

Emerging Zoonosis of Methicillin Resistant *Staphylococcus aureus*

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Staphylococcus aureus (*S. aureus*) has a characteristics property that it can develop resistance against antibiotics. Resistance against methicillin shows resistance against all beta-lactams. *S. aureus* develop its resistance against methicillin by acquiring different genes, which produces specific penicillin binding proteins on which beta-lactams have very little effect [1]. These genes are present in chromosomal cassette mec (*SCCmec*) [2]. During 1970s infections of the methicillin resistant *Staphylococcus aureus* (MRSA) were mainly limited to the environments of hospital i.e. Human associated-MRSA. Furthermore, MRSA transmitted in community i.e. Community associated-MRSA in those peoples who have no risk factors for MRSA infections. Currently MRSA strains associated with livestock have emerged due exposure with livestock i.e. Livestock associated-MRSA. Phenotypically oxacillin and cefoxitin are mainly used to find out MRSA, while genotypic identification can be conducted by different advanced sequencing techniques [3].

MRSA may also be transmitted to humans by handling or consumption of contaminated animals [4]. *S. aureus* is the major cause of mastitis in animals. Emergence of MRSA in milk is of extremely importance because it is directly consumed by humans. Milk infected with MRSA, will be transferred to humans leading to development of resistance to all beta-lactams antibiotics which is a great public health importance.

Prevention of MRSA spread needs proper actions for veterinary infection control. The research work and phylogenetic studies of *Staphylococci* showed that animal strains are evolved from human isolates and in these days there is risk that these can be transmitted back to humans. Various staphylococcal species in animals and in environment provide a large reservoir of MRSA and resistance genes it is therefore emphasized that food animals should be properly monitored to prevent its spread in both populations. Whole genome sequencing and next generation sequencing has played a vital role for the evolution of resistance and new resistant genes can also be found by these techniques. By these technologies the pathways of resistance can be traced back by functional genomics which can then be addressed by appropriate measures.

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