

First report on the antibiotic resistance profiles and virulence genes of *Staphylococcus pseudintermedius* colonizing shelter dogs and dog owners in Nigeria- Moses I. B - Ebonyi State University

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Abstract

The increase in antibiotic-resistant staphylococci among pets and its transfer to humans threaten veterinary medicine and public health. This study was designed to determine the antibiotic resistance patterns and the prevalence of virulence genes among *S. pseudintermedius* obtained from dogs and dog owners in Abakaliki, Nigeria. Exactly 112 swab samples (perineum, nares, and mouth) were obtained from shelter dogs while nasal swabs of 97 dog owners and 150 non-dog owners were collected. Swab 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 *sec*, *siet*, *exi*, and *lukD* genes by PCR. A total of 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 methicillin-resistant *S. pseudintermedius* (MRSP) strains as they harboured *mecA* genes. No *S. pseudintermedius* isolate was recovered from non-dog owners. Isolates were highly resistant to penicillin (100 %) and ampicillin (94.2 %). Equal resistance frequency (51.2 %) was each observed for fluoroquinolones, clindamycin, trimethoprim/sulfamethoxazole, and erythromycin. Isolates also exhibited resistance to gentamycin (46.5 %), chloramphenicol (23.1 %), tetracycline (19.8 %), and tigecycline (8.1 %). Isolates harboured *sec* (73.7 %), *exi* (2 %), *siet* (62.6 %), and *lukD* (55.6 %) virulence genes. *S. pseudintermedius* isolates, including MRSP strains which harboured *mecA* genes in this study were multi-drug resistant and notably more resistant than those reported in literature. *Sec*, *exi*, *siet*, and *lukD* virulence genes were harboured by the isolates. There was phenotypic homogeneity in the antibiogram of

isolates from dogs and their owners, thus depicting a possible zoonotic transmission. The ability of *S. pseudintermedius* to cause human infections highlights its lack of host specificity and the importance of considering inter-species transmission.

Staphylococcus pseudintermedius is a normal flora of dogs but when their immune system is compromised, it becomes pathogenic and thus termed an opportunistic microorganism. It is a well-known cause of dermatologic infections such as; pyoderma, otitis externa and wound infections. It has been isolated from serious human infections particularly from people who are in close contact with pets such as; small animal veterinarians and pet owners. However, it has recently emerged as a dangerous opportunistic pathogen comparable to *S. aureus* in humans. Human infections with *S. pseudintermedius* are rare usually local and associated with bite wounds, but there are isolated reports of bacteremia, brain abscess, endocarditis, sinusitis, otitis, infected leg ulcers and pneumonia. Human infection, mainly acquired from dogs has however only recently been reported. The first case of human infection by *S. pseudintermedius* was described by Van Hoovels et al, causing endocarditis after the implantation of a Cardioverter Defibrillator Device (ICD). Since then human infections have been reported sporadically, including surgical site infections, rhinosinusitis and catheter associated bacteremia. Most importantly, Methicillin Resistant *Staphylococcus pseudintermedius* (MRSP) has recently emerged as a significant public health problem in veterinary medicine and entails further consequences for humans. Moreover, the transmission of *S. pseudintermedius* and *S. aureus*

between human and zoonotic hosts is evident and has resulted in severe infections in humans caused by MRSP. Consequently, the importance of this bacterium as a pathogen appears to be underestimated. This underestimation has been shown in recent genomic data which clearly indicates that *S. pseudintermedius* is equipped with genes homologous to those encoding virulence factors and regulatory systems that are characteristic of *S. aureus*. Because, the therapeutic options are limited both for animals and humans, their increasing incidence is an alarming problem. *Staphylococcus pseudintermedius* harbour various virulence factors which are closely related to those harboured by *S. aureus*. It produces enzymes such as coagulase, DNase, protease, thermonuclease and toxins, including haemolysins and exfoliative toxins. *Staphylococcus pseudintermedius* also produces a leucotoxin known as Luk-I, which is very similar to Panton-Valentine Leucocidin (PVL) from *S. aureus*. Knowledge of the pathogenesis of *S. pseudintermedius* remains yet limited. The resistance of *S. pseudintermedius* depends on geographical distribution as well as on other factors; thus, it is important to obtain data from different countries to better understand the epidemiological spread of resistance. This study, was therefore, designed to determine the antibiotic resistance patterns and to molecularly characterize *Staphylococcus pseudintermedius* isolates obtained from dogs and dog owners for various virulence genes in Abakaliki, South-east Nigeria.

Conclusion:

Staphylococcus pseudintermedius isolates in this study were notably more resistant than those reported in literature. This study revealed that amoxicillin-clavulanic acid, ceftazidime and cefepime are no longer effective in treating bacterial infections caused by *S. pseudintermedius* isolates in Ebonyi state as a large number of the isolates obtained in this study were resistant to these antibiotics. This study also showed that ofloxacin, chloramphenicol,

meropenem and ertapenem are still highly active against *S. pseudintermedius* and MRSP isolates from both dogs and humans in Ebonyi state. The *S. pseudintermedius* isolates from dogs and dog owners in this study harboured *sec*, *sxt*, *exi* and *lukD* virulence genes. High prevalence of isolates positive for a significant number of these toxin genes suggests that these genes may play an important role in infection caused by *S. pseudintermedius*. The strange phenotypic homogeneity in the antibiotic resistance profiles observed among human and dog isolates depicts a likely zoonotic transfer between the dogs and their owners. The ability of *S. pseudintermedius* to cause human infections highlights its lack of host specificity and the importance of considering inter-species transmission.