

Molecular relatedness of methicillin-resistant *s. aureus* isolates from staff, environment and pets at university veterinary hospital in Malaysia

ABSTRACT

Methicillin-resistant *Staphylococcus aureus* (MRSA) has emerged as a problem in veterinary medicine and is no longer considered as a mere nosocomial pathogen. We studied the occurrence of MRSA in veterinary personnel, cats and dogs and the environmental premises in University Veterinary Hospital (UVH). We found the prevalence of MRSA as follows: UVH 2/28 (7.1%) staff, 8/100 (8%) of the pets [5/50 (10%) of the dogs and 3/50 (6%) of the cats], and 9/28 (4.5%) of the environmental samples. Antibiotic sensitivity tests (AST) show multi-resistance characteristics of the MRSA and the minimum inhibitory concentration (MIC) values for the isolates ranged from 1.5 μg to $>256 \mu\text{g/ml}$. Molecular typing by using multi-locus sequence typing (MLST), staphylococcal protein A typing (*spa* typing) and pulsed-field gel electrophoresis (PFGE) was conducted and the results from MLST indicated that an isolate from a veterinary personnel (PG21), typed as ST1241 belonged to the same clonal complex (CC) as the two isolates from two dogs (DG16 and DG20), both being typed as ST59. The PFGE results revealed that the two isolates from two veterinary personnel, PG21 and PG16 belonged to closely related MRSA strains with isolates from dog (DG36) and from environmental surface (EV100) respectively. The fact that PFGE revealed close similarity between isolates from humans, a dog and environmental surfaces indicates the possibility for either of them to be the source of MRSA and the potential routes and risks of spread.

Keyword: Pandemic; MRSA clones; Veterinarians; Molecular epidemiology; *Spa* typing; MLST; PFGE.