

Characterization of methicillin-resistant *Staphylococcus aureus* from ready-to-eat foods in China

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The objective of a new study published in the journal *Zoonoses* was to determine the prevalence, antimicrobial resistance, virulence profiles,

and molecular characteristics of methicillin-resistant *Staphylococcus aureus* (MRSA) obtained from ready-to-eat (RTE) foods in China.

Two hundred seventy-six RTE food-associated *S. aureus* isolates were collected from 25 provinces across China in 2018, then characterized by antimicrobial susceptibility testing, [virulence factors](#) detecting, multi-locus sequence typing (MLST), spa typing, SCCmec typing and pulsed-field gel electrophoresis (PFGE).

Two hundred fifty isolates (90.6%) were resistant to at least one antimicrobial agent; 73 (26.4%) isolates were multi-drug resistant (MDR). Thirty MRSA isolates were identified, among which nine toxin genes (sea, seb, sec, sed, seh, selk, sell, selq, and tst-1) were detected. Sixty percent (18/30) of the MRSA isolates harbored multiple toxin genes.

Four virulence gene patterns were identified, with seb-selk-selq (30/30) being the most common pattern. Thirteen sequence types, as well as 13 spa and four SCCmec types were found among 30 MRSA isolates. The most prevalent MRSA lineages were CC59-t437-SCCmecIV/V (23.3% [7/30]), CC398-t011-SCCmecV (23.3% [7/30]), and CC1-t114-SCCmecIV (16.7% [5/30]).

The findings highlight the importance for the identification of prevalent clones, assessment of drug-resistance and virulence, and formulation of food safety measures for [public health](#).

More information: Wei Wang et al, Antimicrobial Resistance, Virulence, and Genetic Characterization of Methicillin-Resistant *Staphylococcus aureus* Recovered from Ready-to-Eat (RTE) Food in China: A New Challenge for Food Safety, *Zoonoses* (2023). [DOI: 10.15212/ZOONOSES-2023-0025](https://doi.org/10.15212/ZOONOSES-2023-0025)

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