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**Molecular characteristics of antimicrobial resistance and virulence determinants of *Staphylococcus aureus* isolates from clinical infection and food**

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**Background:** *Staphylococcus aureus* (*S. aureus*) is an important human etiologic agent. Researching the characteristics of popular genotype of *S. aureus*, relating to the pathogenicity and antibiotic resistance, can provide reference for the prevention.

**Methods:** This study collected 275 *S. aureus* isolates from Zhengzhou city of China, including 148 isolates from patients and 127 isolates from ready-to-eat food. Antimicrobial susceptibility testing was performed using the broth dilution method. Molecular characteristics of antimicrobial resistance, virulence and genotypes were identified by PCR.

**Results:** 34.18% (94/275) of *S. aureus* isolates were MRSA. Compared with food isolates, clinical isolates had significantly higher antibiotic resistance rates, the carriage rates of resistance genes including *acc(6')*/*aph(2')*, *aph(3')*-III, *ermA*, *ermB* and virulence genes including *tetM*, *sea*, *seb*, *pvl* and *etb*. MRSA-t030-*agrII*-SCC*mecIII* and MSSA-t002-*agrII* were the most common types among the clinical strains, and MRSA-t002-*agrII*-SCC*mecIII* and MSSA-t002-*agrII* among food strains. Besides, some strains found in *agr* group were also *spa* type-specific, suggesting that there may be phenotypic consistency.

**Conclusion:** The clinical isolates contained more resistance genes and had higher antibiotic resistance, while the two sources strains all had high toxicity. It indicates that the bacteria from different origins may have different evolution process. Since resistance and virulence factors in food bacteria can be transmitted to humans, food handlers should strictly follow hygienic measures during the process of food production in order to ensure the safety of human consumers.

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