

P1135 **Molecular epidemiology of clinical *Pseudomonas aeruginosa* isolates in the Tshwane region, South Africa**

Kedisaletse Moloto¹, Johann Pitout², Marthie M Ehlers¹, Farzana Ismail³, Marleen Kock*¹

¹University of Pretoria, Medical Microbiology, Pretoria, South Africa, ²Calgary Laboratory Services (AHS), Division of Microbiology, Calgary, Canada, ³The National Institute of Communicable Diseases, Microbiology, Johannesburg, South Africa

Background: *Pseudomonas aeruginosa* is an important opportunistic pathogen capable of causing life-threatening diseases. High-risk *Pseudomonas aeruginosa* clones belong to mainly sequence type (ST) 111, ST175 and ST235, which are responsible for epidemics of healthcare outbreaks caused by multidrug resistant (MDR) and extensively drug resistant (XDR) strains worldwide. The spread and the genetic diversity of healthcare associated pathogens, such as *P. aeruginosa* can be monitored by molecular typing techniques. Data on the molecular epidemiology of clinical *P. aeruginosa* in South Africa is limited, therefore, the purpose of this study was to investigate the genetic relatedness of *P. aeruginosa* as well as to determine the epidemiological profiles of the *P. aeruginosa* isolates circulating in the Tshwane region.

Materials/methods: A total of 237 consecutive non-repeat *P. aeruginosa* isolates were collected from the National Health Laboratory Service from May to September 2016. The samples were collected from hospitals and clinics in Pretoria and the greater Tshwane region. Clonal relatedness was investigated by pulsed field gel electrophoresis (PFGE) with *SpeI* on all 237 *P. aeruginosa* isolates. This was followed by multi-locus sequence typing (MLST), which was performed on only selected isolates (10) representing different PFGE types, samples and participating hospitals.

Results: A high prevalence of multidrug resistance (resistant to at least one antimicrobial agent in three or more antimicrobial classes) was observed among the studied isolates. Pulsed field gel electrophoresis identified 70 isolates belonging to 30 different minor (< 5 isolates with ≥80% similarity) pulsotypes. The MLST analysis of the 10 selected isolates showed only two previously reported sequence types (STs); ST1712 (PA27) and ST2546 (PA117). Seven new STs, i.e. ST2829, ST2833, ST2836, ST2838, ST2839, ST2843 and ST2845 were identified in this study.

Conclusions: This study revealed that the *P. aeruginosa* isolates circulating in the Tshwane clinical settings have a high genetic diversity. The high prevalence of MDR *P. aeruginosa* in the studied clinical setting has serious implications for the treatment of *P. aeruginosa* infections. None of the common high risk clones were found in this study; however, the spread of the identified clones poses a threat to our healthcare system.