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## Prevalence of Methicillin/Oxacillin Resistant Staphylococcus aureus (MRSA) in Stray and Pet Dogs of Chittagong Metropolitan Area, Bangladesh

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Methicillin resistant Staphylococcus aureus (MRSA) is a multidrug resistant organism that threatens the effectiveness of antibiotics worldwide. The study was carried out in stray (n=108) and pet (n=50) dogs in Chittagong Metropolitan area, Bangladesh to determine the proportionate prevalence of MRSA strains by molecular techniques and their in-vitro antibiotic susceptibility patterns. Oral swabs (N=158) were collected using sterile cotton swabs and were isolated according to cultural properties and molecular amplification of nuc gene. The isolates were subjected to antimicrobial sensitivity testing by Kirby-Bauer method, and resistant mecA gene of MRSA was detected by polymerase chain reaction (PCR). 37 (34.91%) stray and 17 (34%) pet dogs were found positive for S. aureus, of which 18 (16.98%) stray and 7 (14%) pet dogs were found positive for nuc gene of S. aureus. Highest prevalence of MRSA was found in Bayezid (57.89%) and Kotwali (100%), whereas lowest in Pahartoli (22.22%) and Chandgaon (0%) for stray and pet dogs, respectively. A high percentage of MRSA isolates were resistant to antibiotics, including oxytetracycline (83.33%), azithromycin (77.78%), oxacillin (75.93%), sulfamethoxazole + trimethoprim (74.07%), methicillin (74.07%), ciprofloxacin (74.07%), gentamicin (74.07%), amoxicillin (46.3%) and ceftriaxone (42.59%). So, it can be concluded that MRSA in dogs are prevalent in Chittagong, Bangladesh.

### Biography

Tofazzal Md. Rakib received the Doctor of Veterinary Medicine (DVM) and MSc degree from Chittagong Veterinary and Animal Sciences University, Chittagong, Bangladesh. He joined as a Lecturer in the Department of Pathology and Parasitology, CVASU in 2016. His research interest includes pathogenesis of diseases, host-pathogen interaction, pathobiology of infectious diseases, public health concerns of animal diseases, transformation in cancer biology, emerging and reemerging diseases, evolutionary analysis of microorganisms and introducing new economic techniques for the diagnosis and therapy of infections with the application of bioinformatics tools.

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