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# **Molecular epidemiology and antimicrobial susceptibility of methicillin-resistant *Staphylococcus aureus* isolates in Xiangyang, China**

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## **Highlights:**

- A total of 53.75% ( $n=43/80$ ) of *S. aureus* isolates were identified as MRSA.
- MRSA isolates were mainly derived from sputum, wound secretions and fester.
- ST239-t030/t632 and ST59-t437 were the dominant epidemic clones in this region.
- PFGE grouped 43 MRSA isolates into five pattern types.
- Eight of the 43 MRSA isolates were positive for the PVL gene (8/43, 18.6%).
- ST239-t030/t632/t037 were the epidemic clones with the most serious drug resistance.

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