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O0915 Dissemination of high-risk clonal group 307 amongst extended-spectrum beta-lactamase producing *Klebsiella pneumoniae* isolates in neonatal and paediatric wards in Tshwane, South Africa

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Background: *Klebsiella pneumoniae* infections places a burden on healthcare settings. Acquisition of virulence factors *via* plasmid mediated transfer and production of extended spectrum beta-lactamases (ESBLs) makes antibiotic therapy of these infections difficult. Extended spectrum beta-lactamase producing *K. pneumoniae* are often part of the clonal group (CG) 307 consisting of high-risk clones including sequence type (ST) 307. Patients at high risk of obtaining hospital-acquired infections include neonatal and paediatric patients, especially those in intensive care units.

Materials/methods: Non-repetitive *K. pneumoniae* isolates collected from tertiary hospitals around the Tshwane area were identified as ESBL producers using the Vitek® 2 automated system. Representative isolates from neonatal and paediatric patients and wards were confirmed as ESBL producers using a phenotypic combined disk diffusion test. These isolates were screened for three selected beta-lactamase genes using a multiplex polymerase chain reaction (M-PCR) assay. An enterobacterial repetitive intergenic consensus sequence PCR (ERIC-PCR) assay was performed on the isolates and a dendrogram was constructed to assess genetic relatedness. A representative isolate of the most common cluster in the dendrogram was analysed using multilocus sequence typing.

Results: One hundred and four ESBL producing *K. pneumoniae* isolates were collected. Thirty isolates were found to represent the neonatal-paediatric subset population. Twenty-nine isolates were positive for ESBL production using the phenotypic disk diffusion test. Twenty-nine isolates screened positive for the beta lactamase genes cefotaximase-Munich (CTX-M), Temoniera (TEM), and sulfhydryl variable (SHV) enzymes; one isolate tested negative for CTX-M. Analysis of the dendrogram showed a cluster of 10 isolates with the same ERIC-PCR fingerprint. A representative isolate of this cluster was identified as a novel double locus variant of the high-risk ST307 clone. This novel sequence type was spread across four different hospitals in the Tshwane area and across many different neonatal and paediatric wards.

Conclusions: The identification of emerging high-risk *K. pneumoniae* clones, including novel CG307 sequence types, aids in the understanding of evolutionary patterns and the prediction of how these clones will evolve in the future. Revising infection control and prevention strategies would aid in preventing the dissemination of these clones in the Tshwane area.