Abdulaziz Zorgani, J Microb Biochem Technol 2013, 5:4
http://dx.doi.org/10.4172/1948-5948.S1.010

OMICS Group Conferences
Accelerating Scientific Discovery
2nd International Conference on
Clinical Microbiology & Microbial Genomics
September 16-17, 2013 Hampton Inn Tropicana, Las Vegas, NV, USA

Carriage and genetic profile of MRSA isolated from Tripoli paediatric hospital

Abdulaziz Zorgani
University of Tripoli, Libya

Methicillin-resistant Staphylococcus aureus (MRSA) was recognized as one of the most commonly identified antibiotic-resistant pathogen that forms a serious public health problem. There are very limited studies in Libya that address MRSA carriage, and no data is available on the pattern of MRSA among pediatric. We performed a prospective study in Tripoli Pediatric Hospital to determine the nasal carriage rate of MRSA and investigate some resistance and virulence characteristics of MRSA by phenotypic and molecular methods. Traditional and commercial rapid methods were carried out to identify MRSA isolates according to standard guideline methods. Phenotypic and genotypic examinations were applied to MRSA isolates such as PFGE to detect molecular typing and relatedness of MRSA isolates. Over a 16-months period of the study, the overall carriage rate of MRSA was 9.23%. Meanwhile, the prevalence of MRSA among in-patients, their mothers, out-patients, and HCWs was 8.3%, 11%, 2.19% and 12.36% respectively. There was a significant difference between in-patients and out-patients (P=0.044). The highest MRSA carriage rate was observed among ICU patients. 30.7% of in-patients MRSA strains were multi-drug resistance. PCR results exhibited that all tested MRSA (100%) was *mecA*gene carrier, other genes were detected at different rates as following: *luks*PV, *fnbA, icaA/icaD*, and *cna* represents 28.57%, 71.82%, 60% and 34.28% respectively, while *clfA* was not detected. *ermC* was predominant gene (69.23%), followed by *ermB* (46.15%), *msrA* (38.46%) and *ermA* gene (15.38%). Although five PFGE types were recognized among MRSA isolates, but type A was the predominant.Nasal carriage rate of MRSA is low compared to previous local studies. All MRSA isolates carried *mecA* gene and most of erythromycin-resistant isolates carried at least one of macrolide resistant genes. More virulent MRSA strains that harbored PVL-encoding gene and able to form biofilm may increase the possibility of the occurance of severe infection. The majority of MRSA bear at least one adhesion gene, *fnbA* was found the most common gene, but not all of them are able to form biofilm. PFGE type A was the predominant type. Further studies are required to determine the whole genotypic characteristic of MRSA isolates.

zorgania@yahoo.com