

### P-086 - THIRD GENERATION CEPHALOSPORIN-RESISTANT *KLEBSIELLA PNEUMONIAE*: DOES THE ORIGIN MATTER?

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#### Background

Third generation cephalosporins-resistant *Klebsiella pneumoniae* represent an important health-care associated infectious (HAI) agent, whose prevalence is increasing globally<sup>1</sup>. As many other HAI, *K. pneumoniae* end-up in urban wastewater treatment plants, often surviving the treatment process, being released to the environment. If these contaminants maintain the traits of clinical isolates was the question we aimed to answer in this study. With this aim, we obtained and characterized third generation cephalosporins-resistant *K. pneumoniae* isolates from clinical settings and from wastewater.

#### Method

A total of 52 isolates resistant to 3<sup>rd</sup> generation cephalosporins comprising 25 clinical isolates and 27 isolates from wastewater were selected for this study. Isolates were compared based on 1) antibiotic susceptibility to 5 classes of antibiotics ( $\beta$ -lactams, aminoglycosides, quinolones, sulfonamides and tetracyclines) by the disk diffusion method; 2) presence of genetic determinants potentially encoding extended-spectrum  $\beta$ -lactamases, carbapenemases or colistin resistance by PCR; and 3) the plasmids profile of each isolate based on PFGE.

#### Results & Conclusions

Multidrug resistance was observed in 74% (20/27) of the wastewater isolates and in 92% (23/25) of the clinical isolates. The genes *bla*<sub>SHV</sub>, *bla*<sub>CTX-M</sub>, *bla*<sub>TEM</sub>, *bla*<sub>OXA</sub> were highly prevalent in the clinical and wastewater cephalosporin resistant isolates - *bla*<sub>SHV</sub> 96 vs. 89%, *bla*<sub>CTX-M</sub> 76 vs. 81%, *bla*<sub>TEM</sub> 72 vs. 59% and *bla*<sub>OXA</sub> 40 vs. 44%. However, the gene *bla*<sub>KPC</sub> was detected only in clinical isolates (6%). The beta-lactam resistance genes *bla*<sub>VIM</sub> and *bla*<sub>IMP</sub> and the colistin resistance genes *mcr-1* and *mcr-2* were not detected. Curiously, in the wastewater isolates was observed a higher number of plasmids than in clinical isolates –22% vs. 44% of the isolates carried 1 plasmid, 48% vs. 36% carried 2 plasmids, and 26% vs. 16% carried 3 plasmids. Plasmids were not detected in 2% of the isolates and the presence of 4 was uncommon.

These results indicate that clinically relevant bacteria once released into the wastewater might retain clinical relevant traits, representing a threat for human health, either directly or indirectly through the spread of antibiotic resistance genes.

#### References & Acknowledgments

<sup>1</sup> Nordmann, P., Naas, T., Poirel, L., 2011. Global spread of Carbapenemase producing Enterobacteriaceae. Emerging Infectious Diseases 17(10):1791–1798.

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