Survey about the Lower Respiratory Tract Bacterial Infections among children in the ICUs in *Egypt*

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Background

The respiratory tract is one of the most common sites of infection. A 1.4 million children are died from acute Lower Respiratory Tract infections (LRTIs), pneumonia and bronchiolitis. This survey is aim to detect the most prevalent causative bacteria for LRTIs among children in the Intensive Care Units (ICUs) from Cairo/ Egypt, and to detect the multi-drug resistant (MDR) bacteria. For farther protection by a trial to prepare a combined vaccine for the most prevalent bacteria of this cases

Methods

- Two hundreds clinical isolates from Lower Respiratory Tract infected children were collected from the Intensive Care Units (ICUs) in Cairo Egypt
- Isolates were microbiologically identified
- The antimicrobial susceptibility testing to different classes of antibiotics were done and the most prevalent causative bacteria for the LRTIs were determined

Green metallic sheen colonies Of *E. coli* on EMB media

A multiple drug resistant PS

% OF BACTERIA

K = *Klebsiella pneumonia* 40%
PS= *Pseudomonas aeruginosa* 40%
AC = *Acinetobacter* spp. 10%
E.C = *E. coli* 7%
S.A = *Staph. aureus* 3%

Result of susceptibility test

Results

- The survey revealed that there are five causative bacteria : *Pseudomonas aeruginosa* , *Klebsiella pneumonia*, *E. coli*, *Acinetobacter*, *Staph. aureus*.
- The most prevalent Causative bacteria were found to be *Pseudomonas aeruginosa* with a percentage of 40% and also *Klebsiella pneumonia* with a percentage of 40% .

Conclusion

- *Pseudomonas aeruginosa* and *Klebsiella pneumonia* are the most prevalent causative bacteria
- Study show that the prevalent bacteria have also a multiple drug resistance character to most of antibiotics especially penicillins , cephalosporins, imipenam , aztreonam ,gentamicin and amikacin .

Further study

The high Multi Drug Resistance among isolates give us a good reason to start preparation of a **combined vaccine** against the most prevalent causative bacteria