Molecular Epidemiological Analysis of Methicillin-Resistant *Staphylococcus aureus* Isolates From a Medical Intensive Care Unit: A Comparison of Nasal and Clinical Isolates

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Abstract: *Background:* The control of nosocomial transmission of methicillin-resistant *Staphylococcus aureus* (MRSA) represents a significant challenge to infection control professionals. Nasal carriage colonization by MRSA plays a crucial role in the epidemiology and pathogenesis of this infection. *Methods:* Patients in the medical intensive care unit (ICU) between November 2010 and March 2011 were swabbed when hospitalized, reswabbed 1 week later and for a third time, when they were discharged from the ICU. All swabs were examined within 2 hours of collection using ChromID MRSA-Select agar plates to detect MRSA. Positive specimens were determined to have the *mecA* and *femB* gene through amplification with duplex polymerase chain reaction. Repetitive element sequence–based polymerase chain reaction was used to investigate the epidemiological types of MRSA isolates in the third screening and clinical isolates obtained from 2007 to 2010 in West China Hospital. A comparison of molecular types was performed to investigate the genetic relationship between nasal and clinical isolates. *Results:* After the third screening, 16 nasal MRSA isolates were identified. Epidemiological analysis revealed that 16 nasal MRSA isolates and 37 clinical MRSA isolates differentiated into 2 clusters, comprising 9 subclusters. Of the 16 nasal strains, 11 (68.8%) belonged to subcluster I of cluster I; 3 of 9 subclusters consisted of both nasal and clinical isolates, while 4 of 9 subclusters consisted of clinical isolates and only 2 of 9 consisted of nasal isolates. *Conclusions:* Our study indicated a high degree of genetic relatedness between nasal and clinical MRSA isolates. The molecular typing of MRSA is critical for controlling the nosocomial transmission of this pathogen in ICU setting and defining a nosocomial infection control policy.

Key Indexing Terms: Methicillin-resistant *Staphylococcus aureus*; MRSA-select agar; Rep-PCR; Infection control. **[Am J Med Sci 2013;345(5):361–365.]**

INTRODUCTION

Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most common nosocomial pathogens and is associated with significant morbidity and mortality among hospitalized patients in intensive care units (ICUs).[1] Several characteristics of MRSA contribute to its propensity for epidemic spread, including multidrug resistance, long-term survival in medical environments and high virulence. For the control of MRSA infection, strict compliance with infection control measures is required, such as hand hygiene, environmental cleaning and contact isolation. Active surveillance has been implemented to screen and identify patients who are carriers of MRSA.[2] Furthermore, the analysis of MRSA molecular typing may be useful for controlling the nosocomial transmission of this pathogen in ICU settings.[3]

Nasal colonization by MRSA plays a crucial role in the epidemiology and pathogenesis of infection.[4] The rapid screening and early identification of isolates among high-risk patients is critical for reducing the spread of MRSA.[5] According to a study conducted mainly in southern and eastern Europe, South America and the United States in 2002, it was found that pandemic clones of MRSA belong to several genetic lineages.[6,7] Nosocomial MRSA infection rates were dependent on the medical practice of local hospitals and microbial resistance patterns, which vary from 1% to 80% between different hospitals.[1] Detailed information regarding MRSA genetic relatedness and nosocomial transmission among patients is required for the effective control of the infection.

Active surveillance for MRSA involves genetic analysis of pathogens cultured from nasal samples of patients obtained at the time of admission or during hospitalization. The DiversiLab system is a molecular strain typing system that uses the repetitive element sequence–based polymerase chain reaction (rep-PCR) method to determine the similarity of bacterial strains at the genomic level.[8] The most important advantage of using the rep-PCR microbial genotyping system is the potential to trace the sources of nosocomial outbreaks in the hospital setting, and meaningful results will be obtained across consecutive studies over many years. In the present study, the molecular types of nasal MRSA collected after the patient was admitted in the ICU were compared with the strains of MRSA isolated from clinical samples over 4 consecutive years to investigate any potential relationship, or differences, between nasal colonization and clinically significant MRSA.

METHODS

This prospective study was carried out from November 2010 to March 2011 in the 50-bed medical ICU of West China Hospital. A total of 670 nasal swabs from 336 newly admitted or already hospitalized ICU patients were included in this study. All patients were swabbed when hospitalized, reswabbed 1 week later and for a third time, when they were discharged from the ICU. All swabs were examined within 2 hours of collection.

Nasal swabs were collected by nursing personnel who were trained by microbiology and infection control experts. Specimens were transported in COPAN medium (bioMerieux, Inc; Marcy I'Etoile, France), and cultures were processed within 2 hours of collection in the following manner: all swabs were streaked on ChromID MRSA-Select agar plates (bioMerieux, Inc) for the detection of MRSA. MRSA-select agar plates that

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TABLE 1. Epidemiological features of MRSA in this study

Strain ID	Culture date (day/mo/yr)	Infection or colonization	Isolated source	Antimicrobial resistance pattern	
				R	S
71002	31-7-2007	INF	WS	ERY, TET	VAN, SXT, RIF, CIP, GM
71003	18-5-2007	INF	WS	ERY, CIP	VAN, SXT, RIF, GM, TET
71004	12-7-2007	COL	SP	ERY	VAN, SXT, RIF, CIP, GM, TET
71107	3-7-2007	COL	SP	ERY, TET, CIP, GM	VAN, SXT, RIF
71108	18-7-2007	COL	SP	ERY, TET, CIP	VAN, SXT, RIF, GM
71109	1-9-2007	COL	SP	ERY, CIP	VAN, SXT, RIF, GM, TET
71111	25-9-2007	INF	BC	ERY	VAN, SXT, RIF, CIP, GM, TET
71112	20-9-2007	COL	SP	ERY, TET	VAN, SXT, RIF, CIP, GM
71113	20-9-2007	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
81005	16-5-2008	INF	BC	ERY, TET, CIP, GM, RIF	VAN, SXT
81006	8-6-2008	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
81007	19-5-2008	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
81008	16-8-2008	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
81009	22-7-2008	INF	WS	ERY, TET, CIP, GM	VAN, SXT, RIF
81010	6-6-2008	INF	WS	ERY, TET, CIP, GM, SXT	VAN, RIF
81012	25-5-2008	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
81013	15-5-2008	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
81101	15-5-2008	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
81102	19-5-2008	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
81103	18-6-2008	INF	BC	ERY, TET, CIP, GM, RIF	VAN, SXT
81110	19-5-2008	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
94802	24-1-2009	INF	BC	ERY, TET, CIP, GM, SXT	VAN, RIF
94510	29-1-2009	INF	WS	ERY, TET, CIP, GM, RIF, SXT	VAN
94505	1-3-2009	INF	BC	ERY, TET, CIP, GM, SXT	VAN, RIF
94404	24-2-2009	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
95211	26-5-2009	COL	SP	ERY, TET, CIP, GM, RIF, SXT	VAN
94405	27-11-2009	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
95212	25-2-2009	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
94403	30-3-2009	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
94401	2-8-2009	INF	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
104508	20-2-2010	INF	WS	ERY, TET, CIP, GM	VAN, SXT, RIF
104402	20-3-2010	COL	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
104411	12-4-2010	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
104412	16-4-2010	COL	SP	ERY, TET, CIP, RIF	VAN, SXT, GM
105210	7-5-2010	INF	SP	ERY, TET, CIP, GM, RIF	VAN, SXT
104803	19-6-2010	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
104509	27-8-2010	INF	WS	ERY, TET, CIP, GM, RIF	VAN, SXT
SM4808*	29-1-2011	COL	NS	ERY, TET, CIP, GM	VAN, SXT, RIF
SM4811*	8-1-2011	COL	NS	ERY, TET, CIP, GM	VAN, SXT, RIF
SM4812*	23-12-2010	INF	NS	ERY, TET, CIP, GM, RIF	VAN, SXT
SM4813*	28-12-2010	COL	NS	ERY, TET, CIP, GM	VAN, SXT, RIF
SM5201*	29-12-2010	COL	NS	ERY, TET, CIP, GM	VAN, SXT, RIF
SM5203*	17-2-2011	COL	NS	ERY, TET, CIP, GM, RIF	VAN, SXT
SM5204*	20-2-2011	INF	NS	ERY, TET	VAN, SXT, RIF, CIP, GM
SM5205*	24-12-2010	COL	NS	ERY, TET, GM	VAN, SXT, RIF, CIP
SM5206*	26-12-2010	COL	NS	ERY, TET, CIP, GM, RIF	VAN, SXT
SM5208*	13-11-2010	INF	NS	ERY, TET, CIP, GM, RIF	VAN, SXT
SM4810*	20-11-2010	COL	NS	ERY, TET, CIP, GM	VAN, SXT, RIF
SM4804*	6-1-2011	COL	NS	ERY, TET	VAN, SXT, RIF, CIP, GM
SM5207*	23-3-2011	COL	NS	ERY, TET, CIP, GM, RIF	VAN, SXT
SM4409*	30-3-2011	COL	NS	ERY, TET, CIP, GM, RIF	VAN, SXT