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P0915 The emergence of Klebsiella pneumoniae ST307 clade II in private and public sectors in South Africa

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Background: There is a desperate need for molecular surveillance systems, especially in developing countries, with the ability to recognize and track the emergence of high-risk antimicrobial resistant (AMR) clones in a real time fashion. Whole genomic sequencing (WGS) and rapid PCR were used to track the emergence of a novel *K. pneumoniae* clone ST307 with $bla_{\text{OXA-181}}$ in private and public sectors in South Africa.

Materials/methods: A total of 948 clinical *Klebsiella pneumoniae* were collected from 2007 to 2017 across South Africa. Illumina WGS was performed on a sub-collection (n=27) and this information was used to design PCR primers for the identification of ST307 and its association with $bla_{\text{OXA-181}}$ on IncX3 plasmids.

Results: WGS showed that *K. pneumoniae* ST307 belonged to two clades. Clade I was associated with $bla_{\text{CTX-M-15}}$ and corresponded to ST307 sequences deposited in Genbank (n=9). A novel ST307 clade II (that differ from clade I in approximately 100 SNPs) contained $bla_{\text{OXA-181}}$ and was associated with IS*3000* on IncX3 plasmids. PCR screening showed that ST307 clade I with $bla_{\text{CTX-M-15}}$ was present in 2007and clade II with $bla_{\text{OXA-181}}$ emerged during 2012. In 2013 and 2014, 15% (20/135) of *K. pneumoniae* with $bla_{\text{OXA-181}}$ tested positive for ST307 clade II and was found in three Gauteng cities. During 2015 to 2016 the numbers of ST307 increased exponentially; 60% (297/499) belonged to clade II that had subsequently spread to 10 other cities across six different provinces (i.e. Eastern Cape, Gauteng, Free State, Limpopo, Mpumalanga, North West).

Conclusions: This study described the rapid emergence over a 10-year period of *K. pneumoniae* ST307 clade II with $bla_{\text{OXA-181}}$ in South Africa and highlighted the importance of using WGS to develop molecular surveillance methods for tracking emerging AMR clones in a rapid fashion. Our results suggest that clade I with $bla_{\text{CTX-M-15}}$ established itself first in the healthcare system during the mid-2000s and clade II evolved and rapidly spread after acquiring IncX3 plasmids containing $bla_{\text{OXA-181}}$.