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Paper Poster Session V

Carbapenem resistance in Klebsiella

Interregional outbreak of NDM-producing *Klebsiella pneumoniae* ST11 in Poland in 2012-2014

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Objectives

The first case of NDM-positive organism in Poland was identified in 2011 in Warsaw, being *E. coli* ST410 from the Congo (Fiett et al. 2014). In the end of 2012, first isolates of NDM-producing *K. pneumoniae* of unknown origin were reported in a hospital in Poznan, and since then it has been spreading in the country. The aim of this work is to present dynamics of the outbreak and preliminary molecular characteristics of the outbreak isolates.

Methods

Bacterial isolates were collected together with basic clinical and epidemiological data owing to the national AMR surveillance programme. Species identification was confirmed with the VITEK 2 Compact system (bioMérieux). NDM production was detected phenotypically by the Carba NP test and EDTA DDST, and by PCR. Typing was performed by PFGE and MLST. ESBL co-production was assessed by DDST, followed by PCR and sequencing of $bla_{CTX\text{-}M\text{-}1}$-like genes. Plasmid profiling was performed by S1 nuclease analysis. Transfer of plasmids carrying bla_{NDM} and/or $bla_{CTX\text{-}M\text{-}1}$-like genes was performed by conjugation and electroporation assays.

Results

Following the four *K. pneumoniae* NDM cases in the late 2012, 106 cases were identified in Poland in 2013, and 180 cases by the end of September 2014. Most of the cases were hospitalized in areas of Poznan (159 cases in 10 medical institutions) and Warsaw (113 cases in 10 sites), following patient's transfer from Poznan. The outbreak has affected mainly three hospitals in Poznan and one in Warsaw, patients of which were transferred also to nine more distant cities. In two cases, *E. coli* NDM isolates were recovered after or together with *K. pneumoniae*. Fifty-four *K. pneumoniae* and two *E. coli* isolates from different centers were selected for molecular characterization. All *K. pneumoniae* were classified into a single but microheterogeneous PFGE type, split into 23 subtypes. All 16 selected isolates, representing different PFGE subtypes, were of the same sequence type ST11. *K. pneumoniae* isolates varied regarding ESBL expression with 40/54 ESBL-positive isolates, in all cases producing enzymes of the CTX-M-1 type. The isolates differed also by their S1 plasmidic profiles, having 1-4 plasmids of varying size. Twenty-one isolates were used in NDM transfer assays; conjugation worked only for nine isolates and always with low efficiency. Both transconjugants and transformants produced either only NDM or NDM plus the CTX-M-1-like ESBL.

Conclusions

After several years of KPC dissemination (currently stabilized), now epidemiology of carbapenemase producers in Poland is dominated by the dynamic clonal outbreak of *K. pneumoniae* ST11 NDM in two regions, which so far has been very difficult to contain despite active control measures. The preliminary molecular data demonstrate on-going diversification of the outbreak strain, observed in PFGE, plasmid and β-lactamase profiles. The situation is of the highest public health concern.