Molecular Epidemiology of Staphylococcus aureus Carriage ACME-arcA Gene in Healthy Carrier

Ehsanollah Ghaznavi-RAD*; Mohsen Rezazadeh1; Alireza Amouzande; Alireza Japoni-Nejad1; Hamid Kazemian2; Mahsa Tabib-Nejad1; Nasimeh Fard-Mousavi1; Hamid Bornasi1; Mahtab Bonyadi1; Nona Taheri1; Majid Akbari1

1- Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences. Arak, Iran
2- Students Research Committee, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran

mohsen.rezazadeh@yahoo.com

Background & Objectives: Staphylococcus aureus continues to be an important human pathogen in both healthcare and community settings. The arc gene cluster within the arginine catabolic mobile element ACME may have function as a virulence or strain survival factor. This study aimed to determine molecular epidemiology and prevalence of the ACME-associated arcA gene among S. aureus isolated from healthy student of Arak University of Medical Sciences.

Methods: From the 568 nasal swap specimens, 82 S. aureus isolated by S. aureus–specific isolation procedures. Isolates that carriage ACME-arcA gene were identified by PCR, as well as PCR for determination of single-locus spa sequence typing was carried out. Then data were analysed using Ridom StaphType software.

Results: Among 82 S. aureus isolates, 11 (13.4%) were positive for arcA gene. Strain with spa type t660 was the only Methicillin-resistant Staphylococcus aureus (MRSA) and spa type t1149, t074, t790, t002, t021, t084, t4892, t3204, t701 (two isolates) were known as Methicillin-susceptible Staphylococcus aureus (MSSA).

Conclusion: The detection of ACME-arcA in diverse S. aureus types highlights the mobility of the elements encoding ACME-arcA genes. The diversity of strain types among ACME-arcA-encoding S. aureus is a cause for public-health concern and demands continued surveillance and close monitoring.

Keywords: Staphylococcus aureus; Arginine; ACME; ArcA Gene; Ridom StaphType Software