Prevalence of antibiotic resistance genes in Acinetobacter baumannii isolated from clinical specimens from Pretoria Academic Hospital

Bellomo AN, Kock MM, Makgotlho PE, Hoosen AA and Ehlers MM

Department of Medical Microbiology, Faculty of Health Sciences, University of Pretoria/NHLS

INTRODUCTION

- Acinetobacter baumannii (A. baumannii) is an opportunistic pathogenic, which belongs to the family Moraxellaceae
- This bacteria is associated with outbreaks of nosocomial infections in intensive care units
- Incidence of A. baumannii infections have escalated since emergence of drug resistant strains in 1995
- The largest antibiotic resistance island known was identified in A. baumannii and consisted of more than 40 genes
- The bacteria were sensitive to the carbapenem β-lactams and tetracyclines classes of antibiotics until the 1970’s
- Acinetobacter baumannii naturally produces AmpC β-lactamase and oxacillinases
  - Class B: metallo-β-lactamasates (MBL’s)
  - Class D: carbapenem hydrolysing oxacillinases (CHDL’s)
- The first CHDL genes were reported in 1995

AIM

The aim of this study was to investigate the prevalence of antibiotic resistance genes from clinical specimens of A. baumannii, from the Pretoria Academic Hospital, by performing two different Multiplex Polymerase Chain Reactions

MATERIALS AND METHODS

- Ninety seven (97) A. baumannii isolates were obtained from clinical specimens sent from the Pretoria Academic Hospital for microbiological analysis to the Diagnostic Division in the Department of Medical Microbiology, UP/NHLS
- The isolates were identified as A. baumannii and underwent susceptibility testing using the Vitek 2 Automated System (bioMérieux, France)
- Automated DNA extraction was performed using the MagNA Pure Compact (Roche, Germany)
- Multiplex I amplified blaOXA-23, blaOXA-24, blaOXA-51 and blaOXA-58 genes, while Multiplex II amplified IMP, VIM, SPM-1, GIM-1, SIM-1 genes
- The multiplex PCR’s were done using the Qiagen Multiplex PCR kit 1000 (Qiagen, USA) according to the manufacturer’s instructions, using the Perkin Elmer GeneAmp System 9600 (Lab Centraal BV, Haarlem, The Netherlands) and cycling conditions as previously described

RESULTS AND DISCUSSION

- Multiplex I showed that 59% (58/97) of the isolates were positive for OXA-23, 83% (81/97) positive for OXA-51 and 3% (3/97) positive for OXA-58 (Figure 1)
- Figure 2 shows a gel electrophoresis of Multiplex I with bands for OXA-23, OXA-51 and OXA-58 present
- None of the isolates were positive for OXA-24
- Multiplex II showed that only 1% (1/97) of isolates were MBL positive with a VIM-like gene

CONCLUSIONS

- OXA-23 and OXA-51 genes were highly prevalent in clinical isolates of A. baumannii analysed in this study. This is similar to worldwide prevalence
- MBL genes were not prevalent in clinical isolates of A. baumannii in South Africa, however a prevalence of (59%) was reported in Korea
- This multiplex PCR proved to be a rapid technique for antimicrobial susceptibility testing

REFERENCES