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Molecular typing of community acquired MRSA isolated from retail meats by spa typing, PFGE, and MLST

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Recent studies in both Europe and the United States have revealed a high prevalence of *Staphylococcus aureus* including MRSA strains in retail meats, particularly pork. In this study a total of 48 *Staphylococcus aureus* and MRSA isolates were selected and subjected to molecular typing using PFGE, spa typing and MLST. The sources of the 48 isolates were as follows: 6 chicken livers, 6 chicken gizzards, 6 beef, 6 pork, 6 turkey, 6 chicken and 12 chicken MRSA strains. PFGE was able to perfectly separate 23 of the isolates that showed PFGE patterns into groups according to their meat source while twenty five isolates were non-typable by PFGE. Six of the MRSA isolates belonged to PFGE type USA300, which is community acquired (CA-MRSA). The other six MRSA isolates belonged to PFGE type USA500, which is also a community acquired MRSA. The two MRSA PFGE types USA300 and USA 500 showed spa type t008 and t064 respectively, which are also known to be present in community acquired CA-MRSA. These results affirm that the source of MRSA contamination in our study is human based and may be due to improper handling of the meat at the slaughter house, processing facilities, or at the stores. Preliminary MLST analysis of the seven housekeeping genes for the 48 isolates appeared less discriminatory than PFGE to group the isolates according to their meat source and more analysis is underway. In conclusion Molecular typing is an effective tool for source tracking of foodborne pathogens including *Staphylococcus aureus*.

Biography

Mohamed K Fakhr is currently an Assistant Professor of Molecular Microbiology in the Department of Biological Science at the University of Tulsa, USA. After obtaining his PhD from Oklahoma State University in 2002, he moved to North Dakota State University where he worked as a Postdoctoral Research Associate then a Research Assistant Professor at the Department of Veterinary and Microbiological Sciences. In 2008, he moved to Tulsa, where he currently runs an active research program in the area of Molecular Typing and Detection of Foodborne Bacterial Pathogens alongside exploring the mechanisms by which these foodborne pathogens develop resistance to antimicrobials.

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