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## Staphylococcus aureus in a northern Italian region: Phenotypic and molecular characterization

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### Abstract

**Background:** *Staphylococcus aureus* is a leading cause of community-acquired infections and healthcare-associated infections. Epidemiological data are useful for understanding the dynamics of the diffusion of this pathogen, and to plan control activities and monitor their efficacy.

**Methods:** *S. aureus* isolates were collected in 13 public hospital laboratories of Emilia-Romagna (northern Italy region) during February-March 2009; phenotypic and molecular characterizations of these isolates were performed.

**Results:** The study sample included 267 isolates, 57 from blood, 81 from respiratory tract, and 129 from wounds; 106 (40%) were methicillin-resistant *S. aureus* (MRSA). MRSA showed a limited number of circulating clones with 2 predominant spa types - t008 and t041 - accounting for 36% and 27% of MRSA isolates, respectively. The t041 type had a higher prevalence of antimicrobial resistance compared to other spa types and accounted for most of the retrieved hetero-vancomycin-intermediate *S. aureus* (h-VISA), while t008 was more frequently detected in non-hospital isolates. A higher degree of genetic diversity was observed in methicillin-susceptible *S. aureus* (MSSA), with no predominant clones and low prevalence of antimicrobial resistance. The occurrence of community-acquired MRSA infection appears to be rare in Emilia-Romagna.

**Conclusions:** In contrast to previous studies reporting Italian data, t008 was the most frequent spa type among MRSA isolates in Emilia-Romagna. The prevalence of antimicrobial resistance of different MRSA spa types could influence their ability to cause infections with hospital onset. The presence of only 2 major MRSA clones circulating in Emilia-Romagna increases the chances that a regional strategy aimed at MRSA prevention will be effective.