Type: Poster Presentation

Final Abstract Number: 40.033
Session: Antibiotic Resistance
Date: Thursday, April 3, 2014
Time: 12:45-14:15
Room: Ballroom

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 allstrains (n = 277) harboured the β-lactamase (*blaZ*)gene and 2.7% (n = 8) possessed the *mecA* gene. The staphylococcal cassette chromosome *mec* (SCC*mec*) typing of MRSA strains detected only SCC*mec* 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.

http://dx.doi.org/10.1016/j.ijid.2014.03.623

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bla_{OXA-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 aph(3′)-VI*] and their associations with various β-lactamase genes and occurrence of *mexR* and *nfxB* efflux pump regulators.

Results: Presence of bla_{OXA-10} was confirmed in 80% of the isolates, 75% were positive for AmpC β-lactamase while bla_{SHV} and $bla_{CTXM-15}$ were detected in one isolate each. Occurrence of AMEs *aac (6′)-I* 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 *mexR* and *nfxB*.

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 *mexR* and *nfxB* efflux regulator genes in clinical isolates *P. aeruginosa* in Nigeria.

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