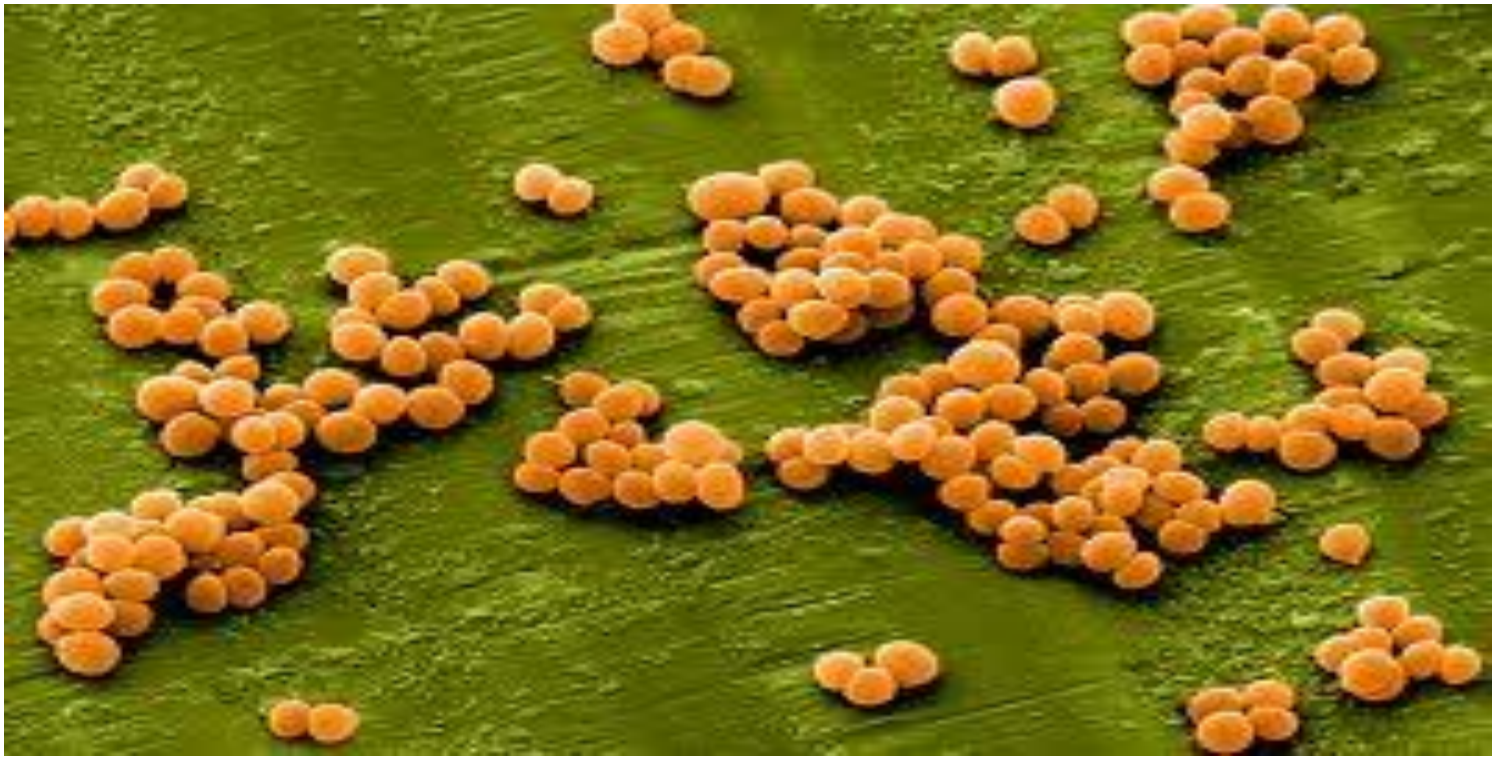
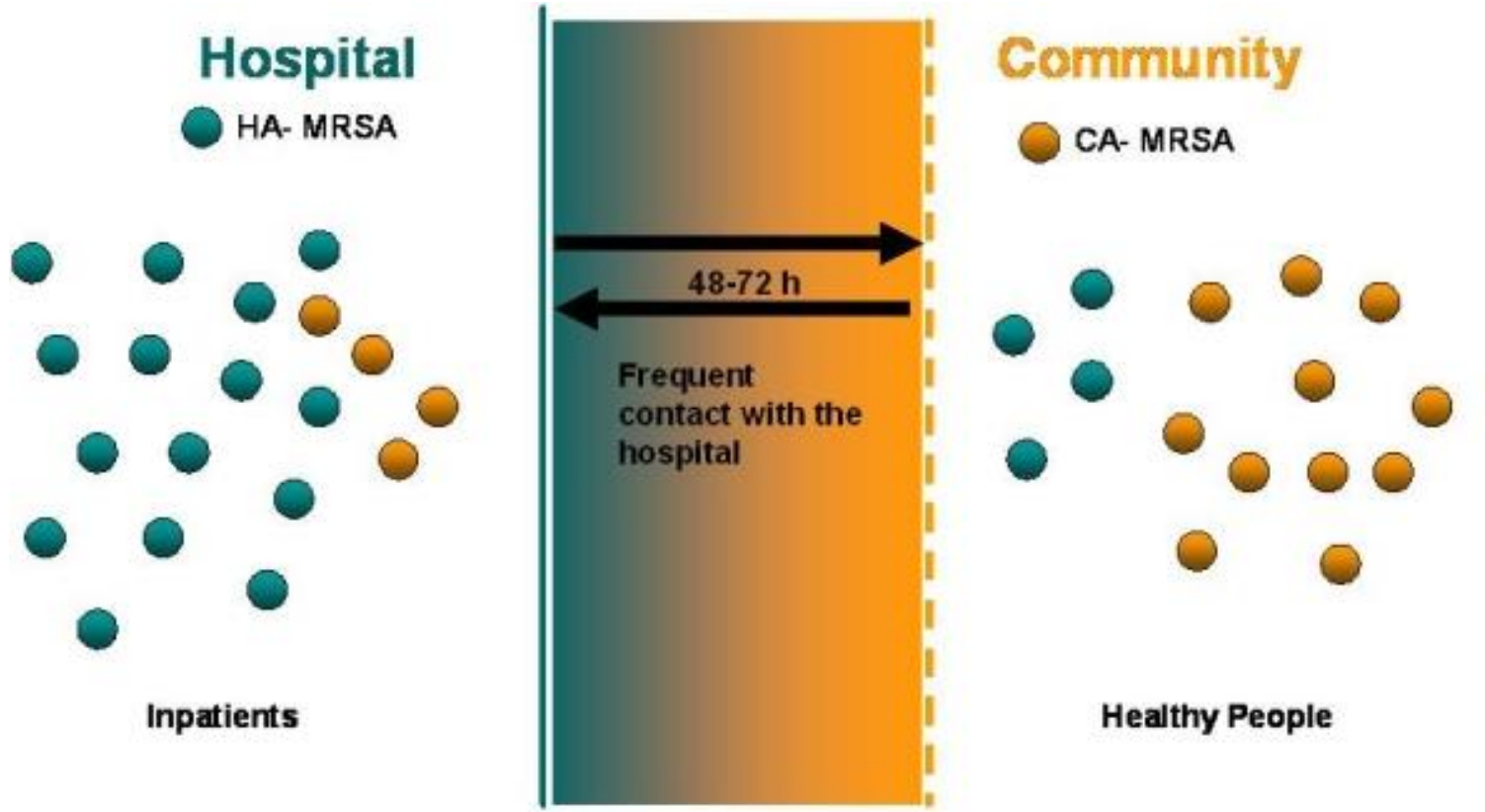
Molecular analysis and susceptibility patterns of methicillin-resistant *Staphylococcus aureus* (MRSA) strains causing community- and healthcare-associated infections in the northern region of Palestine

Kamel Adwan, PhD, Naser Jarrar, MS, Awni Abu-Hijleh, PhD, Ghaleb Adwan, PhD, Elena Awwad, MS and Yousef Salameh, BS.

INTRODUCTION



Nowadays CA-MRSA are beginning to enter hospitals and to acquire resistance to multiple antibiotics, representing a severe public health problem.



Differences Between CA-MRSA and HA-MRSA

	CA-MRSA	HA-MRSA
Most common clinical syndromes	Skin and soft tissue infections (pulmonary, bloodstream, urinary infections much less common)	Nosocomial pneumonia; catheter-related urinary tract, bloodstream, or skin and soft tissue infections
Antimicrobial susceptibility	Usually susceptible to TMP/SMX, doxycycline, clindamycin, rifampin	More often resistant
SCC*mec* type	IV (occasionally V)	I, II, or III
Presence of PVL toxin	Yes (>80%)	Not observed

- SCC*mec* type IV/V has increased mobility and therefore greater potential for horizontal spread to diverse *S. aureus* genetic backgrounds compared with other SCC*mec* types.

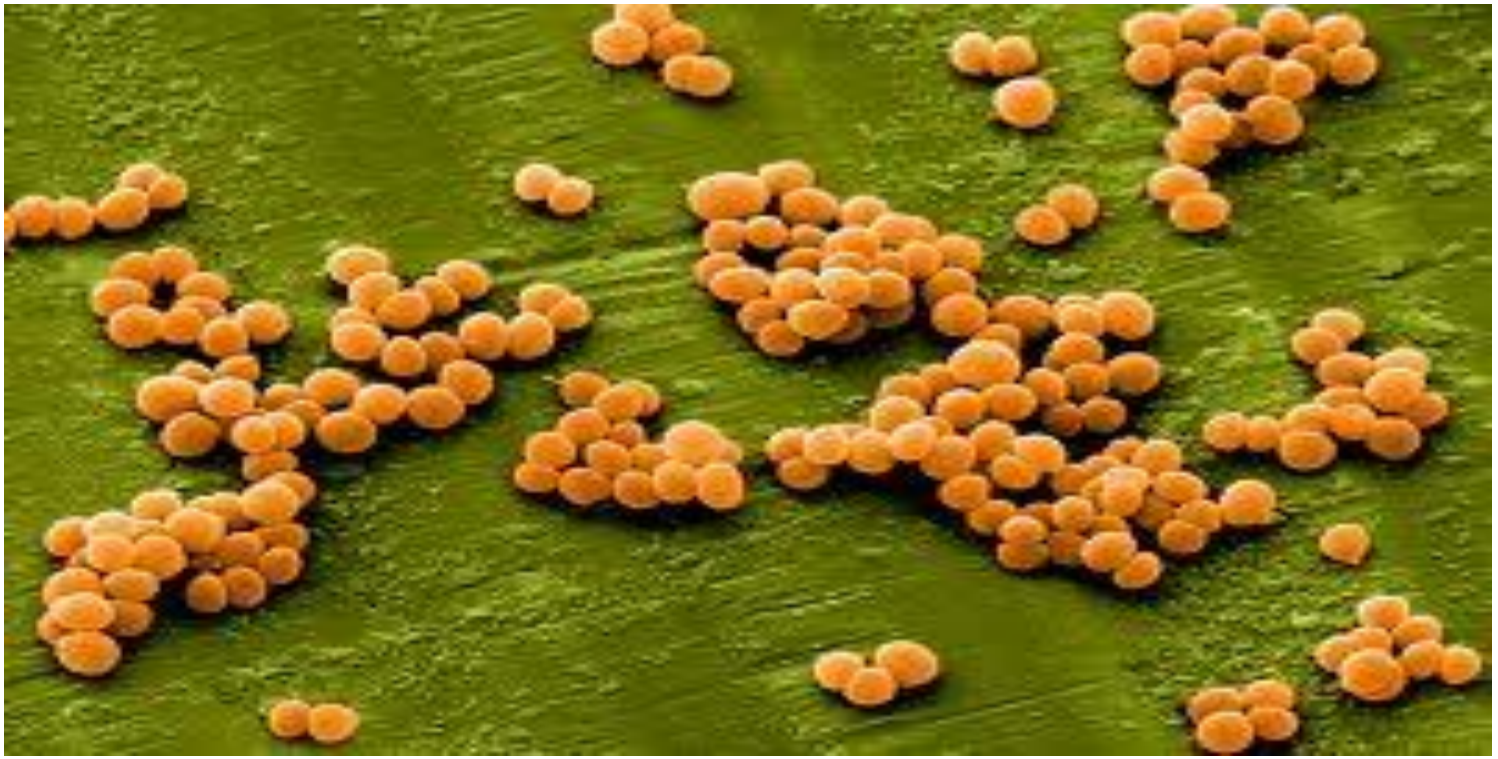
- Nasal carriage of MRSA (include healthy individuals) represents a major risk factor for subsequent infection and transmission of this pathogen.

Objective of study

This study was performed between March and June 2011 at An-Najah National University, Palestine to:

- To obtain a snapshot on the prevalence of nasal carriage of *S. aureus* and MRSA in students of An-Najah National Universityin
- To explore transmission of these strains in healthcare settings,
- To molecularly characterize MRSA strains circulating in Palestine.

MATERIALS AND METHODS



-360 Nasal swabs obtained from healthy students

-46 clinical MRSA isolates obtained from three different health centers in northern Palestine

Identifcation of S. aureus was con?rmed on the basis of Gram stain, production of catalase, and results of Staphytect plus tests

Detection of the mecA gene

SCC*mec* typing

Susceptibility patterns

Partial DNA sequencing of the mecA gene was determined in 6 MRSA isolates representing both nasal and clinical isolates

RESULTS

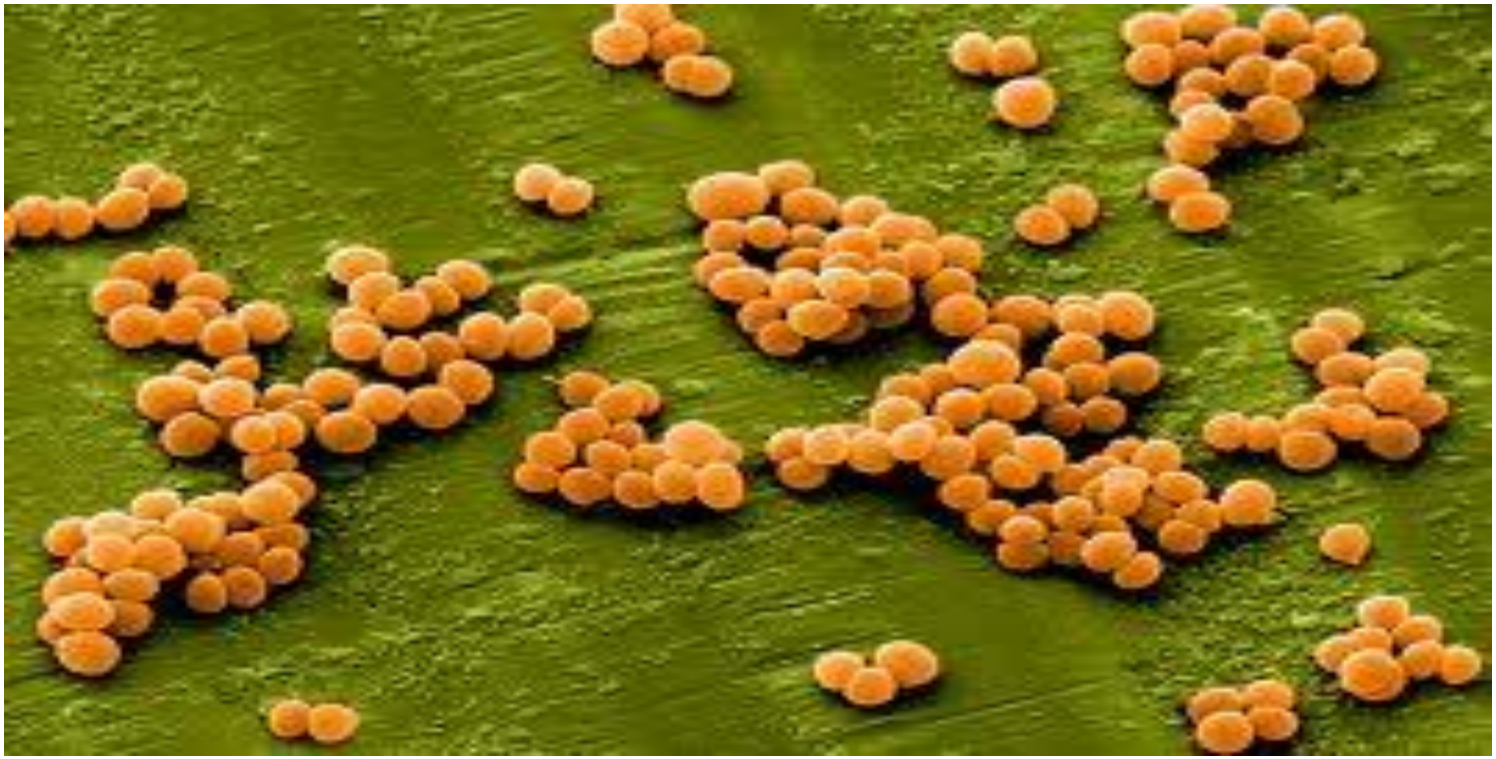


Table 1: Antibiotic resistance of 86 *S. aureus* isolates from healthy students nasal carriers

Antibiotic	Number (%) of resistant isolates
Vancomycin	0
Ciprofloxacin	28 (33)
Penicillin G	84 (98)
Amoxicillin/clavulanic	80 (93)
Erythromycin	20 (23)
Clindamycin	10 (12)
Methicillin	8 (9)

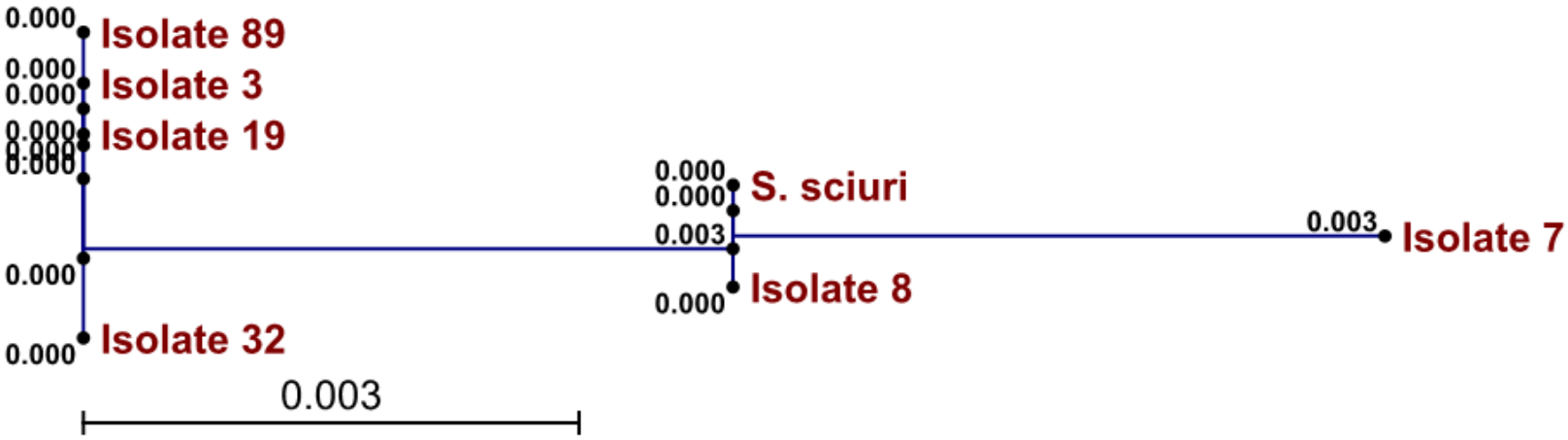
Table 2 : Distribution of 54 clinical and community MRSA isolates by SCC*mec* type and resistance profile.

SCC*mec* type	No. of MRSA strains	No. (%) of Clinical MRSA strains	No. (%) of Nasal MRSA strains	No. (%) of strains resistant to [b] :					
				VAN	CIP	CLI	ERY	AMC	PEN
II	10	10	0	0	6 (60)	8 (80)	10 (100)	10 (100)	10 (100)
III	16	16	0	0	14 (88)	10 (63)	16 (100)	16 (100)	16 (100)
IVa	16	8	8	0	4 (25)	4 (25)	14 (88)	16 (100)	16 (100)
V	12	12	0	0	2 (17)	6 (50)	12 (100)	12 (100)	12 (100)
Total	54	46	8	0	26 (48)	28 (52)	52 (96)	54 (100)	54 (100)

Table 3: Patterns of resistance to individual antibiotics among SCCmec type Iva MRSA isolates

Resistance pattern*	Resistance profile	No. of isolates	
		HA-MRSA	CA-MRSA
CLI, ERY, AMC, PEN	A	2	2
CIP, ERY, AMC, PEN	B	4	-
ERY, AMC, PEN	C	2	4
AMC, PEN	D	-	2

Fig 1. Phylogenetic tree based on the partial nucleotid sequences of the *mec*A gene of three selected CA-MRSA isolates (19, 32, 89), three healthcare settings MRSA isolates (3, 7, 8). The phylogenic tree was rooted with the *S. sciuri* (GenBank accession no. Y13096). Numbers above branches are bootstrap values.



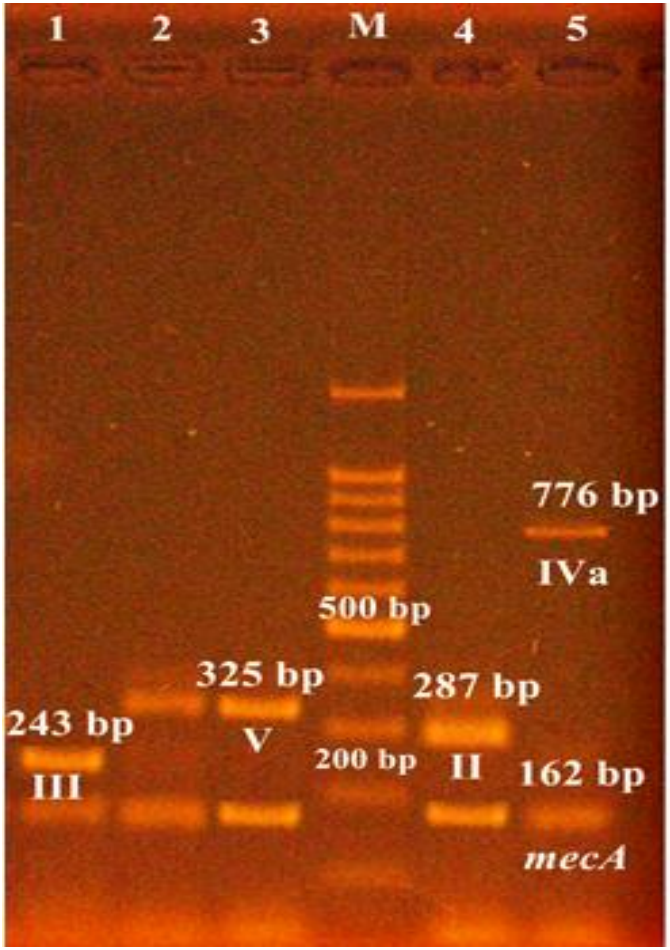
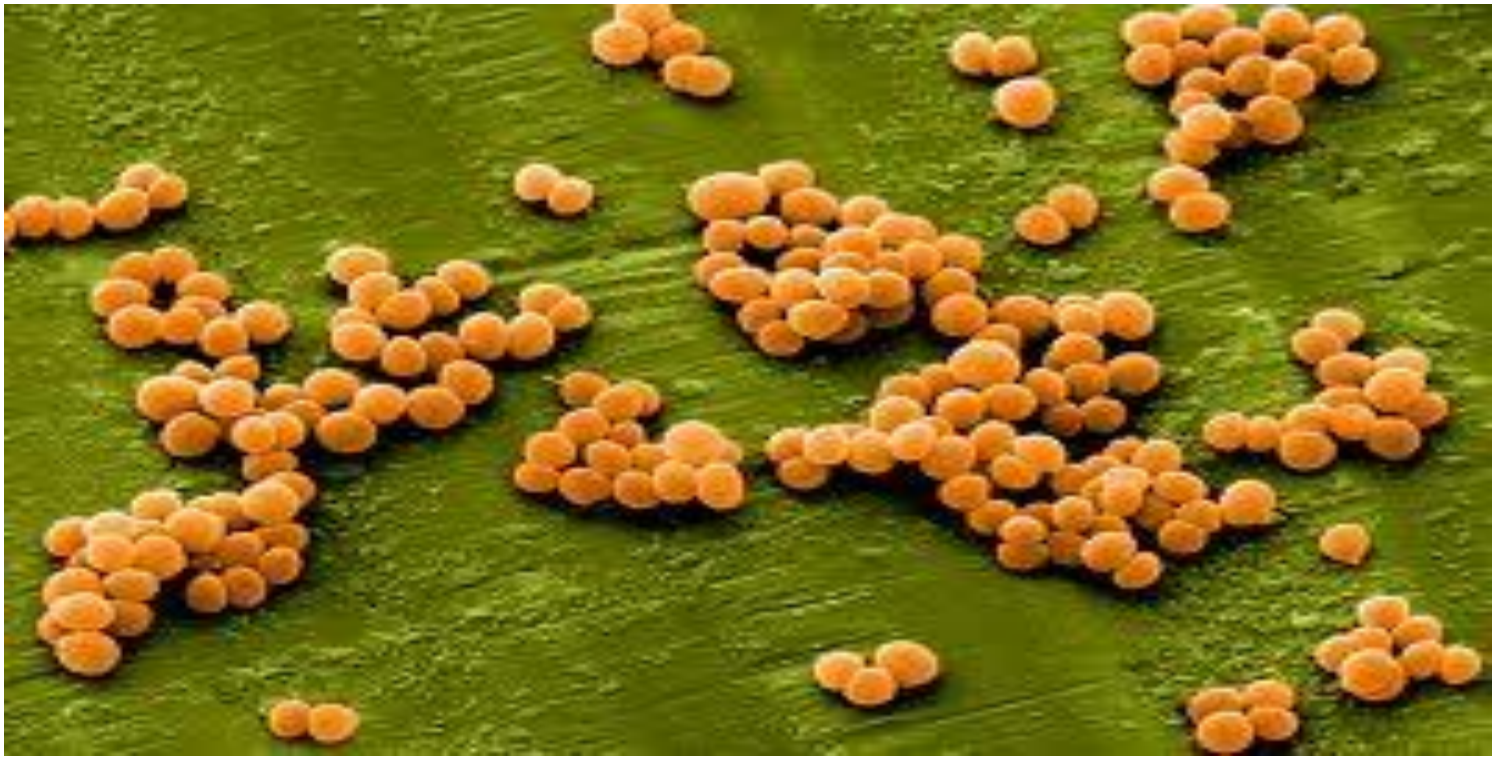


Fig 2. Representative of SCCmec multiplex PCR types detected in MRSA isolates. Lane M, molecular sizes marker (100-bp ladder DNA); 1, type III; 2 and 3, type V; 4, type II; 5, type IVa.

DISCUSSION



- Maximum resistance of *S. aureus* was observed towards penicillin G and amoxicillin/clavulanic acid resulting from uncontrolled, inappropriate use of antibiotics.
- 52% of the MRSA isolates belonged to SCC*mec* types IVa and V, which are traditionally associated with CA-MRSA.
- Nosocomial SCC*mec* types II and III are represented by 48%, whereas SCC*mec* type I was completely absent. These data confirm the tendency of CA-MRSA SCC*mec* type IVa strains to spread in hospital.

- Community associated MRSA strains were less resistant than hospital associated MRSA strains to non-β-lactam, but SCC*mec* types as well, the presence of some CA-MRSA carrying SCC*mec* type IVa resistance profiles within health care settings was observed.
- Sequence analysis shows that the *mecA* genes of the three community associated MRSA isolates were identical to that found in health care settings, and therefore the possibility of horizontal transfer must be considered.


THANK
YOU!


Any
Questions