Staphylococci are widespread in nature, although they are mainly found living on the skin and mucous membranes. The coagulase-positive *Staphylococcus aureus* is well known as a human pathogen. Serious infections produced by *S. aureus* include bacteraemia, pneumonia, osteomyelitis, endocarditis, mastitis, scalded skin syndrome and abscesses of the muscle, urinogenital tract, postoperative wound infection, conjunctivitis, keratitis, endophthalmitis and various nosocomial infections. The organism causes severe diseases in animal, such as suppurative disease, mastitis, arthritis, and UTI that are associated with numerous virulence factors.

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. Methicillin-Resistant *Staphylococcus aureus* (MRSA) was isolated one year after methicillin was introduced. Methicillin resistance in staphylococci is caused by expression of PBP2a encoded by the *mecA* gene. *mecA* is located on a genetic element called the staphylococcal cassette chromosome (SCC) in *S. aureus*. To date, five different types of SCCmec (I-V) have been defined by the particular combination according to their putative recombinase genes (ccrAB) and overall genetic composition of two parts: the ccr complex and the mec complex. Community-acquired MRSA strains possess novel, small, mobile SCCmec type IV or V genetic elements which contain the mecA with or without additional antibiotic resistance genes and are more easily transferred to other strains of *S. aureus*, whereas larger SCCmec types I, II, and III elements are associated with nosocomial infection. MRSA had markedly reduced affinity for all currently available β-lactam antibiotics while maintaining effective cell wall-building activity.

Now MRSA is known to be of the most prevalent nosocomial pathogens throughout the world. 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 in many
countries. MRSA has now also become established outside the hospital environment and is appearing in community populations without identifiable risk factors. Transmission of MRSA is thought to occur primarily from colonized or infected persons to others. In the hospital setting, the most common mode of transmission of resistant *S. aureus* is close contact with infected persons or with health-care workers with contaminated hands or clothing. Evidence suggests, however, that airborne dispersal and transmission may also be important in implicating airborne transmission in hospital setting.

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. The isolation of MRSA from non-human sources including foodstuff and animals has been reported with an increased tendency. The existence of MRSA in non-human sources has aroused curiosity as to whether these MRSA isolates originated from a common source. The *S. aureus* in water resources may also serve as a source for colonizing residents exposed to contaminated water.

Of the total 4885 sampling we isolated 1160 *S. aureus* strains, the prevalence of methicillin resistant (MRSA) among these isolates was 176 (15.1%). The distribution of MRSA in various specimen studied can be summarized as follows: clinical specimen (31.4%) > nosocomial (18.5%) > ocular specimen (11.45) > community personnel (10.2%) > veterinary (5.4%) > food and food handlers (3.2%) > air (2.1%). The highest prevalence was found in clinical specimen and lowest in air, while no MRSA was found in water sources.

According to the results obtained highest resistance was found to penicillin-G, while zero resistance was found to vancomycin when applied to selective sources. Multiple drug resistance in all *S. aureus* (n=1160) and MRSA (n=176) isolates were detected.

The demographic result showed the carriage of *S. aureus* was higher in males than females (57.6%: 42.3%) while, children in the community were the higher colonizer.
(28.3%). The ocular patients of 45 years and above were found to have higher rate of infection.

The results indicated that major reservoir of MRSA in nosocomial infections are colonized/ infected inpatients and colonized health care workers with carriers at risk for developing endogenous infection or cross transmitting MRSA to health care workers and patients. The rate of colonization of MRSA in community personnel was found lower than nosocomial MRSA prevalence (10.2% vs 18.5%). Highest percentage of MRSA (8.3%) was found in clinical dairy herd while carriage rate of MRSA in dairy personnel was insignificant. Major food animals such as cattle meat (10.2%) and chicken (9.0%) were found to be the source of MRSA prevalence. No MRSA dispersion was seen in air from different environment except hospital wards (22.2%, 2/9).

The MIC values of Oxacillin was observed between 4μl/ml to 256μl/ml in which 23.2% MRSA isolates were borderline resistance (2-8μl/ml) and 76.7% were methicillin resistant (≥16μl/ml). The most common resistance pattern “PGMETCI” (n=22) in MRSA isolates was frequently encountered in various sources.

Biotyping: Selective methicillin sensitive S. aureus (n=196) and MRSA (n=176) were subjected to crystal violet test biotyping. The majority of the isolates MSSA (79.5%) and MRSA (80.0%) were classified into human biotype –A, whereas, only 7.1% of MSSA and 0.6% of MRSA of biotype –C (animal origin) was seen among personnel. Biotypic distribution of MRSA (n=165) as described by Coia et al.97 resulted into 4 groups. Maximum strains represented biotype B group (43.6%) followed by group D (30.9%).

Bacteriophage typing: A total of 302 S. aureus with methicillin sensitive and resistant were subjected to bacteriophage typing as many as 51.8% of MSSA and 32.1% of MRSA was found typable at RTD and 100 RTD. Phage group III was predominant in both MSSA and MRSA isolates. Phage patterns 6/75/84, 6, 6/83A (phage group III) were found prevalent in MSSA and 30/33/38 MRSA phage complex resulted predominantly in MRSA isolates of every source.

SCCmec typing: A selective 93 MRSA isolates were subjected to Staphylococcal cassette chromosome mec complex (SCCmec complex). The
SCCmec Type III cassette with Type III-A variant was predominantly found in clinical and ocular specimen and nosocomial isolates. However, few MRSA isolates possessing Type III cassette from community, veterinary and foods sources were resulted. SCCmec Type IV variant IVa was observed in community MRSA isolates and IVb variant was found in veterinary and food MRSA isolates. The results showed that, by and large these, SCCmec cassette complexes were mostly confined to their respective environments. One MRSA isolate from ocular specimen was found to contain SCCmec Type II cassette. The PCR results also showed the positive correlation between MIC values and mecA gene. A 6 MRSA strains with low MIC value were found mecA gene negative.

Furthermore, 70 MRSA strains (Type III) and one MRSA isolate (Type II) were confirmed by specificity of mec gene complex to Class A complex, and 16 MRSA isolates (Type IV) were found to possess Class B complex. The cassette chromosome recombinase (ccrAB) typing, showed 70 MRSA isolates (Type III) containing ccrAB type 3 complex, and 16 MRSA (Type IV) and one MRSA (Type II) possessing ccrAB type 2 complex. The mec complex and ccrAB complex typing showed a positive correlation with SCCmec cassette.

Random Amplified Polymorphic DNA assay (RAPD): the RAPD analysis of selective 15 MRSA isolates resulted into two cluster. Pattern I with 9 MRSA isolates of same antibiogram predominated in our finding.

Pulsed Field Gel Electrophoresis (PFGE): Nine PFGE patterns were identified among 71 MRSA (Type III & II) strains. The largest similarity in diverse sources was found in Pattern D (n=14) followed by pattern C (n=12). The results of pulsotype B (n=7) depicted clonal similarity to the Hungarian clone (Type III).

The 16S rDNA gene analysis of ocular isolate MRSAOC-9 (Type II) had showed >99% homology to N315 (Type II) referral strain. Furthermore, phylogenetic analysis of 16S rDNA gene of 5 selective MRSA strains (Type III) one each from clinical, nosocomial, community, veterinary and food were found to be above 99% similar. Isolates of clinical, nosocomial and community were observed in one cluster, indicating maximum homology among them.