Antibiotic resistance in Staphylococcus aureus from clinical and asymptomatic carriers in Nigeria

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Background: Staphylococcus aureus is an important pathogen causing skin and soft-tissue infections, systemic infections and toxemic syndromes. Treatment options of infections caused by S. aureus are limited due to the problem of antimicrobial resistance. This is why trends in antibiotic susceptibility of S. aureus are constantly being investigated across geographical regions.

Methods & Materials: This study characterized 293 non-duplicate S. aureus isolates obtained from clinical sources and asymptomatic carriers. The Antimicrobial susceptibility testing was performed by disk diffusion and the automated VITEK-2 system. Detection of antibiotic resistance genes in the S. aureus strains was by polymerase chain reaction.

Results: High level resistance was observed against penicillin (97.3%); trimethoprim/sulfamethoxazole (80%) and tetracycline (17.5%). Azithromycin, clarithromycin, erythromycin, clindamycin, linezolid, vancomycin, nitrofurantoin, fusidic acid, mupirocin and rifampicin recorded 100% activity against the isolates. There was no significant difference in antibiotic resistance pattern amongst isolates from clinical and carrier sources at P < 0.05. Ninety-five percent of all strains (n = 277) harboured the mecA gene. The staphylococcal cassette chromosome mec (SCCmec) typing of MRSA strains detected only SCCmec types I and IV in two strains. Eighty-eight percent of MRSA strains were resistant to tetracycline and 50% were resistant to trimethoprim/sulfamethoxazole. All MRSA strains were susceptible to azithromycin, clarithromycin, erythromycin, clindamycin, linezolid, vancomycin, nitrofurantoin, fusidic acid, mupirocin and rifampicin. A particular MRSA strain (Y46) was the only strain resistant to teicoplanin, tigecycline and fosfomycin.

Conclusion: The surveillance of antibiotic resistance in S. aureus is important to prevent the spread of multidrug resistant strains within the hospital environment and the community.

blaOXA-10-efflux pump and aminoglycoside resistance genes in Pseudomonas aeruginosa from Nigeria

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Background: The aim of this study was to characterize the various extended-spectrum β-lactamase (ESBL) and mechanisms of aminoglycoside and fluoroquinolones resistance in clinical isolates of multidrug resistant Pseudomonas aeruginosa from Nigeria.

Methods & Materials: Of the 80 consecutive, non-duplicated clinical isolates of P. aeruginosa obtained from 5 hospitals in 3 southwestern states of Nigeria, 20 class 1 integron positive isolates were selected for the presence of ESBL genes OXA-10, SHV, CTX, AmpC and PER-1 by PCR amplification and gene sequencing. In addition, we investigated the presence of aminoglycosides-modifying enzymes [aac(3)-I, aac(3)-II, aac(6′)-I, aac(6′)-II, ant(2′)-I and ant(3′)-VI] and their associations with various β-lactamase genes and occurrence of mexA and mexB efflux pump regulators.

Results: Presence of blaOXA-10 was confirmed in 80% of the isolates, 75% were positive for AmpC β-lactamase while blaSHV and blaCTXM-15 were detected in one isolate each. Occurrence of AMEs mexA and ant(2′)-I was found among 50% and 45% of the isolates respectively while 35% isolates harboured both enzymes, 45% of the isolates were positive for the two efflux pump regulators mexA and mexB.

Conclusion: This is the first report of the characterization of OXA-10 ESBL in P. aeruginosa from Nigeria, this is also the first report of aac(6′)-I and ant(2′)-I associated with ESBL and occurrence of mexA and mexB efflux regulator genes in clinical isolates P. aeruginosa in Nigeria.

http://dx.doi.org/10.1016/j.ijid.2014.03.624