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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.