Prevalence, Virulence Traits and Antimicrobial Resistance Pattern of *Staphylococcus aureus* Isolated from Chicken

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**ABSTRACT**

*Staphylococcus aureus* isolated from chicken samples of retail market of Shirwal city exhibited 36% (18/50) prevalence, confirmed biochemically as well as by polymerase chain reaction by employing 16s-rDNA and species-specific sau genes. None of the isolates were found to possess virulence genes, viz., *sea*, *seb*, *sec* and *sed*. Antimicrobial resistance pattern revealed that 100% isolates were resistant to 16 among 24 antibiotics, while 5 antibiotics showed more than 70% resistance, except for tobramycin (44.44%) and gentamicin, streptomycin (38.89% each). All isolates were multidrug resistant (MDR). Screening for the presence of antimicrobial resistance genes revealed the presence of *aacA-D,ermA,tetK* and *tetM* genes. None of the isolates carried *mecA, mrsa, mrsB, vanA, vanB* and *ermC* genes, although phenotypic resistance was noted.

**Keywords:** Antimicrobial resistance, Chicken, Prevalence, *Staphylococcus aureus*, Polymerase Chain Reaction (PCR), Virulence Genes

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**INTRODUCTION**

Food-borne disease outbreaks remain a major global health challenge and cross-contamination from raw meat due to poor handling is a major cause in developing countries. *S. aureus*, a ubiquitous food-borne pathogen, may contaminate food materials and is also responsible for the development of antimicrobial resistance (Baghbaderani et al., 2020).

Many investigations have shown that *S. aureus* is resistant to many antibiotics and carries many antimicrobial-resistant genes. Antimicrobial resistance (AMR) has been declared by the World Health Organization as one of the top 10 global public health threats for humans (WHO, 2021). World Health Organization has categorized antibiotic-resistance pathogens into critical, high and medium priority groups for research and development of new antibiotics. Methicillin-resistant and vancomycin-intermediate and resistant *Staphylococcus aureus* is included in the second category as a high priority pathogen (WHO, 2017). *S. aureus* in the food chain is considered as an indicator of bad and poor hygiene; hence the presence of organisms and their exotoxins in food is considered a source of food poisoning (FDA, 2016). Meat derived from poultry reared under intensive management conditions may get contaminated during slaughter procedures due to unhygienic handlings adopted in wet market. It has been well documented that *S. aureus* shows resistance to many antibiotics and carries multiple antimicrobial resistance genes as well as virulence genes. This study aimed to investigate the prevalence of *S. aureus* and its virulence traits, antimicrobial resistance pattern and antimicrobial genes in chicken samples of retail market of Shirwal, Maharashtra (India).

**MATERIALS AND METHODS**

Isolation and Identification of *S. aureus*

Specimens from chicken were collected from 50 different retail shops located in 5 different villages in and around Shirwal, Dist. Satara (Maharashtra, India). The samples were analyzed for the presence of *S. aureus* as per the...
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Bacteriological Analytical Manual (FDA, 2019) with slight modifications. Presumptive isolates were further subjected to biochemical characterization using catalase test, DNA-ase test (Cheesebrough, 2006) and Voges-Prausker test, methyl red test and oxidase test (Cruickshank \textit{et al.}, 1975).

**Antibiogram**

Antibiogram sensitivity and resistance pattern of \textit{S. aureus} was interpreted using the Kirby Bauer disc diffusion method (Bauer \textit{et al.}, 1966) and the results were recorded following the guidelines given by the Clinical and Laboratory Standards Institute (CLSI, 2018).

**PCR Characterization of \textit{S. aureus} for Virulence Genes and Antimicrobial Resistance Genes**

All biochemically confirmed and DNA-ase positive isolates were subjected to a polymerase chain reaction for characterization of various genes, viz., 16S- rDNA and sau genes as per Strommenger \textit{et al.} (2003); virulence genes (sea, seb, sec and sed) according to Mehrotra \textit{et al.} (2000) and antibiotic resistance genes using protocols of Kumar \textit{et al.} (2009) for detection of mecA, tetK, tetM, ermA, ermC, aacA, mrsA and mrsB genes and as per Hizlisoy \textit{et al.} (2018) for \textit{vanA} and \textit{vanB} genes.

**RESULTS AND DISCUSSION**

Biochemically confirmed isolates from 50 chicken specimens revealed, 18 (36%) positive samples of \textit{S. aureus}, which was similar to Patyal \textit{et al.} (2012), Govender \textit{et al.} (2019), Savariraj \textit{et al.} (2020) and Tegegne \textit{et al.} (2021).

Molecular characterization of isolates by targeting 16S-rDNA and sau genes, confirmed only 4/50 (8%) samples as \textit{S. aureus} (Fig. 1). Upon characterization of isolates from chicken for virulence genes, it was noticed that none of the isolates harbored virulence genes. Shylaja \textit{et al.} (2018), Savariraj \textit{et al.}

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out. All isolates were multidrug-resistant showing resistance to more than 3 antibiotics, 5 isolates showed resistance to 16-20 antibiotics and 13 isolates showed resistance to 21-24 antibiotics. Indiscriminate use of antibiotics could be attributed to such a high multidrug resistance rate.

Screening for antimicrobial resistance genes revealed that the prevalence of aacA-D was 55.55% followed by tetM (44.44%), ermA (38.89%) and tetK (11.11%) for, while mecA, vanA, vanB, mrsA, mrsB and ermC were not observed in any of the isolates (Fig. 3). Some isolates have shown phenotypic resistance but were unable to express antimicrobial genes, may be due to alternative mechanisms or genes responsible for resistance. Similar findings were also observed by Zehra et al. (2019), Fazel et al. (2020) and Baghbaderani et al. (2020).

CONCLUSION

Adherence to good meat hygienic practices should be followed to prevent contamination of chicken. Avoiding indiscriminate use of antibiotics and good hygienic practices are necessary to control antimicrobial resistance.

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REFERENCES