28th ECCMID EUROPEAN CONGRESS OF CLINICAL MICROBIOLOGY AND INFECTIOUS DISEASES
Madrid, Spain
21 – 24 April 2018

P1495 Countrywide dissemination of CTX-M-27-producing Escherichia coli ST131 subclade C1-M27 in Hungary, 2015-2017

Laura Jánvári[1], Ivelina Damjanova[1], Júlia Topf[1], Tünde Mag[1], Gyula Mestyán[2], Gizella Szolyka[3], Hilda Osztie[4], Akos Toth*[1]

[1]National Public Health Institute, Budapest, Hungary, *[2]University of Pécs Medical School, Pécs, Hungary*, *[3] Bajcsy-Zsilinszky Hospital and Clinic, Budapest, Hungary*, *[4]Synlab Hungary Ltd, Synlab Budapest Diagnostic Center, Microbiology Laboratory, Budapest, Hungary*

Background: Extended-spectrum β-lactamase (ESBL) producing *Escherichia coli* is one of the most significant multidrug-resistant nosocomial pathogens. Its global spread is associated with the C/H30 clade of the sequence type 131 (ST131) high risk clone. Of the C/H30 clade, the C1-M27 subclade with $bla_{CTX\text{-}M\text{-}27}$ was recently also discovered as an international clade, beside the worldwide disseminated C2/H30Rx clade with $bla_{CTX\text{-}M\text{-}15}$.

The aim of our study was to estimate the proportion of C1-M27 subclade among Hungarian invasive, ESBL-producing *E.coli* isolates submitted to the National Public Health Intsitute between January 2015-October 2017 and to investigate its virulome and resistome.

Materials/methods: CTX-M-1 group specific PCR assay was performed on 200 prescreened ESBL-positive, invasive *E.coli* isolates. Of these 83 isolates gave negative PCR result thus, PCR assay described by Matsumura et al. that can easily and rapidly detect major ST131 clades was performed. Whole-genome sequencing (WGS) of two selected isolates was performed by Illumina 251-bp paired-end sequencing. From WGS data acquired antimicrobial resistance and virulence genes were retrieved using ResFinder and VirulenceFinder online tools.

Results: In 2015 25% (13/52) and in 2016 32.9% (26/79) of the investigated invasive *E. coli* isolates belonged to the C1-M27 subclade, while in 2017 this proportion rose to 47.8% (33/69). Overall, the isolates were submitted from 24 health care institutes in 13 counties and from the Capital of Hungary. In 2015, they appeared in only 6 counties, while in 2017 this subclade disseminated almost the whole country. WGS revealed that the two isolates harboured identical virulence genes: *iha* (encoding adherence protein), *sat* (encoding secreted autotransporter toxin), *gad* (encoding glutamate decarboxylase), *iss* (encoding the increased serum survival factor) and *senB* (encoding the plasmid encoded enterotoxin), but they had different resistome (only $bla_{CTX\text{-}M\text{-}27}$ versus $bla_{CTX\text{-}M\text{-}27}$, *strA*, *strB*, *aadA5*, *sul1*, *sul2*, *dfrA17* and *tet*(A)). The *iss* and *senB* virulence genes could be associated to the higher invasiveness of this strain.

Conclusions: Our results highlight the fact that CTX-M-27-producing *E. coli* ST131 C1-M27 subclade have disseminated rapidly in our country. The increasing number of such isolates demonstrates the need of a continuous surveillance and forceful activities of infection control in Hungary.