

Commensal/opportunistic bacteria pathogens have been implicated severally in bacteremia and knee-joint infection.

Methods & Materials: Fresh samples of feces (n=65) were obtained from a group of invading cattle egrets (\approx 1000) on trees in Vom, Nigeria. These egrets were not deterred by efforts at tree-trimming. Samples were enriched in tryptone-soy broth and plated on MacConkey agar using standard procedures. All positive cultures were sub-cultured on cefixime-rhamnose-sorbitol MacConkey agar (selective medium) and antibiogram was carried out using diffusion disc with 7 different antibiotics.

Results: *E. coli* (n=58) and *Micrococcus spp.* (n=13) were isolated from the faecal material following enrichment. The pooled *E. coli* colonies were sensitive to Ciprofloxacin (+++), Chloramphenicol (+++), Streptomycin (+), Clindamycin (+) and Tetracycline (+) but was resistant to Vancomycin VA (30) and Vancomycin VA (5). The *Micrococcus spp.* was sensitive to Ciprofloxacin (+++), Vancomycin VA (30) (++) and Vancomycin VA (5) (+) but resistant to Streptomycin, Clindamycin, Tetracycline and Chloramphenicol.

Conclusion: Food animal production processes in Africa is particularly opened to abuse of antibiotics with stockmen often treating their cattle without recourse to veterinarians. Since the ecology of cattle egrets and trans-humance cattle are similar with shared environment, food sources, watering points and movement patterns, it is highly likely that drugs and medicaments are also shared by these species inadvertently. While this work has shown evidence of resistant organisms in fecal materials in cattle egret, more studies will become necessary to identify the potential epidemiologic role these species pose in spreading resistant organisms to poultry and other livestock.

<http://dx.doi.org/10.1016/j.ijid.2014.03.591>

Type: Poster Presentation

Final Abstract Number: 40.003

Session: Antibiotic Resistance

Date: Thursday, April 3, 2014

Time: 12:45-14:15

Room: Ballroom

Study of ceftriaxone-resistant *Klebsiella spp.* clinical isolates from a rural hospital in Mozambique



M.J. Pons^{1,*}, P.L. Alonso¹, J. Vila¹, I. Mandomando², B. Sigauque², O. Fraile³, D. Vubil², N. Palma¹, E. Guiral¹, J. Ruiz¹

¹ CRESIB, Barcelona, Spain

² CISM, Manhica, Mozambique

³ ASM, Manhica, Mozambique

Background: *Klebsiella spp.* is among the most clinically relevant enterobacteria, being increasingly reported as a cause of serious infections and has also been associated with an increasing of multidrug-resistant (MDR) strains. The β -lactams and quinolone antibiotics are used as a treatment of infections caused by *Klebsiella spp.* The emergence of extended-spectrum beta-lactamases (ESBL) is an important public health problem, particularly in low income countries where antibiotics armamentarium is limited. The aim was to characterise beta-lactams and quinolone resistance mechanisms (MQR) in clinical isolates from a rural hospital in Manhica, Mozambique.

Methods & Materials: ESBLs and MQR were investigated among ceftriaxone non-susceptible *K. pneumoniae* clinical isolates recovered between 2004–2009. Characterisation of beta-lactams genes

*bla*_{CTX-M}, *bla*_{SHV}, *bla*_{OXA} and *bla*_{TEM} was established by PCR and sequencing. Presence of MQR, target mutations and transferable mechanisms: *aac(6')Ib-cr*, *qnrA,B,C,D,S*, *qepA*, *oqxAB*, were tested by PCR and sequencing. Epidemiological relationship were done by phylogeny, REP-PCR, pulsed field gel electrophoresis and multilocus sequence typing (MLST), while the transferability was evaluated by conjugation. Additionally, the presence of class-1 and 2 integrons was studied.

Results: A total of 19 *K. pneumoniae* were analysed. The *bla*_{CTX-M-15} was found in 18 strains, while the remaining 1 strain presented *bla*_{SHV-5}. Other ESBLs were found concomitantly: *bla*_{SHV-2}, *bla*_{SHV-2A}, *bla*_{SHV-12} and *bla*_{SHV-38} genes. Additionally, other β -lactamases as *bla*_{TEM-1} or *bla*_{OXA-1} were detected. Referent to MQR: 2 *qnrB* and 6 *aac(6')Ib-cr* were found, as well as, described mutations in quinolone targets. The REP-PCR showed 15 different epidemiological profiles. The MLST analysis also showed great variability of ST groups and high transferable capacity of these genes. High presence of class-1 integrons, mainly conferring resistance to trimethoprim and streptomycin, was detected. High levels of MDR was found to the most used antibiotics in the area. Only, no resistance to carbapenems was found.

Conclusion: These strains present a high level of variation at an epidemiological level in the mechanisms of resistance to third-generation cephalosporin, with predominance of *bla*_{CTX-M-15}. While, the presence of TMQR were less important. In general, high level of antimicrobial resistance has been found in a rural hospital with limited access to third-generation cephalosporins, and broad spectrum antibiotics in general.

<http://dx.doi.org/10.1016/j.ijid.2014.03.592>

Type: Poster Presentation

Final Abstract Number: 40.004

Session: Antibiotic Resistance

Date: Thursday, April 3, 2014

Time: 12:45-14:15

Room: Ballroom

Resistance to the chemotherapeutic agents of *Staphylococcus aureus* strains isolated from hospitalized patients



L.M. Junie*, L.M. Simon, S.L. Pandrea

University of Medicine and Pharmacy Iuliu Hatieganu, Cluj Napoca, Romania

Background: In the last years, the percentage of Methicillin resistance staphylococci (MRSA) increased substantially.

The objectives of the study were the identification of the *Staphylococcus* strains; the antibiotic susceptibility testing of the isolates and the detection of the main antibiotic resistance phenotypes.

Methods & Materials: Species identification was achieved by standard procedures and by the automated system Vitek 2 (Biomérieux). The susceptibility to AB was performed using the Vitek 2 (Biomérieux).

Results: We included in this study 96 strains isolated from hospitalized patients in the Emergency Hospital Prof. Dr. O. Fodor Cluj-Napoca. Of all the isolates, 62.5% were *S. aureus* strains: 41.7% of the strains were MRSA and 20.8% of the strains were MSSA. MRSA were isolated from catheters (10.4%), tracheal secretions (24%), abscesses (16.7%), biliary culture (4.2%), vaginal secretions (2.1%) and pleural liquids (3.1%). The MRSA strains showed a high resistance to Tetracycline (100%) and Imipenem (35.4%), a moderate