



Prevalence, genetic diversity, and antimicrobial susceptibility profiles of *Staphylococcus aureus* isolated from bovine mastitis in Zhejiang Province, China*

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Abstract: This study was conducted to determine genetic diversity and antimicrobial susceptibility profiles of *Staphylococcus aureus* recovered from bovine mastitis in Zhejiang Province, China. Out of 3178 quarter milk samples from 846 lactating cows, among which 459 cows (54.3%) were found HMT positive, 890 quarters (28%) were found having subclinical mastitis. From 75 representative *S. aureus* isolates, 16 distinct types were identified by pulsed-field gel electrophoresis (PFGE). Four major PFGE types (A, B, C, and D) accounted for 82.7% of all isolates, and type A (41.3%) was observed in multiple herds across the studied areas. Each region was found to have a predominant type: Hangzhou type A (64.1%), Ningbo type C (34.5%) and type B (23.1%), Jinhua type D (53.3%), and Taizhou type C (62.5%). Results of antimicrobial susceptibility tests showed that 90.7% of the isolates were resistant to at least one antimicrobial. Resistance to penicillin and ampicillin (77.3%), tetracycline (60.0%), or erythromycin (48.0%) was observed. The bacteria resistant to multiple antibiotics such as penicillin, ampicillin, tetracycline, and erythromycin were commonly found. The information obtained from this study is useful for designing specific control programs for bovine *S. aureus* mastitis in this region.

Key words: *Staphylococcus aureus*, Bovine mastitis, Antimicrobial resistance, Genetic diversity, Pulsed-field gel electrophoresis
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INTRODUCTION

Bovine mastitis is a complex and economically important infectious disease for dairy cattle throughout the world, which can result in substantial losses due to reduced milk yield, and increase culling rates and veterinary expenses (Miles *et al.*, 1992). Subclinical mastitis, without any signs of inflammation compared with clinical mastitis, is the main form of the disease, and accounts for the majority of bovine mastitis cases in dairy herds (Oliver *et al.*,

2004). One of the most important causes of bovine subclinical mastitis is the intramammary infection (IMI) caused by *Staphylococcus aureus*, which is difficult to eradicate (Østeras *et al.*, 2006; Ferguson *et al.*, 2007).

Genetic characterization of mastitis-causing *S. aureus* isolates is vital for an effective mastitis control program, especially for developing a vaccine against *S. aureus*. With the development of molecular biology techniques, microbiologists have more choices for epidemiologic typing of *S. aureus* isolates at the present time. A discriminatory and reliable molecular typing method for the identification of bacterial isolates at strain level is the pulsed-field gel electrophoresis (PFGE) (Tenover *et al.*, 1995; Peacock *et al.*,

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