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### Molecular characterization of staphylococci isolated from Retail Mushrooms

*Staphylococcus* spp. is a known cause of food poisoning in humans. The prevalence and virulence of *Staphylococci* in retail mushrooms is understudied despite their proposed role as a *mecA* gene reservoir. One of the objectives of this study was to determine the prevalence of *Staphylococci* in both conventional and organic retail mushrooms sold in the Tulsa, Oklahoma area. Characterizing the isolated strains for their possession of toxin and *mecA* genes was also aimed at. Molecular typing of the isolated strains to determine their origin and genetic diversity was also performed. A total of 420 samples of retail mushrooms were purchased from retail stores including Asian markets across the Tulsa area. *Staphylococcus* spp. was isolated from 14 different domestic and imported brands of fresh mushrooms. Prospective colonies of *Staphylococcus aureus* were identified by PCR and the presence of 18 toxin genes and the *mecA* gene were screened for by PCR. A total of 297/420 mushroom samples (70.71%) was positive for the presence of *Staphylococcus* spp. The prevalence of *S. aureus* in the tested mushroom samples was only 1.6%. The *mecA* gene was detected in 64/297 (21.55%) of the positive samples. A total of 552 isolated *Staphylococcal* strains were also tested for the presence of 18 toxin genes. The prevalence of enterotoxins ranged from 0.1% to 2.1%. The *see*, *sej* and *sei* genes were the most detected enterotoxins among all isolates and the exfoliative toxin (*eta*) gene was detected in only one isolate. The genes of toxic shock syndrome toxin 1, leucocidins (*lukE/lukD* and *lukM*), and Panton-Valentine leucocidin (PVL) were not detected in any of the staphylococcal isolates screened. A subset of 120 staphylococcal isolates was subjected to 16S rDNA gene sequencing and was molecularly identified. A total of 10 different *Staphylococcus* species was detected including *S. aureus*, *S. fleurettii*, *S. saprophyticus*, *S. vitulinus*, *S. sciuri*, *S. xylosum*, *S. succinus*, *S. pasteurii*, *S. warneri*, and *S. haemolyticus*. More than half of the screened *S. fleurettii* strains carried the *mecA* gene. Genetic diversity among the identified *staphylococci* strains showed higher diversity reflecting the mushroom compost environment. Genetic diversity in the *mecA* gene among a selected number of isolated staphylococci in this study showed a higher degree of DNA homology among the isolates, indicating that these isolates can serve as a reservoir of this important gene in the environment. Molecular typing using PFGE for the identified staphylococci showed a high degree of diversity that varied according to the mushroom brand. PFGE, MLST and *spa* typing of the isolated *S. aureus* strains showed two distinct strains of a human origin, supporting that contamination with *S. aureus* was as a result of human handling of the mushrooms during packaging. In conclusion, the prevalence of *Staphylococcus* spp. in fresh mushrooms is high and a subset of the strains was shown to harbor enterotoxin genes, which might lead to foodborne poisoning. The *mecA* screening and genetic diversity results support the hypothesis that those staphylococci other than *S. aureus* can serve as reservoirs for this methicillin resistance gene.

### Biography

Dr. Mohamed K. Fakhr, is currently an Associate Professor of Molecular Microbiology in the Department of Biological Science at the University of Tulsa, USA. After obtaining his Ph.D. from Oklahoma State University in 2002, Dr. Fakhr, 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, Dr. Fakhr 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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