INTRODUCTION
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Staphylococcus aureus is a gram-positive coccoid bacterium named for its tendency to form clusters ("staphylo" is the Greek expression for "bunch of grapes") and its golden pigmentation ("aureus" is Latin for "golden") on culture plates. S. aureus is a versatile and dangerous bacterial pathogen with a genome consisting of a circular chromosome of approximately 2,800 base pairs and additional prophages, plasmids, and transposons. Genes governing virulence and antibiotic resistance reside on both the chromosome and extrachromosomal elements, and these genes are transferred between staphylococcal strains or other bacterial species via extrachromosomal elements. Humans are a natural reservoir of S. aureus, with 30% to 50% of healthy adults colonized, 10% to 20% persistently so. Its importance as a human pathogen has increased in the previous century as a result of the evolution of antimicrobial resistance – to penicillin and subsequently methicillin in particular.

Though, Methicillin-Resistant Staphylococcus aureus (MRSA) was isolated one year after methicillin was introduced, but the mechanism of methicillin resistance was not elucidated until 1981, when Hartman and co-workers discovered altered penicillin-binding proteins (PBP2') in MRSA that had markedly reduced affinity for all currently available beta-lactam antibiotics while maintaining effective cell wall-building activity. Five SCCmec subtypes have officially been identified to date, varying in size from ~20 kilobase pairs (kb) to 68 kb. SCCmec types I, IV and V possess no antimicrobial resistance determinants other than mecA, whereas SCCmec types II and III possess multiple other resistant determinants such as Tn554 (encodes for macrolide resistance). This partially accounts for the larger sizes of the latter, which is thought to have limited their capability for horizontal transference. It is currently postulated that methicillin resistance did not arise within S. aureus, but was transferred from other staphylococcal species.

Since 1961, successive waves of epidemic MRSA have spread throughout hospitals and other chronic healthcare facilities worldwide to the extent that it is now the most commonly isolated antimicrobial-resistant pathogen worldwide. Despite the apparent success of MRSA in the nosocomial setting, it was originally hardly ever isolated from the community. This observation was attributed to the much
slower growth rates of earlier MRSA isolates (probably a result of the fitness costs of SCCmec I to III) compared to methicillin-susceptible S. aureus (MSSA) isolates, a factor which may be of crucial ecological importance in settings where antibiotic selection pressure is not the main evolutionary imperative.

The emergence and spread of methicillin-resistant Staphylococcus aureus (MRSA) isolates from the community that are distinct from their archetypal healthcare associated counterparts (HA-MRSA) marked a critical evolutionary milestone for the organism. In less than 2 decades, particularly in the last 3 years, this initially sporadic phenomenon of community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) has become a global reality, leading to paradigm shifts in the perception and management of staphylococcal infections in countries where CA-MRSA has reached epidemic proportions. For several decades, there has been considerable controversy over whether or not contaminated environmental surfaces contribute to transmission of healthcare-associated pathogens. The proportion of hospital surfaces contaminated with MRSA has varied considerably in published reports, ranging from 1% to 27% of surfaces in patient rooms on regular hospital wards.

Staphylococcus aureus is an important cause of bacterial keratitis and conjunctivitis. This organism infects compromised corneas, such as those with bullous keratopathy, chronic herpetic keratitis, keratoconjunctivitis sicca, ocular rosacea, or atopic keratoconjunctivitis. MRSA warrants particular attention because these strains are frequently resistant to multiple antibiotics, leaving limited treatment options. MRSA is as yet an infrequent cause of external ocular infections. Patients typically have underlying ocular risk factors and/or are medically debilitated. Different strains infect young and old age groups with characteristic antimicrobial sensitivity, this highlights the need for more work to establish the role of MRSA commensals and ocular infections.

Staphylococcus aureus causes severe animal diseases, such as suppurative disease, mastitis, arthritis, and urinary tract infection that are associated with numerous virulence factors, such as the production of extracellular toxins and enzymes. In animals staphylococcal mastitis either a clinical or sub-clinical form is
an important infection that incur considerable economic losses in dairy industry. Many sources of S. aureus spread exist, including housing materials and fodder, equipment and air, bovine skin, non bovine animals, and humans. Teat skin has been suggested as an important reservoir for intra-mammary infection, while bovine-to-human transmission has also been proposed\textsuperscript{12,13}.

For humans, this organism is an important cause of food poisoning. Recently, the isolation of MRSA from non-human sources including foodstuff and animals has been reported with an increased tendency\textsuperscript{14,15}. The existence of MRSA in non-human sources has aroused curiosity as to whether these MRSA isolates originated from a common source. A survey on the non-human MRSA will provide some meaningful data on the importance and similarity between the MRSA strains in the veterinary field. The epidemiological aspects of MRSA infections in animals have not been studied in details; a few veterinary reports have been published on MRSA infections in dairy herds with mastitis and in companion animals. Transmission through food products has not been thoroughly investigated. Therefore, this study examined the characteristics of MRSA isolated from retail meat shops and compared the epidemiological similarity between human and animal isolates.

In the hospital setting, the most common mode of transmission of resistant \textit{S. aureus} is close contact with infected persons or with health-care workers with contaminated hands or clothing. Recent evidence suggests, however, that airborne dispersal and transmission may also be important and case studies implicating airborne transmission in the hospital settings have been published in the literature\textsuperscript{16}. Although drug-resistant \textit{S. aureus} has historically been a significant problem only in hospitals, the urgent need for further study of the ambient airborne concentrations and the role of airborne transmission of this organism in non-hospital environments is demonstrated by the increasing prevalence of methicillin-resistant \textit{S. aureus} (MRSA) infections in the community\textsuperscript{17}. Most alarming about this trend is that infection has been observed among individuals with and without known risk factors. \textit{S. aureus} in water ecosystems may also serve as a source for colonizing residents exposed to contaminated water\textsuperscript{18}. In environmental settings polluted by human or animal waste or both, high frequencies of multiple antibiotic resistance phenotypes
exist. These environments include surface waters receiving runoff from lands occupied by livestock, polluted estuaries, and contaminated water supplies.

In view of the above mentioned lacunae the present study is being undertaken with the aim to extend the knowledge of epidemiology of *Staphylococcus aureus* with the following objectives:

- Isolation, identification and biochemical characterization of *S. aureus* from clinical specimen and healthy personnel and from various environmental sources.
- Incidence of drug resistance in isolated strains of *S. aureus* against various classes of antibiotics and evaluation of minimum inhibitory concentrations (MIC).
- Biotypic differentiation of *S. aureus* strains from various sources.
- Epidemiological investigation of *S. aureus* isolates to trace the source of strain by bacteriophage typing.
- Characterization of methicillin-resistant *S. aureus* (MRSA) strains on the basis of epidemiological marker Staphylococcal cassette chromosome *mec* (SCCmec) complex element by Multiplex PCR strategy.
- Clonal relationship of MRSA isolates among different sources on the basis of randomly amplified polymorphic DNA (RAPD) assay.
- Macrorestriction analysis by *SmaI* digests MRSA isolates by Pulsed Field Gel Electrophoresis (PFGE).
- Phylogenetic analysis of MRSA isolates under study among various sources to establish the genetic relationship.