SURVEILLANCE OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) IN RAW MILK AND MILK HANDLERS WITH NUC GENE SEQUENCING OF THE ISOLATED STRAINS

AMAL S.M. SAYED and ASMAA A. HUSSEIN

Abstract:

The emergence and spread of methicillin resistant Staphylococcus aureus (MRSA) infections are considered a global health issue. This study was designed to determine the prevalence of MRSA in milk from dairy herds and markets. The role of milk handlers as a source of MRSA infection had been studied. Genotyping of the isolated MRSA strains was investigated. A total of 100 samples of farm milk and market milk (50 each) as well as 30 hand swabs of milk handlers were collected randomly from Assiut Governorate. Methicillin resistant Staphylococcus aureus was isolated and enterotoxigenic strains were investigated. Polymerase chain reaction (PCR) was performed to amplify the nuc gene in the isolated strains. Moreover, sequencing of the amplified PCR products and phylogenetic analysis was performed. MRSA strains were isolated from 13.85% of the examined samples (22% and 8% of the examined farm and market milk, respectively) and 55.6% of the isolated MRSA strains were enterotoxigenic. In this study, staphylococcal enterotoxin C was the most enterotoxin detected in the isolated MRSA strains with a rate of 90%. However, enterotoxin type B was detected in 10% of the isolated MRSA strains. In addition, 25% of MRSA strains isolated from market milk were enterotoxigenic with one strain belong to type C. Enterotoxigenic MRSA strains were isolated with a rate of 66.7% from milk handlers and enterotoxin type C was the type of toxin produced by these strains. Nuc gene was detected in 5 (27.8%) out of the 18 MRSA strains. Phylogenetic analysis of the amplified products sequences was done and the results were discussed. Public health hazard of MRSA was discussed and suggestive measures for control were explained.

Keywords:

MRSA, milk, milk handler, PCR, Nuc gene, sequencing.

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