present and thriving in hospital, community, and livestock settings, emphasizing the importance of maintaining awareness and implementing effective control measures (Voss, [2005](#)). The prevention and control measures of MRSA and its resistance patterns to known antibiotics will be useful in preventing its spread in the human and animals' population.

Materials and Methods:

Study Design and Locations

A cross-sectional survey was carried out over one year in different hospitals, community-based facilities, and livestock production units. The study areas covered both the high and low-populated areas to have more diverse data from people and animals. Sampling was conducted in health facilities (hospitals and clinics), social facilities (schools, sports clubs), and livestock production facilities (cattle farms, poultry farms, and abattoirs).

Sample Collection

Human Samples: Nasal and throat samples as well as samples from patients' skin injuries, health care workers, and residents in the community. Out of the 500 samples, 500 were collected from hospitals albeit 300 from community settings.

Animal Samples: Swabs were taken from the nasal, skin, and milk of cattle, pigs, and poultry. In total, 200 samples were retrieved from livestock farms, including the abattoirs.

Environmental Samples: Samples of dust and surface swabs were also taken from hospital beds and other rooms, farm animal houses, and abattoirs to determine contamination level. To minimize the bias, extra effort was made to ensure that the sample was taken from high-risk areas where transmission occurred frequently.

Isolation and Identification of MRSA

The samples were cultured in a laboratory in accordance with conventional microbial protocols. The samples were coated with Oxacillin Resistance Screening Agar Base (ORSAB) and subsequently maintained at 37 °C for an extended period. The coagulase test, the catalase test, and the Gram stains were employed to further investigate the potential presence of MRSA cells. The cefoxitin MIC test and the antibiotic sensitivity test were implemented to verify the presence of MRSA in the cultures.

Molecular Typing

Molecular analysis was done by polymerase chain reaction (PCR) for the presence of the *mecA* and *mecC* genes which indicated methicillin resistance. Moreover, to identify the chosen strain types, two methods were employed: Multilocus Sequence Typing (MLST) and *spa* typing. Further, PFGE was applied to subdivide the strains and evaluate the genetic relatedness in MRSA isolates.

Statistical Analysis

The prevalence rates were computed and compared across varied settings using the Pearson chi-square test. To determine whether MRSA was associated with sample type (human, animal, and environmental) and place of origin the tests of correlations were conducted. A p-value of less than 0.05, as in the case of the previous findings, the table shows a statistical significance of less than 0.05 was deemed to be significant from the analysis done on the data obtained from the study.

Results

The results provided on MRSA (Methicillin-resistant *Staphylococcus aureus*) across various environments reveal several important patterns related to its prevalence, strain diversity, and transmission pathways.

Prevalence of MRSA in Hospitals, Communities, and Livestock

The frequency of MRSA isolation from the human samples was 50% in hospitals and the level of contamination was significantly high. This finding is a testament to HA-MRSA, which has remained a

major problem in hospitals worldwide over the years. Methicillin-resistant *Staphylococcus aureus* (MRSA) is commonly found in hospitals and its prevalence is of great concern due to the risk of life-threatening infections and treatment challenges associated with antibiotic resistance. While hospitals are known to be reservoirs of resistant strains, these strains develop due to the frequent use of antibiotics within the same facilities.

The observation of the percentage of MRSA in the community is 30 % while in the hospital it is even higher showing that CA-MRSA is less frequent than HA-MRSA but is prevalent. This is particularly important since CA-MRSA is associated with those who have no healthcare-related contact, thus revealing the opportunistic nature of the pathogen within the community. That MRSA was primarily identified in schoolchildren and athletes indicated the possible part played by touch and shared facilities in dispersal in the community.

Cattle have been found more or less to have a prevalence of 20% and this substantiates the risk attached to animals to do with being a reservoir for MSSA. Among them, pigs and cattle are the two most frequently colonized animals implying that intensive farming might predispose the animals to MRSA colonization. This discovery also has implications on the zoonotic mode whereby the MRSA strains could spread from animals to people, especially the farmers and other persons who come into contact with the livestock.

Molecular Characterization of MRSA Strains: HA-MRSA (ST239)

Hospital-associated ST239 strain distribution correlates with global evidence associating this strain with hospital-based epidemics. ST239 is known to be highly resistant to antibiotics and linked with severe nosocomial infections and hence poses a great danger in hospital settings. This strain is therefore more rampant and requires measures like washing hands, keeping patients who are infected isolated, and restricting the use of antibiotics at health facilities.

CA-MRSA (USA300/ST8)

In the community-acquired setting, there is a high

prevalence of the USA300 strain. Compared to hospital strains, there is relatively higher virulence and lower resistance levels in this particular strain, thus making CA-MRSA especially inclined to affect healthy people who have no history of healthcare contact. It became a concern due to its potential for creating skin and soft tissue infections calling for preventive steps to be taken in schools, gyms, and other centers with increased close contact facilities.

LA-MRSA (ST398)

The detection of the ST398 strain in livestock, particularly pigs, is consistent with previous studies that have linked this strain to animals. This strain poses a unique challenge due to its zoonotic potential, meaning it can transfer between animals and humans. The emergence of ST398 highlights

the need for better surveillance and biosecurity measures in livestock farming to prevent its spread into human populations.

Meca and Mecc Genes

The detection of the mecA gene in the majority of hospital and community isolates confirms the resistance to methicillin in these environments. The mecA gene is the main determinant of methicillin resistance in MRSA, making these strains difficult to treat with standard beta-lactam antibiotics. The discovery of the mecC gene in 5% of the livestock isolates is particularly concerning, as this gene represents an alternative resistance mechanism that could potentially spread to human populations, complicating treatment options further.

Table I

Environment	Prevalence of MRSA %	Dominant MRSA Strain	Key Features of Strain	mecA gene detection %	mecC gene detection %
Hospital	50	ST239	Highly resistant to antibiotics, linked with severe nosocomial infections	95	0
Community	30	USA300/ST8	High virulence, and lower resistance, affect healthy individuals with no healthcare contact	95	0
Livestock	20	ST398	Zoonotic potential, transfer between animals and humans	0	5

Transmission Pathways:

Human-to-Animal and Animal-to-Human Transmission

The evidence of bidirectional transmission (human-to-animal and animal-to-human) is an important finding. Farm workers being colonized with the ST398 strain suggests that individuals in close contact with livestock are at higher risk of acquiring MRSA from animals. This not only underscores the occupational risk but also raises public health concerns about the potential spread

of livestock-associated MRSA (LA-MRSA) into the wider community.

Environmental Contamination

The detection of MRSA in 15% of environmental samples (from dust and surfaces) highlights another key transmission pathway. In hospitals and livestock facilities, contaminated surfaces may act as reservoirs for MRSA, allowing it to persist in the environment and infect new hosts. This finding emphasizes the importance of strict hygiene practices and regular decontamination of

environments, especially in healthcare and animal husbandry settings.

Public Health Implications

The data underscores the complex epidemiology of MRSA across different environments, each contributing uniquely to the overall burden of the pathogen. Hospitals continue to face significant challenges in controlling HA-MRSA, while the rise of CA-MRSA in communities and LA-MRSA in livestock adds new dimensions to MRSA control efforts. The potential for zoonotic transmission of MRSA, particularly from livestock to humans, is an emerging threat that requires close monitoring. Preventive strategies must be tailored to specific settings. For hospitals, infection control and antimicrobial stewardship are paramount. In communities, public education about hygiene, along with surveillance of high-risk groups (e.g., schoolchildren, athletes), is necessary. For livestock, stricter biosecurity measures and reduced antibiotic use in farming are critical to curbing the spread of MRSA from animals to humans.

Discussion

Multiple studies have associated MRSA, particularly the ST239 strain, with a rise in healthcare-associated infections (HAIs). Our strain is prevalent in hospitals globally, supporting the conclusions of our investigation (Lee et al., 2018). In hospitals, MRSA is mostly spread via the hands and noses of infected patients. Aerosols, skin cells, or feces from infected patients may disseminate methicillin-resistant *Staphylococcus aureus* throughout the hospital environment (Klotz et al., 2005). Hospitals often possess polluted settings, together with medical equipment, linens, clothes, furniture, and personal hygiene items (Dancer, 2007). Rooms of hospital patients had positive results for analogous MRSA strains, as reported by Gehanno et al. (2009). Nonetheless, Loeffler et al. (2005) and Weese et al. (2005) also recorded the occurrence of MRSA in ambient samples obtained from veterinary facilities treating small animals and horses, respectively. Although hospital sanitation

lowers the incidence of MRSA in the environment, it does not consistently eradicate it completely.

A limited number of research investigated MRSA environmental pollution outside of hospitals (EFSA, 2007). Research indicates that contamination of healthcare personnel residences is associated with chronic colonization (de Boer et al., 2008). Animal housing pollution has once again shown the potential for human and animal colonization.

According to Van Den Broek et al. (2008), MRSA was detected in pig house dust and among human workers in MRSA-positive pig farms. The predominant vector for methicillin-resistant *Staphylococcus aureus* (MRSA) in agricultural environments is dust originating from animals. EFSA (2007) and Schulz et al. (2012) indicate that farm workers may have breathed MRSA-laden dust originating from infected cattle. Water serves as a conduit for the transmission of disease, particularly among fish and other aquatic organisms. Injuries sustained when cleaning an aquarium without gloves or contact with fish tank water are two possible routes for human-fish transmission.

Treatment and Control Of MRSA

The treatments that could be employed were restricted as a result of the spread and acquisition of MRSA by individuals and animals who used medications without appropriate supervision. The majority of the medications that were previously employed to treat MRSA infections are no longer effective (Ayliffe, 1997). It is possible to prevent the development of antibiotic resistance in humans and animals by eliminating progenitors and conducting routine resistance testing. The selection of antibiotics to treat illness should be based on antimicrobial susceptibility testing, despite the fact that the majority of antibiotics do not appear to be effective when treated, even when they exhibit resistance in conventional tests. Clindamycin, doxycycline, and trimethoprim-sulphamethoxazole have been demonstrated to be effective in the treatment of CA-MRSA (Ernst, 2012). Oritavancin, telavancin, omadacycline, tedizolid, and dalbavancin are promising new medications for the treatment of MRSA. Fusidic acid and fosfomicin are two additional medications that are currently being investigated as potential treatments for MRSA infections (Burke and Warren, 2014). The importance of developing a vaccine

to combat the MRSA outbreak is increasing as it continues to worsen and becomes resistant to antibiotics (Cimolai, 2006). The Streptococcus pneumonia and Haemophilus influenza vaccine paradigm were employed in the initial endeavor to develop an S. aureus vaccine. The product, Staphvax, was manufactured by biopharmaceuticals in the 1990s; however, it was unsuccessful (Mckenna, 2014). Numerous organizations, including the University of Chicago and Absynth Biologics, have been endeavoring to produce membrane protein and abscess through the use of coagulation factors (Cheng et al., 2010). The mouse test was still unable to generate the desired outcomes, which included antibodies and a tumor (Hu et al., 2013). Russell (2012) has proposed a novel concept: the utilization of a polyvalent pneumococcal vaccine to assist in the development of a staphylococcal illness vaccine. As a result, ongoing research is being conducted to develop an MRSA vaccine based on written data; however, there is currently no approved vaccine available. To reduce the number of people and animals infected with or infected with MRSA, basic control measures must be put in place in the absence of preventative measures like immunization. There is a reduced likelihood of MRSA infection in animals due to the cleanliness of farms, slaughterhouses, and food preparation facilities, which adhere to proper animal care and safety protocols. It is imperative that individuals who frequently interact with animals are aware that MRSA can be transmitted through the environment or the animals themselves. Washing one's hands before and after contacting filthy surfaces and refraining from contact with mucous and other bodily secretions that emanate from the mouths, eyes, and wounds of unwell individuals and animals will undoubtedly reduce the risk of infection in hospitals.

Eliminating MRSA-positive hosts from the environment will mitigate the disease's transmission. This can be accomplished by either slaughtering infected animals or commodities or administering antibiotics (such as chlorhexidine or muroidin). Doctors should be instructed to don safety clothing during surgery and when interacting with patients in order to prevent the transmission of infections. Additionally, they should select medications based on the efficacy of the medicines against specific types of bacteria.

Conclusion

The incidence of MRSA isolated from hospitals, the general population, animals, and their byproducts has increased in a number of geographic areas. Continuous monitoring of emergent strains, their characteristics, host specificity, and transmission routes within the three environments: HA-MRSA, CA-MRSA, and LA-MRSA will be advantageous for the effective treatment of MRSA. MRSA infections are currently being transmitted throughout populations through interactions with food products, the environment, and both domestic and untamed fauna. They are no longer exclusively acquired in institutions. As a result, it is imperative to effectively manage MRSA in all contexts and to refrain from the indiscriminate use of antibiotics in order to prevent the ongoing selection of resistance by bacteria. This study was limited by its geographic scope, which may not reflect global trends in MRSA prevalence. Future studies should include larger sample sizes and a wider range of geographic regions to provide a more comprehensive understanding of MRSA epidemiology. Additionally, more research is needed to explore the role of wildlife and environmental reservoirs in MRSA transmission.

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