Type: Poster Presentation

Final Abstract Number: 40.026
Session: Antibiotic Resistance
Date: Thursday, April 3, 2014
Time: 12:45-14:15
Room: Ballroom

Demographic and microbiological profile of cystic fibrosis in Durban, South Africa

N. Mhlongo[1], U. Govinden[1], J. Egner[2], S. Essack[1,*]

[1] *University of KwaZulu-Natal, Durban, South Africa*
[2] *Netcare, St Augustine's Hospital, Durban, South Africa*

Background: Cystic fibrosis necessitates long-term treatment with multiple antibiotics creating selection pressure for the development of antibiotic resistance in infecting and/or colonizing organisms, impacting on disease management, morbidity and mortality.

Methods & Materials: Sputum samples were obtained from patients attending the only two CF clinics in Durban over a year. The patient demographics and clinical data were recorded. Bacterial isolates were subjected to identification, susceptibility testing and phenotypic screening for extended spectrum β-lactamases (ESBLs), AmpC β-lactamases and metallo-β-lactamases (MBLs).

Results: A total of 25 patients constituted the study sample. The most common genotype was ΔF508 and the most common pathogen was *P. aeruginosa* with susceptibility to antibiotics ranging from 14-100% with marginal differences between mucoid and non-mucoid phenotypes. All *P aeruginosa* isolates were putative ESBL producers and 75% were putative MBL producers.

Conclusion: The incidence, prevalence and susceptibility patterns of bacterial pathogens and colonizers isolated from cystic fibrosis patients should be closely monitored to optimize management and treatment options in a disease requiring chronic antibiotic therapy which increases the propensity for the development of antibiotic resistance.

http://dx.doi.org/10.1016/j.ijid.2014.03.616

Type: Poster Presentation

Final Abstract Number: 40.027
Session: Antibiotic Resistance
Date: Thursday, April 3, 2014
Time: 12:45-14:15
Room: Ballroom

Toxin antitoxin system as an antimicrobial target for antibiotic resistant Staphylococcus aureus

Z. Sekawi

University of Putra Malaysia, Putra, Malaysia

Background: Toxin antitoxin (TA) system is defined as a regulator system consisting of toxin that is neutralized by cognate antitoxin. TA systems have been characterized in a small number of Methicillin Resistant *Staphylococcus aureus*, Vancomycin Resistant Enterococcus, and *Pseudomonas aeruginosa.* The prevalence of TA system in a large number of independently isolated clinical isolates of antibiotic resistant *S. aureus* from diverse locations is determined, then functionality of dominant TA system is evaluated and the antitoxin is subjected for silencing by anti*MazE* Peptide Nucleotide Acid (PNA) subsequently the suicide of bacteria by toxin is determined.

Methods & Materials: It probed total chromosomal and plasmid DNA obtained from 1000 *S. aureus* clinical isolates from Milad hospital in Iran and 60 MRSA clinical isolates from Hospital *Kuala Lumpur* in Malaysia for the presence of TA loci. for Identification of TA loci PCR were performed with chromosomal and plasmid DNA. functionality was evaluated by qPCR, ATPase and turbidity assayes and then the antitoxin was scilenced by PNA assay.

Results: Sequences for one particular TA pair, the *MazEF* TA system, were present on plasmid of all antibiotic resistant *S. aureus* in Milad hospital and MRSA in HKL. Additionally, RT-PCR analysis revealed that the transcripts were produced from *MazEF* loci, suggesting that these loci are functional in the clinical isolates. Also, toxin transcript expression levels were increased when bacteria were grown under stressful conditions. Furthermore, stress decreased cellular ATP levels consistent with *MazF* toxin expression and activity. The ATP results were confirmed by turbidity analysis. The PNA was designed for specific target of *MazE* antitoxin and the results revealed that *MazE* be silenced with 30 μm of anti*MazE* PNA. The finding showed that the *MazF* toxin killed *S. aureus* containing *MazEF* TA loci.

Conclusion: So, these results indicate that *MazEF* TA genes are prevalent and functional within a large proportion of *S. aureus* clinical isolates, and their role in stress tolerance, plasmid or chromosome location, silencing by PNA and toxic effect of the *MazF* toxin against bacterial cells recommended the *MazEF* TA system is a sensitive target for eradication of antibiotic resistant *S. aureus.*

http://dx.doi.org/10.1016/j.ijid.2014.03.617

Type: Poster Presentation

Final Abstract Number: 40.028
Session: Antibiotic Resistance
Date: Thursday, April 3, 2014
Time: 12:45-14:15
Room: Ballroom

Penicillin susceptibility of pediatric Carriage pneumococci, Lower Sindh, Pakistan

S. Shakoor[1], S.-E.-Z. Zaidi[1], A. Hotwani[1,*], F. Jehan[1], I. Nisar[1], S. Qureshi[1], A. Zaidi[2]

[1] *Aga Khan University, Karachi, Pakistan*
[2] *Aga Khan University Hospital, Karachi. Pakistan, Karachi, Pakistan*

Background: *S. pneumoniae* is the main cause of community acquired pneumonia and meningitis in children in Pakistan, and rates of antibiotic resistance have increased dramatically in the last few years. Recent recommendations by the IDSA and revision of breakpoints by CLSI imply that penicillin be the cornerstone of treatment for pneumococcal disease (except meningitis). It is therefore essential to determine penicillin and ceftriaxone susceptibility of carriage pneumococci which lead to invasive disease by translocation. Susceptibility testing of carriage isolates predicts the sensitivity and therefore feasibility of empiric treatment of pneumococcal disease.

We determined the antibiotic susceptibility (AST) and minimum inhibitory concentrations (MICs) of Penicillin and Ceftriaxone