P1190
Paper Poster Session
Deciphering carbapenem resistance

Genetic context of blaNDM-1 isolated from Acinetobacter baumannii and Klebsiella pneumoniae from India, Belgium and Iraq

Xavier Basil Britto*[1], Hadi Ameen[2], Jasmine Coppens[1], Lavanya Vanjari[3], Runak Hawrame[4], Azad O Maged[5], Youri Glupczynski[6], Christine Lammens[1], Lakshmi Vemu[3], Herman Goossens[1], Surbhi Malhotra-Kumar[7]

[1]*University of Antwerp, Laboratory of Medical Microbiology, Wilrijk, Belgium*

[2]*University of Antwerp, Wilrijk, Belgium*

[3]*Nizam's Institute of Medical Sciences, Department of Microbiology, Panjagutta, Hyderabad, Telangana, India*

[4]*Sulaymanyha Teaching Hospital,, Laboratory of Medical Microbiology, Sulaymanyha, Iraq*

[5]*Raparin Paediatric Teaching Hospital, Erbil, Iraq*

[6]*Chu Ucl Namur (Université Catholique de Louvain), Site Godinne, Laboratory of Microbiology, Yvoir, Belgium*

[7]*University of Antwerp, Laboratory of Medical Microbiology, Wilrijk, Antwerpen, Belgium*

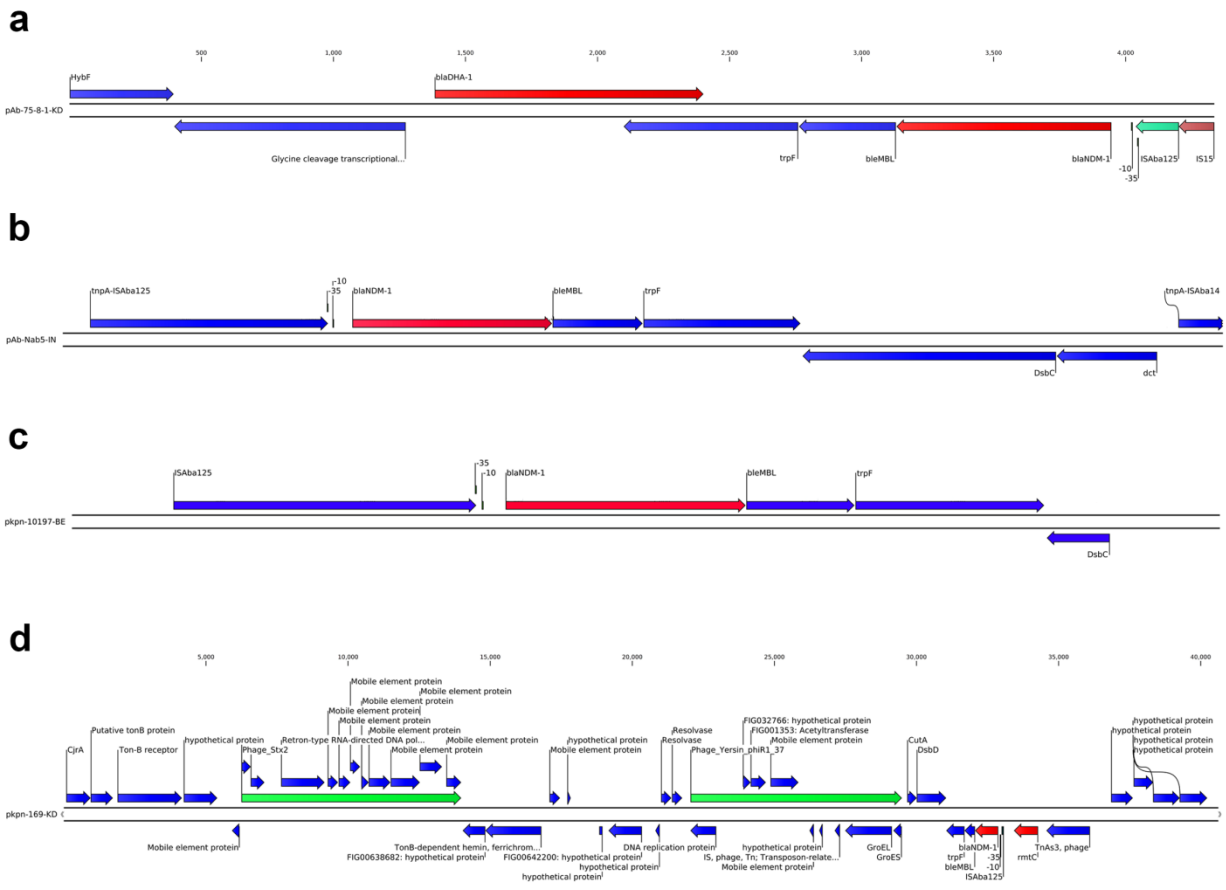
Background: Widespread dissemination of carbapenem resistance due to rapidly spreading resistance determinants such as *bla*$_{NDM}$ (New Delhi metallo-β-lactamase) is now a global crisis. *bla*$_{NDM}$ is *harbored* on various multi-drug resistant plasmids that transfer easily within and between Gram-negative bacterial species. Here, we investigated the genetic context of the *bla*$_{NDM-1}$ gene present in *A. baumannii* and *K. pneumoniae* isolated from hospitalized patients in Kurdistan (Iraq), India and Belgium.

Material/methods: Two strains each of *K. pneumoniae* and *A. baumannii* exhibiting phenotypic carbapenem resistance were isolated from hospitalized patients in Kurdistan (KD), Belgium (BE) and India (IN). The strains (Kpn-169-KD, Ab-Nab5-IN, Ab-75-8-1-KD and Kpn-10197-BE) were screened for carbapenemase genes by PCR and sequencing.
Whole genome sequencing (WGS) of strains was performed via 2×150b paired end sequencing (Nextera XT sample) preparation kit and Miseq, Illumina. The sequences of strains were independently assembled using SPAdes v3.6.1 (denovo assembly). *De novo* contigs were screened for plasmid origin by using Plasmid Finder (https://cge.cbs.dtu.dk//services/PlasmidFinder/). The identified plasmid specific contigs were used as reference template for reference mapping using CLC Genomics Workbench v7.5.1 (CLCbio, Denmark). Mapped reads were extracted and *de novo* assembly was performed, then contigs were annotated using online server BASys to understand the genetic context.

Results: *Bla*$_{NDM-1}$ was harbored in *K. pneumoniae* on IncF1B (pkpn-10197-BE) and IncFII (pkpn-169-KD) plasmids while the same for *A. baumannii* could not be defined indicating that the gene might be chromosomally integrated. *Bla*$_{NDM-1}$ harboring elements isolated from the *A.baumannii* strains from Iraq (pAb-75-8-1-KD) and India (pAb-Nab5-IN) were highly similar and in both strains, the gene was harbored along with ISAba125 (Figure a and b). However, in contrast to pAb-Nab5-IN, the ISAba125

in pAb-75-8-1-KD was truncated by IS15 and also co- harbored other resistance genes such as the cephalosporinase, *bla*$_{DHA-1}$ that showed a 73 amino-acid long C-terminal extension. The *bla*$_{NDM-1}$ plasmids in *K. pneumonaie* from Belgium (pkpn-10197-BE) and Iraq (pkpn-169-KD) also differed in the genes that were co-carried. Of note, the pkpn-169-KD harbored an intact shiga-toxin (Stx2)-encoding bacteriophage, the *rmtC* 16S rRNA methyltransferase as well as the *senB* gene and the *cjr* operon (Figure d). The shiga-toxin genes are a major virulence attribute of enterohemorrhagic (EHEC) *Escherichia coli*, while the *senB*-encoded enterotoxin and the *cjr* operon have been shown to be crucial during early pathogenesis and invasion of the urinary tract by uropathogenic (UPEC) *E. coli*.

Conclusions: We demonstrate here remarkable differences in the genes co-harbored along with *bla*$_{NDM-1}$ in *A. baumannii* and *K.pneumoniae* isolated from different geographic locations. However presence of major virulence factors of EHEC and UPEC *E.coli* on the *bla*$_{NDM-1}$ plasmid isolated from *K. pneumoniae* in Iraq might imply an enhanced virulence capacity of these multi-drug resistant strains and is of special concern.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