

**Table 7. Identification of *S. aureus* with the common tests compared with the PCR detection of *nuc* gene.**

Tube Coagulase Test		PCR detection of <i>nuc</i> Gene		% Sensitivity	% Specificity
		Positive	Negative		
Human Plasma	Positive	1	0	100	70
	Negative	3	7		
Rabbit Plasma	Positive	1	0	50	66.7
	Negative	3	7		
DNase	Positive	1	1	36.4	100
	Negative	3	6		
MSA	Positive	4	7	50	66.7
	Negative	0	0		
MSA/DNase/rabbit plasma	Positive	1	1	50	66.7
	Negative	3	6		

## Discussion

Recently, the emergence of MRSA infections in the community among healthy individuals without any risk factors had increased steadily and become a great concern of the community<sup>(10,37)</sup>. In this study, all the three MRSA isolates originated from female students. In addition, all of these three did not have history of cold/flu. The resistant *mecA* gene was predominantly present in the female isolates (8 persons, 88.9%) and seldom present in male isolate (1 person, 11.1%). All of the multiresistant CoNS and *S. aureus* were mainly isolated from female, 13.7% (10 out of 73 females) and 3.7% (1 out of 27 males) from male. Figure 9 shows the distribution of *mecA* gene among the students with different gender.

It was mentioned that the presence of *mec A* gene does not always mean that the *Staphylococcus spp.* show resistance to methicillin as shown in the susceptibility test of E-test and disk diffusion test. This may be due to the presence of the incomplete regulator genes (*mecI* and/or *mecRI*) or maybe because of the inability to express the *mecA* gene<sup>(38)</sup>. The current study proposed that MRSA can colonize nail just like skin and anterior nares (unpublished data). During physical contact, the MRSA may attach to the skin but they also retain underneath nail of the person. In addition, MRSA

may transmit from our daily use item such as cell phones, coins, keys, doorknobs and others (unpublished data).

The resistance to erythromycin was mainly due to the presence of either, *ermA*, *ermB*, *ermC* or combination of the *erm* genes. It was indicated that *ermA* and *ermC* genes are responsible for most of the erythromycin resistance in *S. aureus* which is similar to the result obtained from the current study. All of the isolates contain only *ermC* gene. The *ermA* is part of the transposon Tn554 in the chromosome, while the *ermC* is located on the plasmid<sup>(39)</sup>. *ermC* gene is the most prevalent form where it was found in all eight isolates. None of the isolates contained *ermA* and *ermB* genes. As described previously, *ermB* gene is commonly found on animal strains<sup>(39)</sup>. The results also coincide with the research done by Eady *et al.*; who documented that *ermC* is predominant in clinical and commensal coagulase-negative staphylococci<sup>(39)</sup>.

Resistance towards macrolides is due to the presence of *msr* gene. In this study, *msrA* instead of *msrB* was chosen. Ten of 11 isolates (90.9%) tested contain *msr A* gene. Previous studies reported that no *S. aureus* contains both *erm* and *msrA* genes<sup>(40)</sup>. However, all of the *S. aureus* (100%) in the current study possessed combination of these two genes. Most of the CoNS also contain both *erm* and *msrA* genes.