Board no 239

Extensively Antibiotic Resistant Acinetobacter spp.: A Life-threatening Infectious Agent for Neonatal Deaths and Illnesses in Bangladesh

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Background

- Genus *Acinetobacter* consists of heterogenous group of organisms associated with hospital environment.
- *Acinetobacter baumannii* is most commonly associated with wide range of infection including sepsis and pneumonia.
- The hospital surfaces such as bed, curtains, furniture, hospital equipment are reservoir of the organism as it can survive in dry condition.
- *Acinetobacter baumannii* resistant to carbapenem, the last resort of antibiotics, is listed as a priority-1 critical pathogen by the WHO and is a cause of nosocomial infection.

Methods

Study: Child Health and Mortality Prevention Surveillance (CHAMPS)

Objective: To understand the causes of stillbirths and under-5 deaths by a panel of experts using laboratory and clinical data in Bangladesh.

Specimens: Bacterial isolates from post-mortem blood specimens and routine clinical specimens of stillbirths and under-5 children with suspected sepsis at a paediatric ward from Aug 2017- Jun 2021.

Laboratory diagnosis: Microbial culture was done using blood culture and identification was done using automated bacterial identification instrument. Antibiotic susceptibility was tested using Kirby-Bauer method. Whole genome sequencing was performed for isolates from post mortem specimens using Illumina NexSeq Platform.

Bioinformatics analysis: Genomic assembly was done with SPAdes 3.13.2. Identification was confirmed with pubMLST, 16S rRNA blast, FastANI and KmerFinder. Sequence type was determined using Pasteur MLST scheme. AMR genes were idenfied using ResFinder and CARD-Resistance Gene Identifier.

Results

Neonates are more susceptible to Acinetobacter infection

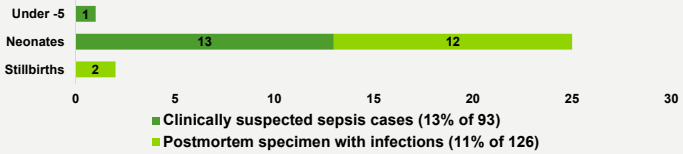

Fig 1. Age distribution of cases with infection among clinically suspected sepsis cases and post-mortem cases

Multidrug resistant A. baumannii are highly associated with the cases

All isolates were resistant to first-line antibiotics used in neonates (ampicillin and gentamicin) and >80% against second-line antibiotics (meropenem and amikacin). Isolates were all susceptible to tigecycline, colistin and polymyxin B. Over 80% isolates contain carbapenemase resistance gene.

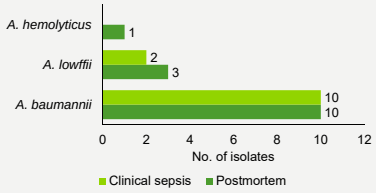

Fig 2a. Frequency of different species determined by bacterial culture

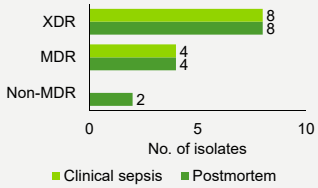

Fig 2b. Distribution of antibiotic resistance across isolates

Genomic level analysis identified diversity among the Acinetobacter isolates compared to biochemical assay based identification

Whole genome analysis was performed with the isolates from post-mortem specimens. Identification using different bioinformatics tool yielded different species compared to biochemical identification.

Total 5 genomic sequence types were identified (2, 23, 575, 622, 976). Interestingly, the data identified a possible outbreak by ST 575 from 2020-21.

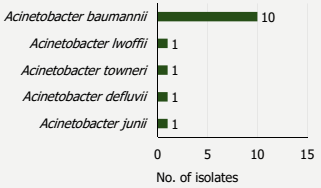

Fig 3a. Frequency of different species determined by genomic analysis

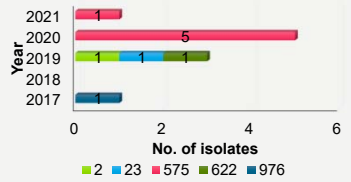

Fig 3b. Distribution of several sequence types over the years

Diverse carbapenem resistance genes were identified from Acinetobacter spp.

Genomic investigation identified bla_{OXA-23} gene among 65% of the isolates. bla_{NDM-1} was identified from two *A. baumannii* and one *A. towneri* isolate.

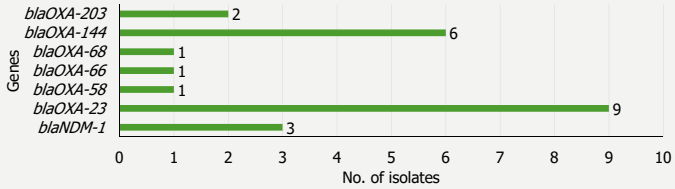

Fig 4. Frequency of carbapenemase resistance genes identified from the Acinetobacter isolates from post-mortem genes

Conclusions

A concerning proportion of neonatal deaths and suspected sepsis were caused by carbapenem-resistant *Acinetobacter* infections. Implementation of hospital infection control and improved clinical management is necessary to control unwanted child death and sufferings.

CHAMPS

https://champshealth.org/

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