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Paper Poster Session
Surveillance of carbapenemases: they will not stop!

Characterization of carbapenemase-producing Escherichia coli isolates from France between 2012-2013

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Background: Although less frequent than carbapenem-producing (CP) *Klebsiella pneumoniae*, the threat represented by CP-*Escherichia coli* (CP-Ec) is considered as even more serious. Indeed, whereas *K. pneumoniae* strains are mostly found in the hospital, *E. coli* is one of the most frequent cause of community- and hospital-acquired infections. There is therefore a significant risk of the dissemination of CP-*Ec* in the community, as it has occurred with the fluoroquinolone-resistant and ESBL-producing *Ec* ST131 clone. A global dissemination of CP-*Ec* clones would lead to considerable burden in terms of mortality and economical cost. Here we aimed to characterize the diversity of CP-*Ec* strains received at the French National Reference Centre (NRC) and to assess the risk of dissemination of specific clones.

Material/Methods: 140 CP-*Ec* were received at the NRC for carbapenemase-producing Enterobacteriaceae between 2012 and 2013. Antimicrobial susceptibility testing was performed according to Eucast guidelines. ß-lactamase genes were sought by PCR. Bacterial typing was performed by semi-automated REP-PCR and MLST.

Results: Most of the isolates came from the largest urban areas of France (Paris, Marseille, and Lille). OXA-48 was the most frequent carbapenemase isolated (78%) followed by NDM (18%). A link with a foreign country could be clearly evidenced in 37% of the cases (most often north African countries for OXA-48 and India for NDM), suggesting autochtonous dissemination for more then halve of the cases. 56% of the bacteria were from screening samples and 27% from urinary samples. 11 % of the bacteria were sent by community-serving microbiology laboratories.

Our study revealed a great genetic variability among CP-*Ec*. Nevertheless some clones seem to be more prevalent. An outbreak of *E. coli* ST-90 OXA-204(+) linked to a contaminated duodenoscope could be evidenced. 21 isolates of *E. coli* ST-38 harboring bla_{OXA-48} gene have been identified in several areas of France, suggesting importation into France from Turkey and subsequent dissemination. 5 isolates of E. coli ST-410 producing OXA-181 have been isolated from 5 patients with no epidemiological link. Several other ST-types have been isolated several times (ST-10, and ST-23).

Conclusions: MLST and REP-PCR typing of 130 isolates sent to the CPE-NRC in 2012 and 2013 revealed a broad diversity of strains with three over-represented lineages: ST10 expressing bla_{OXA-48}, ST410 expressing $bla_{OXA-181}$ gene or bla_{NDM-1} gene and ST23 expressing bla_{OXA-48} gene. The emergence of these variants, especially in the community, seem to be confirmed among CP-*Ec* isolated in 2014 and 2015, as suggested by preliminary whole genome sequencing results.