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

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INTRODUCTION

- *Acinetobacter baumannii* (*A. baumannii*) is an opportunistic pathogen, 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 carbapenems, β-lactams and tetracyclines classes of antibiotics until the 1970's
- *Acinetobacter baumannii* naturally produces AmpC β-lactamase and oxacillinases
  - Class B: metallo-β-lactamases (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 manufacturers 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

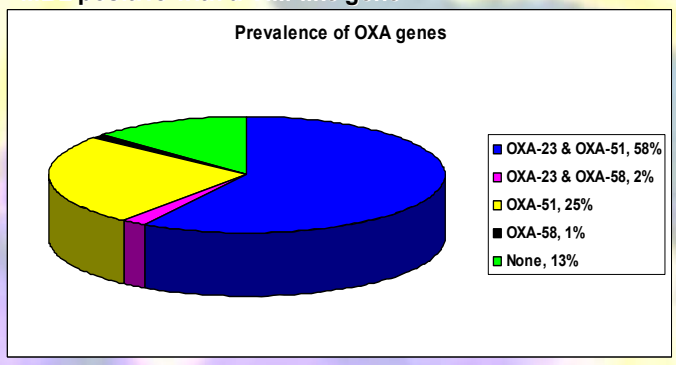

Figure 1: Pie chart showing the results of the Multiplex I for the prevalence of the OXA genes in the selected clinical isolates

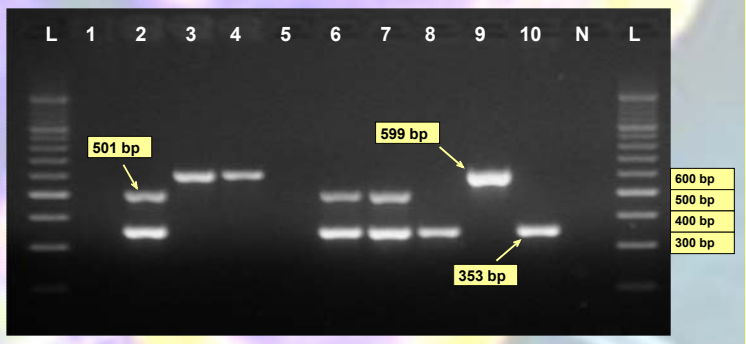

Figure 2: Multiplex I simultaneously amplified OXA-23 (501 bp), OXA51 (353 bp) and OXA-58 (599 bp). Lanes 1 and 5 were negative for all of the OXA genes. Lanes 2, 6 and 7 were positive for OXA-23 and OXA-51. Lanes 3,4 and 9 were positive for only OXA-58. Lanes 8 and 10 were positive only for OXA-51. Lane N was the Negative control. (O'Range Ruler 100 bp DNA Ladder)

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

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