Prevalence of extended-spectrum-β-lactamase (ESBL) and metallo-β-lactamase (MBL) antibiotic resistance genes in Enterobacter species in Pretoria Academic Hospital

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Introduction

- Enterobacter spp are opportunistic pathogens that rarely colonise healthy humans
- The pathogenic Enterobacter spp harbour extended-spectrum β-lactamase (ESBL) and metallo-β-lactamase (MBL) enzymes
- The ESBL enzymes were first identified in 1980 in Germany and are frequently the products of three genes bla<sub>CTX-M</sub>, bla<sub>SHV</sub> and bla<sub>TEM</sub>
- The MBL enzymes were first reported from a Bacillus cereus strain in 1999 in Italy. The bacteria harboured the VIM and IMP genes
- Multi-drug resistance due to the presence of the ESBL and MBL resistance genes in Enterobacteriaceae is the cause of therapy failure during treatment with 3<sup>rd</sup> generation cephalosporins and carbapenemns
- Detection of ESBL and MBL producing bacteria is based on phenotypic and genotypic techniques
- A multiplex PCR can be used for the simultaneous detection of these resistance genes

Aim

- To investigate the prevalence of ESBL and MBL antibiotic resistance genes in Enterobacter species in Pretoria Academic Hospital using a multiplex PCR assay

Materials and Methods

- Ninety-seven (97) consecutive clinical Enterobacter isolates were collected from the diagnostic division of the Department of Medical Microbiology
- The study included 16 E. aerogenes and 81 E. cloacae isolates
- Identification and antibiotic resistance was determined using the Vitek 2 (bioMérieux, France)
- The MagNA Pure Compact (Roche Applied Science, Germany) was used for the extraction of total DNA according to the manufacturer’s protocol
- The multiplex PCR amplification assay was performed using the QIAGEN Multiplex PCR kit (QIAGEN, USA) following the manufacturer’s instructions on a PX2 Thermal Cycler (Thermo Electron Corporation, MA, USA)

Results and Discussion

- The multiplex PCR successfully detected the presence of the bla<sub>CTX-M</sub>, bla<sub>SHV</sub> and bla<sub>TEM</sub> genes in the Enterobacter spp isolates from the Pretoria Academic Hospital (Figure 1)
- In total, the prevalence of ESBL antibiotic resistance genes in Enterobacter species was 56% (54/97) in this clinical setting
- ESBL genes were detected in 25% (4/16) of E. aerogenes isolates, while 75% (12/16) were negative (Figure 2)
- In E. cloacae, 62% (50/81) of the isolates harboured ESBL genes, while 38% (31/81) were negative (Figure 3)
- None of the Enterobacter isolates analysed in this study were positive for the VIM gene
- A 22% ESBL prevalence in Enterobacter spp was reported in the Tel Aviv Medical Centre (Israel) in 2005 (Schlesinger et al., 2005), while a much lower ESBL prevalence of 2% was reported in the United States (Schwaber et al., 2004)

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References

- Sanders WEJR and Sanders CC (1997) Enterobacter spp.; pathogens poised to flourish at the turn of the century. Clinical Microbiology Reviews 10:220-241

Conclusion

- The results of this study showed a high prevalence of 56% ESBL genes in Enterobacter spp in Pretoria Academic Hospital
- It is essential to include molecular techniques as part of surveillance to monitor the circulation of these resistant genes in a clinical setting