

First Report on the Molecular and Antimicrobial Susceptibility Studies of Staphylococcus Pseudintermedius Colonizing Shelter Dogs and Dog Owners in Abakaliki, Eastern Nigeria

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Abstract:

Background: The increase in antibiotic-resistant staphylococci among pets and its transfer to humans threaten veterinary medicine and public health.

Objectives: This study was designed to determine the prevalence, antibiotic resistance patterns, and the molecular characteristics of S. pseudintermedius obtained from dogs and dog owners in Abakaliki, Nigeria.

Methods: Exactly 112 swab samples and 97 nasal swabs were obtained from shelter dogs and dog owners respectively. Samples were processed and isolates were identified using standard microbiological procedures. MIC was determined by broth micro-dilution using the sensititre system. Isolates were screened for mecA, mecC, cfr, tetM, tetK, tetL, tetO, sec, siet, exi, and lukD genes by PCR. Sequencing of tetM genes was also done.

Results: Exactly 99 S. pseudintermedius isolates [86 (76.8 %) from dogs and 13 (13.4 %) from dog owners] were obtained, out of which 52 (52.5 %) were identified as MRSP strains as they harboured mecA genes. Isolates were resistant (100 % - 51.2 %) to beta-lactams, fluoroquinolones, clindamycin, trimethoprim/sulfamethoxazole, and erythromycin. Isolates also exhibited resistance to gentamycin (46.5 %), chloramphenicol (23.1 %), tetracycline (19.8 %), and tigecycline (8.1 %). Tetracycline-resistant isolates harboured tetM gene and their DNA sequences were deposited in the NCBI database with their respective accession numbers. Cfr and mecC genes were not detected in the isolates. Isolates harboured sec (73.7 %), exi (2 %), siet (62.6 %), and lukD (55.6 %) virulence genes. Isolates in our study were multi-drug resistant and exhibited homogeneity in their pathogenic factors, thus depicting a possible zoonotic transmission event.



Biography:

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Publication of speakers:

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